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(54) Title: NOVEL GENETIC MARKERS FOR LEUKEMIAS

(57) Abstract: The present invention is related to methods for detecting leukemia cells by determing the expression profile of a group of markers. In particular, the type or subtype of leukemia cells in a sample is determined. Further, uses of the group of markers is discloses and compositions comprising these markers.

Novel Genetic Markers for Leukemias

The present invention is related to methods for detecting leukemia cells by determing the expression profile of a group of markers. In particular, the type or subtype of leukemia cells in a sample is determined. Further, uses of the group of markers are disclosed and compositions comprising these markers.

In the present specification, a number of documents is cited. The disclosure content of these documents including manufacturers' manuals, is herewith incorporated by reference. This holds particular true for the documents such as gene accession numbers cited in Tables 43a, b, 44 and 45 providing the complete nucleotide sequence of marker genes/cDNAs. In other terms, by reciting these documents, applicant intends to incorporate the complete nucleotide/amino acid sequence of those markers where only a partial sequence has been identified in the appended Tables. It is also intended to include the (poly)peptide sequences translated from these nucleotide sequences within the disclosure content of the present specification.

Today leukemias are classified into four different groups or types: acute myeloid (AML), acute lymphatic (ALL), chronic myeloid (CML) and chronic lymphatic leukemia (CLL). Within these groups, several subcategories can be identified further using a panel of standard techniques as described below. The incidence of leukemias is increasing with age and is 5/100.000/year in AML, 1/100.000/year in ALL, 1/100.000 in CML and 6/100.000/year in CLL. Several methods for classification have to be applied at diagnosis and before treatment starts: cytomorphology and cytochemistry, multiparameter –immunophenotyping, cytogenetics including fluorescence in situ hybridization, and molecular techniques such as polymerase chain reaction (PCR). So far only a combination of these techniques allows a precise diagnosis which is necessary to apply state of the art treatment. As the exact diagnosis is mandatory for example in CML the detection of a specific cytogenetic abnormality, the translocation (9;22) or its molecular counterpart, the BCR/ABL rearrangement is required to establish the diagnosis of CML. While all patients with CML show a BCR-ABL-rearrangement and are therefore homogenous with regard to the primary genetic abnormality, in AML and

ALL at least 10-15 different subgroups have been identified on the morphological, genetical or molecular level. Also in CLL several subgroups can be clearly separated. These different subcatgories in leukemias are associated with varying clinical outcome and therefore are the basis for different treatment strategies. The importance of highly specific classification may be illustrated in detail further for the AML as a very heterogeneous group of diseases.

Data from clinical trials showed that outcome of patients with AML differs in a broad range. Several parameters influencing prognosis have been identified. These can be assigned to different categories: patients' characteristics (i.e. age, comorbidity), therapy, and biology of the AML. Therefore, a lot of effort was invested to identify biological entities and to distinguish subgroups of AML which are associated with a favorable, intermediate or unfavorable prognosis, respectively. In order to allow a comparison between different studies a classification of AML was mandatory. In 1976 the FAB classification was proposed by the French-American-British co-operative group which was based on cytomorphology and cytochemistry in order to separate AML subgroups according to the morphological appearance of blasts in the blood and bone marrow. In addition, it was recognized that genetic abnormalities occurring in the leukemic blast had a major impact on the morphological picture and even more on the prognosis. So far, the karyotype of the leukemic blasts is the most important independent prognostic factor regarding response to therapy as well as survival. For clinical purposes karyotype analysis allows to discriminate between three major prognostic groups. A favorable outcome under currently used treatment regimens with cure rates from 50 % up to 858 was observed in several studies in patients with a) t (8;21) (q22; q22) occuring in AML M2, b) inv (16) (p13q22) occurring in; AML M4eo and c) t(15;17) (q22; qll-12) occurring in AML M3/H3v. In contrast, chromosome aberrations with an unfavorable clinical course are -5/del(5q), -7/de1(7q), inv(3)/t(3:31 and complex aberrant karyotypes with cure rates of only 10%. The remainder of AML patients are assigned to a prognostically intermediate group. This latter group is very heterogeneous because it includes patients with a normal karyotype as well as those with rare chromosome aberrations with yet unknown prognostic impact.

The sub-classification of leukemias becomes increasingly important to guide therapy. Thus, the development of new, specific treatment approaches requires the identification of specific subtypes that may benefit from a distinct therapeutic protocol. It has already been shown in two entities that the development of specific

drugs can improve outcome of distinct subsets of leukemia. One important example is the development of a new therapeutic drug (STI571) for the treatment of chronic myeloid leukemia (ML): this designed molecule inhibits the CML specific chimeric tyrosine kinase BCR-ABL generated from the genetic defect observed in CML, the BCR-ABL-rearrangement due to the translocation between chromosomes 3 and 22 (t(9;22) (q34; q11)). First data show that therapy response is dramatically higher in patients treated with this new drug as compared to all other drugs that had been used so far. Another example is the subtype of acute myeloid leukemia AML M3 and its variant M3v both with karyotype t[15;17)(q22; q11-12). The introduction of a new drug (all-trans retinoic acid - ATRA) has improved the outcome in this subgroup of patient from about 50% to 85 % long-term survivors; As it is mandatory for these patients suffering from these specific leukemia subtypes to be identified as fast as possible so that the best therapy can be applied, diagnostics today must accomplish sub-classification with maximal precision. Not only for these subtypes but also for several other leukemia subtypes different treatment approaches could improve outcome. Therefore, rapid and precise identification of distinct leukemia subtypes is the future goal for diagnostics.

So far a combination of methods is necessary to obtain the most important information in leukemia diagnostics: Analysis of the morphology and cytochemistry of bone marrow blasts and peripheral blood cells is necessary to establish the diagnosis. In some cases the addition of immunophenotyping is mandatory to separate very undifferentiated AML from acute lymphoblastic leukemia and CLL. Leukemia subtypes investigated can be diagnosed by cytomorphology alone, only if an expert reviews the smears. However, a genetic analysis based on chromosome analysis, fluorescence in situ hybridization or RT-PCR and immunophenotyping is required in order to assign all cases in to the right category. The aim of these techniques besides diagnosis is mainly to determine the prognosis of the leukemia. A major disadvantage of these methods, however, is that viable cells are necessary as the cells for genetic analysis have to divide in vitro in order to obtain metaphases for the analysis. Another problem is the long time of 72 hours from receipt of the material in the laboratory to obtain the result. Furthermore, great experience in preparation of chromosomes and even more in analyzing the karyotypes is required to obtain the correct result in at least 90% of cases. These experts in their field are necessary for all other techniques

mentioned above as well. Accordingly, standard diagnosis of leukemia uses a combination of complementary methods, is expensive, time-consuming, and requires experienced experts in the field. Methods that have to be combined are cytomorphology or histomorphology, multiparameter-immunophenotyping, cytogenetics, fluorescence in situ hybridization, and molecular genetics such as polymerase chain reaction based assays.

Using these techniques in combination, hematological malignancies in a first approach are separated into chronic myeloid leukemia (CML), chronic lymphoid (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within the latter three disease entities several prognostically relevant subtypes have been established. As a second approach this further subclassification is based mainly on genetic abnormalities of the leukemic blasts and clearly is associated with different prognoses. Therefore, this subclassification is increasingly important to guide therapy. Furthermore, the development of new, specific treatment approaches requires precise identification of leukemia subtypes.

In a first study Golub et al. (Science 1999) showed that gene expression profiles can be used for class prediction and discriminated AML from ALL samples. However, for his analysis of acute leukemias the selection of the two different subgroups was performed using exclusively morphologic-phenotypical criteria. This was only descriptive and does not provide deeper insights into the pathogenesis or the underlying biology of the leukemia. The approach reproduces only very basic knowledge of cytomorphology and intends to differentiate classes. The data is not sufficient to predict prognostically relevant cytogenetic aberrations.

Thus, the technical problem underlying the present invention was to provide means for leukemia diagnostics which overcome the disadvantages of the prior art diagnostic methods.

The solution to said technical problem is achieved by providing the embodiments characterized in the claims. Accordingly, the present invention relates to a method of determining whether a patient sample contains leukemia cells or other cells comprising the steps of a) determining the expression profile of a group of markers in a patient sample and b) concluding from the expression profile whether the

patient sample contains leukemia cells or other cells characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 3 to 6, tables 15 to 20, tables 29, 30, 41, or 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42. In a particular embodiment therof, the present invention pertains to a method wherein leukemia type and subtype are simultaneously determined whereby a microarray for the detection of the expression level of a marker or a group of markers is used.

It is important to note that in accordance with the invention in all pertaining embodiments any possible combination of markers, said markers being disclosed in the respective table or tables is encompassed within the scope of the invention.

As used herein, the term "expression" refers to the process by which mRNA or a polypeptide is produced based on the nucleic acid sequence of a gene. The process includes both transcription and translation, i.e. „expression" shall also include the formation of mRNA upon transcription.

In accordance with the present invention, the term „determining the expression profile" preferably refers to the determination of the level of expression, namely of said group of markers.

As used herein, the term „marker" refers to a DNA, in particular cDNA, or RNA or a fragment thereof or a protein or a fragment thereof which are in the case of RNA (or cDNA) formed upon transcription of a nucleotide sequence which is capable of expression. The nucleic acid molecule fragments refer to fragments preferably of at least 8 such as ten, twelfe, fifteen or eighteen nucleotides in length representing a consecutive stretch of nucleotides of a gene, cDNA or mRNA such as of 20 or 25 nucleotides that are, for example, further specified in the appended Tables or a complementary sequence thereto. In other terms, markers include any fragment (or complementary sequence thereto) of the sequences depicted in the appended tables as long as these fragments unambiguously identify the marker. Typical fragment lengths are provided above. The determination of the expression profile of markers may be effected at the transcriptional or translational level. In other terms, the method of the invention envisages the determination at the level of mRNA or at the protein level. Protein fragments such as peptides advantageously

comprise at least 6 consecutive amino acids representative of the corresponding full length protein. 6 amino acids are generally recognized as the lowest peptidic stretch giving rise to a linear epitope recognized by an antibody, fragment or derivative thereof. Alternatively, the proteins or fragments thereof may be analysed using nucleic acid molecules specifically binding to three-dimensional structures (aptamers). In principle, the investigator may determine, in accordance with the method of the invention, whether a gene is expressed at all in a leukemic or other cell. Alternatively, an investigator may determine the difference in the expression level, for example, between a leukemic and a non-leukemic cell or between two or more different types or subtypes of leukemia. If the sample comprises only other, i.e. non-leukemia cells, then the patient's suffering from a leukaemia may safely be denied. Insofar, the above main embodiment is to be understood that if the presence of other cells is determined then this determination includes an assessment to the effect that only other cells but no leukemic cells are comprised in the sample. On the other hand, the determination of leukemic cells may include the further characterization of such cells including the differentiation status of the cells as well as the distinction from other types of cancer cells or other subtypes of leukaemia cells. Particular embodiments in this regard are further outlined herein below.

In accordance with the above, the present invention also contemplates methods where simply the assessment of leukaemia cells but not necessarily of other cells is effected. This holds true for all embodiments where the determination of other cells is mentioned. It is to be understood that with the exception of the possible determination of other cells, the steps of the various methods of the invention remain unchanged. Thus, the invention also relates to a method of determining whether a patient sample contains leukemia cells comprising the steps of a) determining the the expression profile of a group of markers in a patient sample and b) concluding from expression profile whether the patient sample contains leukemia cells characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 3 to 6, tables 15 to 20, tables 29, 30, 41, or 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 3 to 6,

tables 15 to 20, and tables 29, 30, 41, or 42. Thus, the invention further relates to a method of determining whether a patient sample contains leukemia cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, comprising the steps of a) determining the expression profile of a group of markers in a patient sample and b) concluding from the expression profile whether the patient sample contains leukemia cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 16 to 20 or table 29 or 30 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 16 to 20 or table 29 or 30, to name two important embodiments of the invention.

Determination of the expression profile/levels may be effected by a variety of methods, depending on the nature of the marker. Thus, if the marker is mRNA, cDNA may be prepared into which a detectable label, such as a fluorescent, chemiluminescent, bioluminescent, radioactive (such as ^{3}H or ^{32}P) label is incorporated. Said detectably labelled cDNA, in single-stranded form, may then be hybridised, preferably under stringent or highly stringent conditions to a panel of single-stranded oligonucleotides representing different genes and affixed to a solid support such as a chip. Upon applying appropriate washing steps, those cDNAs will be detected or quantitatively detected that have a counterpart in the oligonucleotide panel. Various advantageous embodiments of this general method are feasible. For example, the mRNA or the cDNA may be amplified wherein it is, for quantitative assessments, preferable that the number of amplified copies corresponds relative to further amplified mRNAs or cDNAs to the number of mRNAs originally present in the cell. Also, the cDNAs may be transcribed into cRNAs wherein only in the transcription step a label is incorporated into the nucleic acid and wherein the cRNA is employed for hybridisation. Alternatively, the lable may be attached subsequent to the transcription step. Similarly, proteins from a cell or tissue under investigation may be contacted with a panel of aptamers or of antibodies or fragments or derivatives thereof. The antibodies etc. may be affixed to a solid support such as a chip. Binding of proteins indicative of a

leukemia or a subtype of leukaemia may be verified by binding to a detectably labelled secondary antibody or aptamer. For the labelling of antibodies, it is referred to Harlow and Lane, "Antibodies, a laboratory manual", CSH Press, 1988, Cold Spring Harbor. As regards further test assays and formats, it is referred to further embodiments of the invention as specified herein below as well as to the appended examples. In addition, a number of applicable assay formats are available in the art that can applied to the method of the invention without further ado. Specifically, a minimum set of proteins necessary for diagnosis of all leukemia types may be selected for creation of a protein array system to make diagnosis on a protein lysate of a diagnostic bone marrow sample directly. Protein Array Systems for the detection of specific protein expression profiles already are available (for example: Bio-Plex, BIORAD, München, Germany). For this application preferably antibodies against the proteins have to be produced and immobilized on a platform e.g. glasslides or microtiterplates. The immobilized antibodies can be labeled with a reactant specific for the certain target proteins as discussed above. The reactants can include enzyme substrates, DNA, receptors, antigens or antibodies to create for example a capture sandwich immunoassay.

The level of the expression of the „marker" is indicative of a leukemic condition, of a cell or an organism. The level of expression of a marker or group of markers is measured and is compared with the level of expression of the same marker or the same group of markers from other cells or samples. The comparison may be effected in an actual experiment or in silico. When the expression level also referred to as expression pattern or expression signature (expression profile) is measurably different, there is according to the invention a meaningful difference in the level of expression. Preferably the difference at least is 5 %, 10% or 20%, more preferred at least 50% or may even be as high as 75% or 100%. More preferred the difference in the level of expression is at least 200%, i.e. two fold, at least 500%, i.e. five fold, or at least 1000%, i.e. 10 fold.

The present invention allows to diagnose a wide variety and at least 14 different clinically relevant leukemia subtypes. Therefore, the invention of a combination of marker genes and their specific expression level it is possible to substitute all other mandatory diagnostic approaches including the approach of Golub and colleagues (cytomorphology or histomorphology, multiparameter-immunophenotyping,

cytogenetics, fluorescence in situ hybridization, and molecular genetics) in one single step with a specifity and sensitivity that had never been achieved in all other techniques used so far.

In more detail, based on biomathematical analysis of gene expression profiles a new method could be provided which forms the basis for designing and developing a novel diagnostic approach preferably based on microarray technology. Further, subsets of markers, preferably genes could be introduced which allow the determination of leukemia type and subtype. The method according to the invention abolishes today's standard procedures in diagnosis of leukemia. These standard diagnostic procedures require more and more centralized core facilities with both personal experts in the fields of cytomorphology, cytogenetics and molecular genetics and expensive lab equipment, which causes increasing costs for adequate diagnosis. The present invention provides novel cost-effective methods and diagnostic tools, which are less time consuming, easy to operate but nevertheless as accurate and safe as all standard methods combined today. The genes or sets of genes allows to assign clinical samples either as healthy or malignant simply based on their gene expression profiles. The genes, representative fragments thereof or transcription or translation products thereof form the basis for the methods of the invention or diagnostic tools, corresponding thereto. Furthermore, these genes etc. allow to predict the diagnoses based on the genetic abnormality of the expression pattern and to discriminate between different prognostic relevant entities. When comparing two groups of microarray experiments, Golub's method (Science 286 (1999), 531-537) sorts the genes with respect to the signal-to-noise ratio of gene x: $S_x = (\mu_1-\mu_2)/(\sigma_1+\sigma_2)$, where μ_k and σ_k denote the mean expression and standard deviation of gene x in group k.

According to a specified number of "informative" genes the 20 best discriminating genes are selected. For each informative gene a decision limit is calculated as $b_x = (\mu_1+\mu_2)/2$. To classify a new sample of an independent test set, the gene expression levels of informative genes are taken and for each gene x and sample y a so-called vote is calculated as $V_x = S_x (g_x^y - b_x)$, where g_x^y denotes expression level of gene x in sample y. The votes of all informative genes are summed up ("weighted voting") and depending upon the sign of this sum the new sample is

classified as group 1 or group 2. The *confidence* in the prediction is calculated as $|\Sigma V_x / \Sigma |V_x| |$.

To assess the significance of each gene, a permutation test is performed, which determines signal-to-noise ratios when class labels are permuted randomly. To assess the robustness of the classifier, a leave-one-out crossvalidation is performed. *Accuracy* is the rate of correctly classified test samples.

The decision limit proposed by Golub does not provide optimal classification accuracy in all situations. When the standard deviation of expression levels within the two groups are very different, the decision limit is biased towards the group with the higher standard deviation.

A decision limit for a particular gene can be considered optimal, if it achieves maximum classification accuracy for a given dataset. By determining systematically classification accuracies for a set of possible decision limits, an optimal decision limit can be calculated. The underlying statistics as described in Example 3 select an optimal decision limit from the following set of decision limits L_x:

$$L_x = \{ (g_x^y + g_x^{y-1})/2 \mid 1 < y <= n \}$$

where g_x^y denotes expression level of gene x in sample y, n denotes the total number of samples in the training set.

Golubs method selects an arbitrary number of "informative" genes to discriminate between two classes of samples according to their signal-to-noise ratio, typically in the range of 10 to 50 genes.

Choosing too many genes like in Golub's method carries the risk of overfitting, which causes poor generalization features of the model.

Therefore the present invention applies an heuristic approach to select a minimal set of discriminative genes, which provides maximum classification accuracy in

leave-one-out-crossvalidation. I.e. for a given set of genes weighted voting as described by Golub is applied and the classification accuracy is calculated by crossvalidation used in accordance with the present invention and representing a further embodiment in accordance with this invention.

The method for achieving this used in accordance with the present invention and representing a further embodiment in accordance with this invention consists of the following steps:

(a) calculating of the top 20 discriminating genes according to the signal-to-noise ratio (top 20 SNR's);

(b) calculating classification accuracy and confidence based on optimal decision limits for each of the top 20 genes;

(c) selecting the gene which provides best classification accuracy and confidence out of step 2; and

(d) testing for each of the remaining 19 genes, whether adding this gene to the model improves accuracy and confidence.

If the gene improves accuracy and confidence, it is added to the weighted voting model, otherwise it is discarded.

Preferably, the decision limit is set according to the formula recited above.

In a pilot study consisting of 103 Affymetrix Genechip microarrays with 12625 genes each as shown in the appended examples we compared the results achieved with Golub's method and with our extended method.

Table A presents an analysis of 18 samples class A versus 85 samples class non-A. Based on 20 informative genes Golub's method results in a crossvalidation accuracy of 0,87 (confidence 0,77); achieves with three genes out of the top 20 set a crossvalidation accuracy of 0,96 (confidence 0,88).

The same analysis was performed for one versus all (OVA) and all pairs (AP) comparisons in this dataset consisting of 5 different classes. Figure 13 b presents accuracy and confidence obtained by both methods: the method of the invention outperforms Golub's method clearly both in terms of accuracy and confidence of classifications.

The development of a leukemia diagnostic tool, preferably microarray based, allows for all patients which are preferably humans and specimens a reproducible, highly specific and rapid method to obtain important information for treatment strategies in leukemia. This technique can be established in every laboratory using basic methods of molecular biology, and preferably makes use of hybridization and amplification such as PCR or LCR based techniques and does not require hematologists or cytogeneticists with several years of experience in leukemia diagnostics. Material for the analysis can be sent over large distances as it is not necessary that cells arrive viable in the laboratory. Therefore, a centralization of leukemia diagnostics with very high quality is possible.

Moreover, the accumulation of an immense knowledge about gene expression profiles in leukemia types and subtypes, which are not characterized by specific genetic abnormalities, leads to a more precise classification compared to all other methods used so far. In addition, the data compiled in accordance with the invention are helpful for the understanding of the pathogenesis of leukemia and will allow to identify genes which are specifically dysregulated. They may be considered as potential targets for therapeutic interventions specifically designed for the different leukemia subtypes.

Preferably the method according to the invention is characterized in that the group of markers consists of between two, such as three, four, five, six, seven, eight, nine or ten and the total number of markers listed in one or more of the tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42. Most preferred, the group consists of all markers listed in one or more tables, whereby the tables are selected from the the tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42. The invention also contemplates that all markers in all tables are analysed. This holds true for the presently discussed as well as for embodiments discussed further below.

Another embodiment of the invention relates to a method of determining whether a patient sample contains leukemia cells or other cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, comprising the steps of determining the expression profile, preferably the level of expression of a group of markers in a patient sample and concluding from the (altered) expression profile i.e. the difference in the level of expression, whether the patient sample contains leukemia cells or other cells and at the same time determining the type and subtype of leukemia cells, if leukemia cells are present, characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 16 to 20 or table 29 or 30 and whereby the number of markers in the group is between one, preferably two such as three, four, five, six, seven, eight, nine or ten and the total number of markers listed in one or more of the tables 16 to 20 or table 29 or 30. It is preferred that the group of markers consists of all markers listed in one or more tables, whereby the tables are selected from the tables 16 to 20 or table 29 or 30. In a preferred embodiment it is differentiated between four types of leukemia cells and the other cells in the patient sample. The other cells are preferably normal cells.

The "other cells" may be, for example, cells affected by a disease which is not a leukaemia. It is preferred, in accordance with the present invention that said other cells are normal cells, i.e. cells not affected by any disease.

This embodiment of the present invention allows for the differentiation between four different types of leukemias, i.e. AML, CLL, CML and ALL. As has been surprisingly demonstrated in accordance with the present invention, the qualitative and/or quantitative determination of an expression profile of a number of genes allows the unambiguous classing with any of the above and currently established types of leukemias. In principle and more preferred, the relation of the gene expression profile to the leukaemia type may take place at the same time at which the determination of the leukaemia cells in the sample takes place. Alternatively, the classification may be effected at a later time point. It was surprising that the distinction between the large number of leukemia types and subtypes, including the cytogenetically and immunophenotypically defined, as well as types

characterized by complex chromosomal aberations, could be accomplished preferably by the use of a microarray for the detection of the expression level of a marker or a group of markers with such ease and accuracy. In particular, certain preferred subsets of genes are provided which can either be used to determine the leukemia type and subtype, or only determine the subtypes of a certain leukemia type or differentiates certain types or subtypes, respectively, from one another.

In another embodiment a method is disclosed which allows differentiating between two types of leukemia cells or one type of leukemia cells and normal cells or non-leukemia cells in a patient sample comprising the steps of determining the expression profile preferably the level of expression, of a group of markers in the patient sample and concluding from the (altered) expression profile, i.e. the difference in the level of expression, which type of leukemia cells the patient sample contains or whether it contains (only) normal cells or non-leukemia cells characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 3 to 6 or tables 7 to 12 and whereby the number of markers in the group is between one, preferably two such as three, four, five, six, seven, eight, nine or ten and the total number of markers listed in one or more of the tables 3 to 6 or tables 7 to 12. In a preferred embodiment the group of markers consists of all markers listed in one or more of the tables 3 to 6 or tables 7 to 12.

In another embodiment of the invention a method is disclosed allowing the differentiation between the subtypes of AML cells or between the subtypes of AML cells and normal cells in a patient sample comprising the steps of determining the expression profile, preferably the level of expression of a group of markers in the patient sample and concluding from the the (altered) expression profile, i.e. the difference in the level of expression, which subtypes of AML cells the patient sample contains or whether it contains normal cells characterized In that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36 and whereby the number of markers in the group is between one, preferably two such as three, four, five, six, seven, eight, nine or ten and the total number of markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36. In a preferred

embodiment the group of markers consists of all markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36. It is preferred that three, four or more subtypes of AML cells are determined.

In another embodiment of the invention a method is disclosed allowing the differentiation between and thus the determination of the subtypes of ALL cells in a patient sample comprising the steps of (a) determining the level of expression of a group of markers in the patient sample and (b) concluding from the differences in the level of expression which subtypes of ALL cells the patient sample contains whereby the group of markers consists of markers selected independently from the markers listed in one or more of the tables 18, 32 or 33 and whereby the number of markers in the group is between one, preferably two such as three, four, five, six, seven, eight, nine or ten and the total number of markers listed in one or more of the tables 18, 32 or 33. It is preferred that the group of markers consists of all markers listed in one or more of the tables 18, 32 or 33.

In another embodiment of the invention a method is disclosed allowing the differentiation between and thus the determination of the subtypes of CLL cells in a patient sample comprising the steps of determining the level of expression of a group of markers in the patient sample and concluding from the differences in the level of expression which subtypes of CLL cells the patient sample contains whereby the group of markers consists of markers selected independently from the markers listed in one or more of the tables 38 or 39 and whereby the number of markers in the group is between one, preferably two such as three, four, five, six, seven, eight, nine or ten and the total number of markers listed in one or more of the tables 38 or 39. It is preferred that the group of markers consists of all markers listed in one or more of the tables 38 or 39.

In another embodiment of the invention, a method is disclosed of assessing the efficacy of a test compound for inhibiting leukemia, the method comprising comparing the expression profile of a group of markers in a first sample obtained from the patient and maintained in the presence of the test compound and the expression profile of a group of markers in a second sample obtained from the

patient and maintained in the absence of the test compound, wherein a significantly altered expression profile of the group of markers in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting leukemia in the patient characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two such as 3, 4, 5, 6, 7, 8, 9 or 10 and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

In accordance with this embodiment of the present invention, it is again preferred that in the comparison of expression profiles expression levels and differences in expression levels are determined and compared. It is further preferred that the alteration determined in accordance with the method of the invention in the expression profile or expression level must be in the direction of the expression profile of normal cells or at least diseased but non-leukemic cells. More preferably the alteration should be in the direction of normal blood cells, more preferably cells of the certain type. Accordingly, it is also preferred that the comparison includes an internal standard of expression levels of analysed markers wherein the internal standard represents the expression profile of non-leukemic and preferably normal cells. The comparison may be effected by relying on actual experimental data or on in silico obtained reference data.

In another embodiment of the invention a method is disclosed of assessing the efficacy of a therapy for inhibiting leukemia in a patient, the method comprising comparing the expression profile, preferably the level of expression of a group of markers in the first sample obtained from the patient prior to providing at least a portion of the therapy to the patient and the expression profile, preferably the level of expression of a group of markers in a second sample obtained from the patient following provision of the portion of the therapy, wherein a significantly (altered) expression profile, i.e. a significantly (altered) difference in the level of expression of the group of markers in the second sample, relative to the first sample, is an

indication that the therapy is efficacious for inhibiting leukemia in the patient characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two such as 3, 4, 5, 6, 7, 8, 9 or 10 and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, or 42.

As with the previous embodiment, the alteration determined in accordance with the method of the invention in the expression profile or expression level must be in the direction of the expression profile or normal cells or at least diseased but non-leukemic cells. Accordingly, it is also preferred in accordance with this embodiment that the comparison includes an internal standarad of expression levels of analysed markers wherein the internal standarad represents the expression profile of non-leukemic and preferably normal cells. The comparison may – again – be effected by relying on actual experimental data or on in silico obtained reference data.

Within the therapy of the patient, compounds may be administered that have at least passed phase II and preferably are whithin phase III of clinical trials. Advantageously, in one embodiment, a therapeutical composition or medicinal product is administered that comprises one pharmaceutically active compound. In alternative embodiments, pharmaceutical compositions or medicinal products are administered that comprise more than one pharmaceutically active compound. If the composition or product comprises more than at least one pharmaceutically active compound then one of the compounds may aim at the direct reduction of tumor load wherein at least one further compound may fulfil an accessory function such as the general stimulation of the immune system. Compounds of the latter class are also well known in the art and comprise plant derived products as well as immunostimulatory molecules selected from the group of interleukins, interferons and others.

Additionally, the invention contemplates a method of refining a compound identified by the method as described herein above, said method comprising optionally the steps of said methods and:

(1) identification of the binding sites of the compound and the target molecule by site-directed mutagenesis or chimeric protein studies;

(2) molecular modeling of both the binding site of the compound and the binding site of the target molecule; and

(3) modification of the compound to improve its binding specificity for the target.

The target may in accordance with the above be DNA, mRNA or protein. All techniques employed in the various steps of the method of the invention are conventional or can be derived by the person skilled in the art from conventional techniques without further ado. Thus, biological assays based on the herein identified nature of the proteins/(poly)peptides may be employed to assess the specificity or potency of the drugs wherein the increase of one or more activities of the proteins/(poly)peptides may be used to monitor said specificity or potency. Steps (1) and (2) can be carried out according to conventional protocols. A protocol for site directed mutagenesis is described in Ling MM, Robinson BH. (1997) Anal. Biochem. 254: 157-178. The use of homology modeling in conjunction with site-directed mutagenesis for analysis of structure-function relationships is reviewed in Szklarz and Halpert (1997) Life Sci. 61:2507-2520. Chimeric proteins are generated by ligation of the corresponding DNA fragments via a unique restriction site using the conventional cloning techniques described in Sambrook (1989), loc. cit.. A fusion of two DNA fragments that results in a chimeric DNA fragment encoding a chimeric protein can also be generated using the gateway-system (Life technologies), a system that is based on DNA fusion by recombination. A prominent example of molecular modeling is the structure-based design of compounds binding to HIV reverse transcriptase that is reviewed in Mao, Sudbeck, Venkatachalam and Uckun (2000). Biochem. Pharmacol. 60: 1251-1265.

For example, identification of the binding site of said drug by site-directed mutagenesis and chimerical protein studies can be achieved by modifications in the (poly)peptide primary sequence that affect the drug affinity; this usually allows to precisely map the binding pocket for the drug.

As regards step (2), the following protocols may be envisaged: Once the effector site for drugs has been mapped, the precise residues interacting with different parts of the drug can be identified by combination of the information obtained from mutagenesis studies (step (1)) and computer simulations of the structure of the binding site provided that the precise three-dimensional structure of the drug is known (if not, it can be predicted by computational simulation). If said drug is itself a peptide, it can be also mutated to determine which residues interact with other residues in the (poly)peptide of interest.

Finally, in step (3) the drug can be modified to improve its binding affinity or ist potency and specificity. If, for instance, there are electrostatic interactions between a particular residue of the (poly)peptide of interest and some region of the drug molecule, the overall charge in that region can be modified to increase that particular interaction.

Identification of binding sites may be assisted by computer programs. Thus, appropriate computer programs can be used for the identification of interactive sites of a putative inhibitor and the (poly)peptide by computer assisted searches for complementary structural motifs (Fassina, Immunomethods 5 (1994), 114-120). Further appropriate computer systems for the computer aided design of protein and peptides are described in the prior art, for example, in Berry, Biochem. Soc. Trans. 22 (1994), 1033-1036; Wodak, Ann. N. Y. Acad. Sci. 501 (1987), 1-13; Pabo, Biochemistry 25 (1986), 5987-5991. Modifications of the drug can be produced, for example, by peptidomimetics and other inhibitors can also be identified by the synthesis of peptidomimetic combinatorial libraries through successive chemical modification and testing the resulting compounds. Methods for the generation and use of peptidomimetic combinatorial libraries are described in the prior art, for example in Ostresh, Methods in Enzymology 267 (1996), 220-234 and Dorner, Bioorg. Med. Chem. 4 (1996), 709-715. Furthermore, the three-dimensional and/or crystallographic structure of activators of the expression of the (poly)peptide of the invention can be used for the design of peptidomimetic

activators, e.g., in combination with the (poly)peptide of the invention (Rose, Biochemistry 35 (1996), 12933-12944; Rutenber, Bioorg. Med. Chem. 4 (1996), 1545-1558).

In accordance with the above, in a preferred embodiment of the method of the invention said at least one compound is further refined by peptidomimetics.

The invention furthermore relates to a method of modifying a compound identified or refined by the method as described herein above as a lead compound to achieve (i) modified site of action, spectrum of activity, organ specificity, and/or (ii) improved potency, and/or (iii) decreased toxicity (improved therapeutic index), and/or (iv) decreased side effects, and/or (v) modified onset of therapeutic action, duration of effect, and/or (vi) modified pharmakinetic parameters (resorption, distribution, metabolism and excretion), and/or (vii) modified physico-chemical parameters (solubility, hygroscopicity, color, taste, odor, stability, state), and/or (viii) improved general specificity, organ/tissue specificity, and/or (ix) optimized application form and route by (i) esterification of carboxyl groups, or (ii) esterification of hydroxyl groups with carbon acids, or (iii) esterification of hydroxyl groups to, e.g. phosphates, pyrophosphates or sulfates or hemi succinates, or (iv) formation of pharmaceutically acceptable salts, or (v) formation of pharmaceutically acceptable complexes, or (vi) synthesis of pharmacologically active polymers, or (vii) introduction of hydrophylic moieties, or (viii) introduction/exchange of substituents on aromates or side chains, change of substituent pattern, or (ix) modification by introduction of isosteric or bioisosteric moieties, or

(x) synthesis of homologous compounds, or (xi) introduction of branched side chains, or (xii) conversion of alkyl substituents to cyclic analogues, or (xiii) derivatisation of hydroxyl group to ketales, acetales, or (xiv) N-acetylation to amides, phenylcarbamates, or (xv) synthesis of Mannich bases, imines, or (xvi) transformation of ketones or aldehydes to Schiff's bases, oximes, acetales, ketales, enolesters, oxazolidines, thiozolidinesor combinations thereof; said method optionally further comprising the steps of the above described methods.

The various steps recited above are generally known in the art. They include or rely on quantitative structure-action relationship (QSAR) analyses (Kubinyi, "Hausch-Analysis and Related Approaches", VCH Verlag, Weinheim, 1992), combinatorial biochemistry, classical chemistry and others (see, for example, Holzgrabe and Bechtold, Deutsche Apotheker Zeitung 140(8), 813-823, 2000).

The invention moreover relates to a method of producing a pharmaceutical composition comprising optionally the steps of the aforementioned methods and further the step of formulating the at least one compound identified, refined or modified by the method of any of the preceding embodiments with a pharmaceutically active carrier or diluent.

The pharmaceutical composition produced in accordance with the present invention may further comprise a pharmaceutically acceptable carrier and/or diluent and/or excipient. Examples of suitable pharmaceutical carriers are well known in the art and include phosphate buffered saline solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions etc. Compositions comprising such carriers can be formulated by well known conventional methods. These pharmaceutical compositions can be administered to the subject at a suitable dose. Administration of the suitable compositions may be effected by different ways, e.g., by intravenous, intraperitoneal, subcutaneous, intramuscular, topical, intradermal, intranasal or intrabronchial administration. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. A typical dose can be, for example, in the range of 0.001 to 1000 μg (or of nucleic acid for expression or for inhibition of expression in this range); however, doses below or above this exemplary range are envisioned, especially considering the aforementioned factors. Generally, the regimen as a regular administration of the pharmaceutical composition should be in the range of 1 μg to 10 mg units per day. If the regimen is a continuous infusion, it should also

be in the range of 1 μg to 10 mg units per kilogram of body weight per minute, respectively. Progress can be monitored by periodic assessment. Dosages will vary but a preferred dosage for intravenous administration of DNA is from approximately 10^6 to 10^{12} copies of the DNA molecule. The compositions of the invention may be administered locally or systemically. Administration will generally be parenterally, e.g., intravenously; DNA may also be administered directly to the target site, e.g., by biolistic delivery to an internal or external target site or by catheter to a site in an artery. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, and inert gases and the like. Furthermore, the pharmaceutical composition of the invention may comprise further agents such as interleukins or interferons depending on the exact intended use of the pharmaceutical composition.

The above methods referring to downstream developments also apply to therapeutically effective compounds referred to in additional embodiments herein below.

In another embodiment of the invention a method is disclosed of selecting a composition for inhibiting leukemia in a patient, the method comprising separately maintaining aliquots of cells of a patient sample in the presence of a plurality of test compositions, comparing the expression profile, preferably the level of expression of a group of markers in each of the aliquots, and selecting one of the test compositions which induces an altered expression profile of the group of markers in the aliquot containing that test composition, relative to other test compositions characterized In that the group of markers consists of markers

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selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two such as 3, 4, 5, 6, 7, 8, 9 or 10 and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

Again, as with the previously recited embodiments, the alteration determined in accordance with the method of the invention in the expression profile or expression level must be in the direction of the expression profile of normal cells or at least diseased but non-leukemic cells. Accordingly, it is also preferred in accordance with this embodiment that the comparison includes an internal standarad of expression levels of analysed markers wherein the internal standarad represents the expression profile of non-leukemic and preferably normal cells. The comparison may – again – be effected by relying on actual experimental data or on in silico obtained reference data.

The expression "in the direction of the expression profile of normal cells" as used herein preferably relates to cells that comprise blood cells, more preferably a single type of blood cells. Most preferably, the single type of cells corresponds to the type of the leukemic cell. For example, an AML type of leukemic cell would preferably be compared to a healthy myeloic blast cell whereas a ALL type of leukemic cell would preferably be compared to a healthy lymphatic blast cell. Myeloic blast cells and lymphatic blast cells may be isolated from healthy bone marrow using well known methods, such as cell sorting based on flow cytometry using established cell surface markers.

In this method of the invention, it is preferred that the test composition comprises only one putatively active test compound. Insofar, the correlation with the activity of the test compound and the readout is particularly convenient. If the test composition comprises more than one putatively pharmaceutically active compounds, it may be considered to separately test each compound in a composition that has tested positive in a first round of the assay. Consequently, in a second round, i.e. in a repetition of steps (a) and (b), the various compositions

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tested positive, if any, in the first round, may be subdivided into single compounds and these single compounds tested again for their efficacy. The goal of such an approach, of course, is to obtain a composition comprising a single active compound only.

In another embodiment a method of determining new subtypes of leukemia cells is diclosed, the method comprising determining. the expression profile, preferably the level of expression of a group of markers of leukemia cells of unknown subtype, comparing the expression profile to the level of expression, ie. the expression profile, of a group of markers of leukemia cells of known subtype, thereby concluding that a new subtype is determined when the expression profile, preferably the level of expression is different to all known subtypes characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

The term "subtype of leukemia cells" in accordance with the present invention may be better understood in accordance with the following Leukemias are subdivided according to their natural clinical course into acute and chronic leukemias. Based on the cell line they are derived from they are further subdivided into myeloid and lymphatc leukemias. This results in four leukemia types, i.e. acute myeloid leukemia (AML), acute lymphoblastic leukemia (ALL), chronic myeloid leukemia (CML), and chronic lymphatic leukemia (CLL). Based on genetic, phenotypic, and biological characteristic, which are assessed by cytomorphology, cytochemistry, cytogenetics, immunophenotyping, and molecular genetics, AML, ALL, and CLL are further subdivided into subtypes. These subtypes are associated with highly differing prognoses. Treatment approaches specific for these subtypes are applied and are being further optimized. Thus, an exact diagnosis based on a reliable and reproducible method is essential for the selection of the appropriate subtype-specific treatment.

The new subtypes identified in accordance with the invention may then be subjected in the same or in further patients to the other methods/embodiments of the invention.

In another embodiment a method is disclosed for guiding the therapy of leukemia in a patient depending on the leukemia subtype and/or the risk of relapse of disease, the method comprising determining the expression profile, preferably the level of expression of a group of markers in the patient sample, and deciding about the therapy strategy depending on the leukemia subtype or the risk of relapse of disease characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two such as 3, 4, 5, 6, 7, 8,.9 or 10 and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

This embodiment is particularly important for the quick and reliable recovery of the patient from the leukemia that effects him or her. As has been stated above, the early and reliable diagnosis of the leukaemia type or subtype is particularly important for the instigation of a useful and straightforward treatment regimen. An incorrect diagnosis may result in the application of a wrong treatment regimen which, in turn, may lead to significant health risks including premature death of the patient. In accordance with the present invention, a reliable means has been provided that, based on the inventive selection of markers provided, will overcome the prior art problems of an insecure or an inappropriate time frame demanding diagnosis. In particular, the present method of the invention provides in step (a) an unambiguous and safe basis for the decision step (b). Again, the patient may safely rely on the conclusion drawn in step (b) due to the strong inherent correlation that has been achieved between the selection of markers and the leukemia subtype. The relation of tables to leukemia subtypes has also been demonstrated elsewhere in this specification.

In another embodiment of the invention, a method for monitoring the progression of leukemia in a patient is disclosed, the method comprising determining the the expression profile, preferably the level of expression of a group of markers in a patient sample at a first point in time, and repeating this step at a subsequent point in time; and comparing the expression profile, preferably the level of expression detected in the previous steps and therefrom monitoring the progression of leukemia in the patient, characterized In that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two such as 3, 4, 5, 6, 7, 8,.9 or 10 and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. In a preferred embodiment, the patient has undergone chemotherapy between the first point in time and the subsequent point in time (including repetitions of step (b).

In this embodiment of the present invention, the skilled artisan may repeat step (b) one or more times in order to collect additional data from different (more) time points. The additional data obtained by such further measurements may provide an overall better overview on the progress of the disease.

In accordance with this embodiment of the disease, the term "progression of leukemia" includes the interpretation of "regression of leukemia", i.e. includes the interpretation of a negative progression. This is of course in line with the aim of the therapy and the desire of the patient.

In the methods according to the invention it is preferred that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two and the total number of markers listed in the at least one of tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. In a preferred embodiment, the number of markers in the group is between five, more preferably between 7, 10 or 15 and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. It is feasible that the

group of markers not only consists of those markers but also comprises them as the data will then be still statistically significant, i.e. the preferred groups may additionally contain 10, 50 or 100 other markers and comprise the other markers according to the invention and mentioned above. It is, however, also feasible for the expert skilled in the art that only a single suitable marker is determined with the methods according to the invention.

Particulary preferred markers used in a method where only one or a few as e.g. one, preferably two markers are used are described in Table 22 and Example 3, Fig. 12 or the markers marked with an asterisk in table 20 and shown in tables 16 to 19 as the preferred set of markers. In detail, example 3 mentions (see example 3 for more details) the following markers including their expression level:

- *ADCY3*
- adenosine deaminase (*ADA*)
- *ARGHGAP4*
- B-cell specific coactivator of octamer binding transcription factors
- *CAPN3* is a member of the papain superfamily and was higher expressed in CML
- *CBFß-MYH11*
- *CD24*
- *CD27*, was identified to assign samples either ALL or CLL
- *CD74* plays a critical role in MHC class II antigen processing
- connective tissue growth factor (*CTGF*)
- *CTGF*
- *CTSW*
- *MYH11*
- glucocorticoid receptor beta
- higher expression of *CBFA2T1* (formerly *ETO*)
- *HLA-DMB*
- *HOXA9*
- *HOXB5*
- *IRF4*, an immune system-restricted interferon regulatory factor
- *KIAA1013*

- *LCN2* that shown to be a modulator of inflammation
- *LEF-1* was absent in myeloid leukemias but highly expressed in lymphoid leukemias
- *MBNL*
- *MSF* translocation partner of the mixed-lineage leukemia gene (MLL) in AML
- *NCOA1* expressed higher in CLL as compared to ALL
- *OS-9*differentially expressed between AML and ALL (14)
- Phospholipidscramblase 1 (*PLSCR1*) to be lower expressed in AML and ALL as compared to normal BM
- *POU2AF1*
- *POU2F2*
- *POU4F1*
- *SCYA3*
- *SGP28*
- *SOCS-2*
- *TRB and CD3D*

Particulary preferred markers used in a method where only one or a few as e.g. one, preferably two markers are used are described in tables 30, 33, 36 and 42 and Example 7, Figures 189 to 234, 254 to 272, 338 to 371, 433 to 465, respectively, or the markers marked with an asterisk in tables 29, 32, 35, 38, and 41 and Figures 24 to 188, 235 to 253, 273 to 337, 372 to 405, 406 to 432, respectively as the preferred set of markers. In detail, example 7 mentions (see example 7 for more details) the following markers including their expression level:

geneID	gene symbol	feature
201162_at	IGFBP7	CLL low
201163_s_at	IGFBP7	CLL low
201362_at	NS1-BP	CML high

201496_x_at	MYH11	AML inv(16) high
201497_x_at	MYH11	AML inv(16) high
201998_at	SIAT1	CLL high
202095_s_at	BIRC5	CLL low
203074_at	ANXA8	AML t(15;17) high
204150_at	STAB1	AML t(15;17) high
204511_at	KIAA0793	CLL high
205528_s_at	CBFA2T1	AML t(8;21) high
205529_s_at	CBFA2T1	AML t(8;21) high
205805_s_at	ROR1	CLL high
206940_s_at	POU4F1	AML t(8;21) high
207819_s_at	ABCB4	CLL high
208091_s_at	DKFZP564K0822	CLL high
208456_s_at	RRAS2	CLL high
209061_at	NCOA3	CLL high
209101_at	CTGF	ALL t(4;11) high, ALL Ph high, T-ALL high
209374_s_at	IGHM	CLL high
209616_s_at	CES1	AML MLL high

210997_at	HGF	AML t(15;17) high
212285_s_at	AGRN	AML t(15;17) high
213539_at	CD3D	T-ALL high
214450_at	CTSW	AML t(15;17) high
215925_s_at		ALL t(4;11) high
218223_s_at	LOC51177	CML low
222166_at		AML +8 high
224520_s_at	MGC13168	ALL t(8;14) high
224794_s_at	LOC51148	AML t(15;17) high
225660_at	SEMA6A	ALL B not Ph high, ALL Ph high
226496_at	Homo sapiens, Similar to hypothetical protein FLJ22611, clone MGC:24716 IMAGE:4277726, mRNA, complete cds	ALL high, CLL high
228827_at	Homo sapiens clone 25023 mRNA sequence	AML t(8;21) high

228904_at	ESTs	AML normal high, AML +8 high, AML complex high
236301_at	Homo sapiens, clone IMAGE:3866403, mRNA	CLL high
236892_s_at	HOXB6	AML normal high, AML +8 high, AML complex high
239214_at	ESTs	ALL t(4;11) high
239393_at	ESTs	ALL t(4;11) high
239791_at	HOXB6	AML normal high, AML +8 high
240581_at	ESTs	ALL t(4;11) high
241464_s_at	ESTs	AML MLL high, AML normal high, AML +8 high, AML complex high
241525_at	ESTs	AML inv(16) high
243362_s_at	LEF1	ALL high, CLL high
36566_at	CTNS	T-ALL low
38487_at	FLJ12442	AML t(15;17) high
201105_at	LGALS1	ALL t(4;11) high

204044_at	QPRT	ALL t(4;11) high
205899_at	CCNA1	ALL t(4;11) high
209168_at	GPM6B	ALL t(4;11) high
213539_at	CD3D	T-ALL high
213894_at	KIAA0960	ALL t(4;11) high
215925_s_at		ALL t(4;11) high
218224_at	PNMA1	T-ALL high
219463_at	C20orf103	ALL t(4;11) high
219631_at	FLJ12929	T-ALL high
225563_at	ESTs	ALL t(4;11) high
225592_at	NRM	ALL t(4;11) high
228083_at	Homo sapiens mRNA; cDNA DKFZp434I1216 (from clone DKFZp434I1216)	ALL t(4;11) high
228988_at	ZNF6	T-ALL high
235749_at		ALL t(8;14) high
242414_at	ESTs	ALL t(4;11) high
243756_at	ESTs	ALL t(4;11) high

201497_x_at	MYH11	AML inv(16) high
228827_at	Homo sapiens clone 25023 mRNA sequence	AML t(8;21) high
38487_at	FLJ12442	AML t(15;17) high
203074_at	ANXA8	AML t(15;17) high
205528_s_at	CBFA2T1	AML t(8;21) high
205529_s_at	CBFA2T1	AML t(8;21) high
206940_s_at	POU4F1	AML t(8;21) high
211341_at	POU4F1	AML t(8;21) high
201496_x_at	MYH11	AML inv(16) high
228660_x_at	SEMA4F	other high
202718_at	IGFBP2	AML t(15;17) high
205380_at	PDZK1	other high
202746_at		AML MLL low
201596_x_at	KRT18	AML t(8;21) low
34210_at	CDW52	AML t(15;17) low
212850_s_at	LRP4	AML inv(16) high

228904_at	ESTs	AML t(8;21) low, AML t(15;17) low, AML inv(16) low, AML MLL low
203151_at	MAP1A	AML t(8;21) low
201137_s_at	HLA-DPB1	AML t(15;17) low
200675_at	CD81	AML inv(16) low
201425_at	ALDH2	AML t(8;21) low
202085_at	TJP2	AML inv(16) low
202619_s_at	PLOD2	AML MLL low
203092_at	TIMM44	AML inv(16) low
204425_at	ARHGAP4	AML t(15;17) low
205366_s_at	HOXB6	AML t(8;21) low, AML t(15;17) low, AML inv(16) low, AML MLL low
205472_s_at	DACH	AML MLL high
206761_at	TACTILE	AML MLL low
222166_at		AML +8 low
222335_at	ESTs	AML MLL low
223318_s_at	MGC10974	AML complex low

225330_at	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds	AML inv(16) low
231277_x_at	ESTs	AML complex low
635_s_at	PPP2R5B	other low
202503_s_at	KIAA0101	CLL low
202580_x_at	FOXM1	CLL low
202709_at	FMOD	CLL high
204882_at	KIAA0053	CLL high
205049_s_at	CD79A	ALL high, CLL high
205051_s_at	KIT	AML high
205382_s_at	DF	AML high
205599_at	TRAF1	CML low CLL high
206255_at	BLK	ALL high, CLL high
206398_s_at	CD19	ALL high, CLL high
210487_at	DNTT	ALL high
210948_s_at	LEF1	ALL high, CLL high
211352_s_at	NCOA3	CLL high

211404_s_at	APLP2	AML high
214761_at	OAZ	ALL high
217950_at	NOSIP	CLL high
218090_s_at		CLL high
218516_s_at	FLJ20421	normal BM low
218916_at	FLJ23436	normal BM low
219753_at	STAG3	ALL high
221969_at	PAX5	ALL high, CLL high
223703_at	CDA017	AML high, CML high, normal BM high
226147_s_at	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385	CLL high
228471_at	ESTs	CLL high
229487_at	ESTs	ALL high
229790_at	TERF2	CML low, BM low
231736_x_at	MGST1	AML high, CML high, normal BM high
231854_at	Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391	CML low

239287_at	ESTs	CLL high
243362_s_at	LEF1	ALL high
243363_at	LEF1	ALL high, CLL high
41577_at	PPP1R16B	CML low

Preferred methods for detection and quantification of the amount of nucleic acids, i.e. for the methods according to the invention allowing the determination of the level of expression of a marker or a group of markers, are those described by Sambrook et al. (1989) or real time methods known in the art as the TaqMan® method disclosed in WO92/02638 and the corresponding US patents US 5,210,015, US 5,804,375, US 5,487,972. This method exploits the exonuclease activity of a polymerase to generate a signal. In detail, the (at least one) target nucleic acid component is detected by a process comprising contacting the sample with an oligonucleotide containing a sequence complementary to a region of the target nucleic acid component and a labeled oligonucleotide containing a sequence complementary to a second region of the same target nucleic acid component sequence strand, but not including the nucleic acid sequence defined by the first oligonucleotide, to create a mixture of duplexes during hybridization conditions, wherein the duplexes comprise the target nucleic acid annealed to the first oligonucleotide and to the labeled oligonucleotide such that the 3'-end of the first oligonucleotide is adjacent to the 5'-end of the labeled oligonucleotide. Then this mixture is treated with a template-dependent nucleic acid polymerase having a 5' to 3' nuclease activity under conditions sufficient to permit the 5' to 3' nuclease activity of the polymerase to cleave the annealed, labeled oligonucleotide and release labeled fragments. The signal generated by the hydrolysis of the labeled oligonucleotide is detected and/ or measured. TaqMan® technology eliminates the need for a solid phase bound reaction complex to be formed and made detectable. Other methods include e.g. fluorescence resoance energy transfer between two adjacenly hybridized probes as used in the LightCycler® format described in US 6,174,670.

Protocols for carrying out the methods according to the invention are known to the expert in the field and are described in the examples, preferably in example 1 and 4. A preferred protocol is described in Example 1(A), where total RNA is isolated, cDNA synthesized and biotin incorporated during the transcription reaction. The purified cDNA was applied to commercially available arrays which can be obtained e.g. from Affymetrix. The hybridized cDNA is detected according to the methods described in Example 1(A). The arrays are produced by photolithography or other methods known to experts skilled in the art e.g. from US5,445,934, US5,744,305, US5,700,637, US5,945,334 and EP619 321 or EP 373 203. The latter methods are also suitable for producing the composition according to the inventions in particular the composition wherein polynucleotides or oligonucleotides are bound to a solid phase in particular in the form of arrays. In a further preferred embodiment of the methods according to the invention, a transcribed polynucleotide or portion thereof is the marker or at least one of the markers. A particularly preferred transcribed polynucleotide is an mRNA or a cDNA. In a preferred embodiment of the methods according to the invention, the step of determining the expression profile further comprises amplifying the transcribed polynucleotide. In another preferred embodiment, the level of expression, i.e. the expression profile, of the group of transcribed polynucleotides is determined by annealing the transcribed polynucleotides with a complementary polynucleotide or a portion thereof under stringent hybridization conditions. The term "stringent hyberidisation conditions" is equivalent to the term "highly stringent hyberdisation conditions". Such highly stringent hybridization conditions may be determined in accordance with the teachings provided in Hames and Higgins (eds) "Nucleic acid hybridization, a practical approach", IRL Press 1985, Oxford, and include hybridization at 55-65°C in 0.2-0.5xSSC, 0.1% SDS followed by appropriate washing conditions such as 0.5-1xSSC at 55°C and 0.1% SDS.

In a most preferred embodiment, the patient sample is blood, i.e. blood mononuclear cells, or bone marrow, i.e. mononuclear cells. The methods according to the invention may be performed on fresh or frozen blood, i.e. blood mononuclear cells or bone marrow, i.e. mononuclear cells.

In a preferred embodiment the marker or at least one of the markers is a protein. In another preferred embodiment the expression profile of the proteins is detected using a reagent which specifically binds to one of the proteins whereby preferably the reagent is selected from the group consisting of an antibody, an antibody derivative, and an antibody fragment.

The term "antibody" comprises monoclonal antibodies as first described by Köhler and Milstein in Nature 278 (1975), 495-497 as well as polyclonal antibodies, i.e. entibodies contained in a polyclonal antiserum. Monoclonal antibodies include those produced by transgenic mice. Fragments of antibodies include $F(ab')_2$, Fab and Fv fragments. Derivatives of antibodies include scFvs, chimeric and humanized antibodies. See, for example Harlow and Lane, loc. cit.

Another embodiment of the invention is a kit preferably for assessing the suitability of each of a plurality of compounds for inhibiting leukemia in a patient, the kit optionally comprising the plurality of compounds; and a reagent for assessing the expression profile of a group of markers characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. Another embodiment is a kit preferably for assessing whether a patient is afflicted with leukemia, the kit comprising reagents for assessing the expression profile of a group of markers characterized In that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. Another embodiment is a kit preferably for assessing the presence of human leukemia cells, the kit comprising an antibody, wherein the antibody specifically binds with a protein corresponding to a marker characterized In that the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. Another

embodiment is a kit preferably for assessing the leukemia cell carcinogenic potential of a test compound, the kit comprising leukemia cells and a reagent for assessing expression of a marker, wherein the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

Advantageously, the kit of the present invention further comprises, optionally (a) storage solution(s) and/or remaining reagents or materials required for the conduct of scientific and/or diagnostic and/or therapeutic methods. Furthermore, parts of the kit of the invention can be packaged individually in vials or bottles or in combination in containers or multicontainer units.

Another embodiment of the invention is related to a protein or the RNA, cDNA or cRNA corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 or the use thereof for the treatment of or vaccination against leukemia. Alternatively and depending on the exact purpose, inhibitors of these compounds such as antibodies, fragments or derivatives thereof may be employed for said purpose.

The invention also contemplates a method for the development or preparation of a pharmaceutical composition for the treatment of leukemia characterized in that a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds. Another embodiment of the invention is related to a method for the development or preparation of a pharmaceutical composition for the treatment of leukemia characterized in that a vector comprising a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds. Another embodiment of the invention is a method for the development or preparation of a pharmaceutical composition for the treatment of leukemia characterized in that an antisense oligonucleotide complementary to a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds. Alternatively, inhibitors such as

antibodies specific for the markers may be used for the preparation or development of a pharmaceutical composition.

The term "pharmaceutical compounds" is preferably to be understood to mean pharmaceutically acceptable carriers, diluents or excipients, only in connection with the embodiments recited in this paragraph. In another embodiment of the invention a marker or a group of markers selected individually from one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is used for the determination of leukemia cells, the type or subtype of leukemia cells.

In another embodiment of the invention a marker or a group of markers selected individually from one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 or 36 is used for the determination of the subtype of AML cells.

In a preferred embodiment, the invention is related to a composition comprising a group of markers and substances chemically different to the markers characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one, preferably two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. It is preferred that the composition according to the invention is characterized in that the group of markers consists of all markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42. More preferred the composition according to the invention is characterized in that the group of markers consists of all markers listed in one or more of the tables 14, tables 16 to 20, or table 29 or 30, most preferred the group of markers consists of all markers listed in the tables 16 to 20 or tables 29 or 30. Preferably the markers are polynucletides or oligonucleotides, whereby the polynucleotides are bound to a solid phase in the form of an array.

The present invention also relates to a method of determining the subtypes of ALL cells in a patient sample comprising the steps of a) determining the level of expression of a group of markers in the patient sample and b) concluding from the differences in the level of expression which subtypes of ALL cells the patient sample contains characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 18, 32 or 33 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 18, 32 or 33.

Preferably the group of markers consists of all markers listed in one or more of the tables 18, 32 or 33.

The present invention further relates to a method of determining the subtypes of CLL cells in a patient sample comprising the steps of a) determining the level of expression of a group of markers in the patient sample and b) concluding from the differences in the level of expression which subtypes of CLL cells the patient sample contains characterized in that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 38 or 39 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 38 or 39.

It is preferred that the group of markers consists of all markers listed in one or more of the tables 38 or 39.

The present invention is also related to a diagnostic composition comprising at least one nucleic acid molecule, preferably (a) single-stranded nucleic acid molecule(s), which is capable of specifically hybridizing to the mRNA of at least one gene listed in Table 1. The use of said nucleic acid molecules for diagnosis of leukemia subtypes, preferably based on microarray technology, offers the following advantages: (1) more rapid and more precise diagnosis, (2) easy to use in laboratories without specialized experience, (3) abolishes the requirement for analyzing viable cells for chromosome analysis (transport problem), (4) very experienced hematologists for cytomorphology and cytochemistry, immunophenotyping as well as cytogeneticists and molecularbiologists are no longer required, and (5) improves the subclassification of leukemia due to the

definition of new entities based on gene expression profiles in those subtypes that are not clearly defined with the methods of the prior art (class discovery).

As used herein, the term "capable of specifically hybridizing" has the meaning of hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook, J., et al., in "Molecular Cloning: A Laboratory Manual" (1989), Eds. J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY and the further definitions provided above. Also contemplated are nucleic acid molecules that hybridize at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation, preferably of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH2PO4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 mg/ml salmon sperm blocking DNA, followed by washes at 50°C with 1 X SSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5x SSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

As a hybridization probe (or primer) nucleic acid molecules can be used, for example, that have exactly or basically the nucleotide sequence of at least one of the genes depicted in the appended tables or parts of these sequences. The term nucleic acid molecule as used herein also comprises fragments which are understood to be parts of the nucleic acid molecules that are long enough to specifically hybridize to transcripts of at least one of the genes of the appended tables. These nucleic acid molecules can be used, for example, as probes or primers in a diagnostic assay. Preferably, the nucleic acid molecules of the present invention have a length of at least 8, 10, 12, 13, 15, 18 in particular of at least 20 and particular preferred of at least 25 nucleotides. The nucleic acid molecules of the invention or parts therefrom* can also be used, for example, as primers for a PCR reaction. The fragments used as hybridization probe can be

synthetic fragments that were produced by means of conventional synthesis methods.

In a preferred embodiment, the diagnostic composition of the present invention comprises at least nucleic acid molecules which are capable of specifically hybridizing to the mRNAs of at least one of the genes listed in the appended tables, preferably 2-5, more preferably 8-12 genes.

In a more preferred embodiment, the diagnostic composition of the present invention comprises at least nucleic acid molecules which are capable of specifically hybridizing to the mRNAs of at least one of the genes listed in the appended tables. In a further preferred embodiment, the diagnostic composition of the present invention comprises at least nucleic acid molecules which are capable of specifically hybridizing to the mRNAs of all genes listed in the appended tables.

In a further preferred embodiment, the nucleic acid molecules of the diagnostic composition of the present invention are bound to (a) a solid support, for example, a polystyrene microtiter dish or nitrocellulose membrane or glass surface or (b) to non-immobilized particles in solution.

In an even more preferred embodiment, the nucleic acid molecules of the diagnostic composition are present in a microarray format which can be established according to well known methods; for details see, e.g., www.affymetrix.com/technology/tech_spotted.html; www.affymetrix.com/technology/tech_probe.html.

The present invention also provides the use of (a) nucleic acid molecule(s) of the present invention for the preparation of a diagnostic composition for the diagnosis of a leukemia or for the diagnosis of several subtypes or a disposition to a leukemia. For the diagnosis of a particular leukemia subtype, preferably, at least 5 different nucleic acid molecules are used as probes. For diagnosis, preferably, bone marrow or peripheral blood can be used. For diagnosis, the target sample is contacted with a (a) nucleic acid molecule(s) of the present invention and the concentration of individual mRNAs is compared with the mRNA expression profile levels of a test sample obtained from healthy donors.

It is a further embodiment of the invention to provide a method of determining whether a patient sample contains leukemia cells or other cells and at the same

time determining the type and subtype of leukemia cells, comprising the steps of providing a patient sample, isolating RNA from the patient sample, transcribing the RNA into cDNA and transcribing the cDNA into cRNA while simultaneously labelling the cRNA, hybridising the cRNA to a microarray, and determining the level of expression of a marker or a group of markers.

Further, the invention contemplates the use of a marker or a group of markers for determining whether a patient sample contains leukemia cells or other cells and whereby preferably the type and subtype of leukemia cells is simultaneously or subsequently is determined. The markers specified in the appended examples and tables may, in accordance with the invention, be used to differentiate, for example, between ALL, CLL, CML and AML.

The nucleic acid molecule is typically a nucleic acid probe for hybridization or a primer for PCR. The person skilled in the art is in a position to design suitable nucleic acids probes based on the information provided in in the appended tables.

The target cellular component, i.e. mRNA e.g., in bone marrow or blood (BM) may be detected directly in situ, e.g. by in situ hybridization or it may be isolated from other cell components by common methods known to those skilled in the art before contacting with a probe. Detection' methods include Northern blot analysis, RNase protection, in situ methods, e.g. in situ hybridization, in vitro amplification methods (PCR, LCR, QRNA replicase or RNA-transcription/amplification (TAS, 3SR), reverse dot blot disclosed in EP 0 237 362)) and other detection assays that are known to those skilled in the art. Preferably, detection is based on a microarray.

Amplification methods include the polymerase chain reaction (PCR) which specifically amplifies target sequences to detectable amounts. Other possible amplification reactions are the ligase Chain Reaction (LCR, Wu and Wallace, 1989, Genomics 4:560-569 and Barany, 1991, Proc. Natl. Acad. Sci. USA 88:189-193); Polymerase Ligase Chain Reaction (Barany, 1991, PCR Methods and Applic. 1:5-16); Gap-LCR (PCT Patent Publication No. WO 90/01069); Repair Chain Reaction (European Patent Publication No. 439,182 A2), 3SR (Kwoh et al., 1989, Proc. Natl. Acad. Sci. USA 86:1173-1177; Guatelli et al., 1990, Proc. Natl. Acad. Sci. USA 87:1874-1878; PCT Patent Publication No. WO 92/0880A), and NASBA (U.S. Pat. No. 5,130,238). Further, there are strand displacement amplification (SDA), transciption mediated amplification (TMA), and Q□-

amplification (for a review see e.g. Whelen and Persing (1996). Annu. Rev. Microbiol. 50, 349-373; Abramson and Myers, 1993, Current Opinion in Biotechnology 4:41-47).

Products obtained by in vitro amplification can be detected according to established methods, e.g. by separating the products on agarose gels and by subsequent staining with ethidium bromide. Alternatively, the amplified products can be detected by using labeled primers for amplification or labeled dNTPs.

The probes can be detectably labeled, for example, with a radioisotope, a bioluminescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate, biotin or an enzyme.

The invention further contemplates a method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with leukemia, the method comprising isolating a protein corresponding to a marker selected from the group consisting of the markers listed in Tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 immunizing a mammal using the isolated protein, or a peptide corresponding to its sequence or a part thereof; isolating splenocytes from the immunized mammal-, fusing the isolated splenocytes with an immortalized cell line to form hybridomas; and screening individual hybridomas for production of an antibody which specifically binds with the protein to isolate the hybridoma. Further, an antibody produced by this method is contemplated by the invention. The antibody may be fragmented or derivated to obtained fragment or derivatives retaining the antibody specificity as has been described herein above.

The invention further contemplates a method of assessing the leukemia cell carcinogenic potential of a test compound, the method comprising maintaining separate aliquots of leukemia cells in the presence and absence of the test compound; and comparing expression of a marker in each of the aliquots, wherein a significantly altered level of expression of the marker in the aliquot maintained in the presence of the test compound, relative to the aliquot maintained in the absence of the test compound, is an indication that the test compound possesses human breast cell carcinogenic potential wherein a marker according to the invention is used.

The invention further contemplates a system for identifying selected polynucleotide records that identify a leukemia cell, the system comprising:a digital computer-, a database coupled to the computer; a database coupled to the database server having data stored in, the data comprising records of data comprising a polynucleotide corresponding to a marker according to the invention and a code mechanism for applying queries based upon a desired selection criteria to the data file in the database to produce reports of polynucleotide records which match the desired selection criteria.

The invention also relates to a method for detecting a leukemia cell, using a computer having a processor, memory, display, and input/output devices, the method comprising the steps of

a) providing a sequence of a polynucleotide isolated from a sample suspected of containing a leukemia cell,

b) providing a database comprising records of data comprising a polynucleotide corresponding to a group of markers according to the invention;

c) using a code mechanism for applying queries based upon a desired selection criteria to the data file in the database to produce reports of polynucleotide records of step a) which provide a match of the desired selection criteria of the sequences in the database of step b), the presence of a match being a positive indication that the polynucleotide of step 1) has been isolated from a cell that is a-leukemia cell.

Also, the present invention relates to a method for assessing the leukemia cell carcinogenic potential of a test compound, comprising (a) contacting a non-leukemia cell with a test compound, and (b) assessing an increase or decrease of marker expression in said non-leukemia cell wherein the marker is selected from the tables 1 to 20, 25 or 27, 29, 30, 32, 33, 35, 36, 38, 39, 41 or 42.

The assessment may be effected on the nucleic acid level such as by hybridization techniques or PCR or on the protein level such as by using antibody or aptamers based technologies.

Finally, the invention relates to a diagnostic composition comprising at least one nucleic acid molecule which is capable of specifically hybridizing to the mRNA corresponding to the marker gene of any of the appended tables. The nucleic acid

molecule may be an antisense DNA or RNA an RNAi molecule a siRNA molecule or the like inhibitory molecule capable of specifically blocking trnascription and/or translation and/or modification and/or localization of the RNA and/or protein corresponding to the marker gene.

The nucleic acid may also be a sense-strand nucleic acid e.g. RNA or preferably DNA which is capable of expressing the protein product of the marker gene, or a protein product of substantially similar activity, in a target cell into which it is introduced.

The invention further comprises pharmaceutical compositions comprising a compound capable of specifically binding to a protein or RNA corresponding to a marker of the invention as listed in any of the appended tables. The marker is preferably selected from the markers designated as particular preferred markers as described herein above . The compound is preferably a compound capable of inhibiting or increasing the function of the protein or of enhancing or decreasing translation of the RNA. The compound is preferably selected from aptameres, aptazynes, RNAzynes, antibodies, affybodies, trinextins, anticalins, or the like compounds. The effect of the compounds on the RNA may be tested by assaying for increased/decreased synthesis of the corresponding protein. The effect of the compounds on the protein may be assayed the testing the effect of the compound in an assay of the proteins function, which e.g. may be an anzymathic function. Alternatively, the effect may be tested by contacting a leukemic cell that expresses large amounts of such protein with the compound and assay cellular parameters associated with the leukemic state of the cell, such as cell growth, growth factor dependency and/or differentiation state of the cell.

In a further embodiment, the invention provides a method of determining wether a patient sample contains leukemia cells or other cells comprising the steps of

a) determining the expression profile of a group of markers in a patient sample and

b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells, and optionally, to which subtype said leukemia cells belong, wherein

a subtype or a type of leukemia listed in table 28 b or c is identified, and a sensitivity and/or specificity of at least 80, 85, 88, 90, 92, 95, 97, 98, 99, 99.1, 99.2, 99.3, 99.4 or 99.5% is achieved, preferably using at least one marker of the group of markers listed in table 29 and/or 30.

In a further embodiment, the invention provides a method of determining wether a patient sample contains leukemia cells or other cells comprising the steps of

(a) determining the expression profile of a group of markers in a patient sample and

(b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells, and optionally, to which subtype said leukemia cells belong, wherein

a subtype or a type of leukemia listed in table 31 b or c is identified, and a sensitivity and/or specificity of at least 80, 85, 88, 90, 92, 95, 97, 98, 99, 99.1, 99.2, 99.3, 99.4 or 99.5% is achieved, preferably using at least one marker of the group of markers listed in table 32 and/or 33.

In a further embodiment, the invention provides a method of determining wether a patient sample contains leukemia cells or other cells comprising the steps of

(a) determining the expression profile of a group of markers in a patient sample and

(b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells, and optionally, to which subtype said leukemia cells belong, wherein

a subtype or a type of leukemia listed in table 34 b or c is identified, and a sensitivity and/or specificity of at least 80, 85, 88, 90, 92, 95, 97, 98, 99, 99.1, 99.2, 99.3, 99.4 or 99.5% is achieved, preferably using at least one marker of the group of markers listed in table 35 and/or 36.

In a further embodiment, the invention provides a method of determining wether a patient sample contains leukemia cells or other cells comprising the steps of

(a) -determining the expression profile of a group of markers in a patient sample and

(b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells, and optionally, to which subtype said leukemia cells belong, wherein

a subtype or a type of leukemia listed in table 37 b or c is identified, and a sensitivity and/or specificity of at least 80, 85, 88, 90, 92, 95, 97, 98, 99, 99.1, 99.2, 99.3, 99.4 or 99.5% is achieved, preferably using at least one marker of the group of markers listed in table 38 and/or 39.

In a further embodiment, the invention provides a method of determining wether a patient sample contains leukemia cells or other cells comprising the steps of

(a) determining the expression profile of a group of markers in a patient sample and

(b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells, and optionally, to which subtype said leukemia cells belong, wherein

a subtype or a type of leukemia listed in table 40 b or c is identified, and a sensitivity and/or specificity of at least 80, 85, 88, 90, 92, 95, 97, 98, 99, 99.1, 99.2, 99.3, 99.4 or 99.5% is achieved, preferably using at least one marker of the group of markers listed in table 41 and/or 42.

Description of the Figures

Figure 1a:	Principal Component Analysis
Figure 1b:	Hierarchical Cluster Analysis
Figure 2:	Classification Accuracy
Figures 3a, 3b1, 3b2:	PCA of AML data based on 312 genes Decision Trees according to I(E)
Figure 4:	Pair-wise Comparison of Normal BM and AML
Figure 5a:	Principal Component Analysis
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Figure 6a:	Principal Component Analysis
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Figure 8a:	Principal Component Analysis
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Figure 9a:	Principal Component Analysis
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Figure 9c:	Comparison of Normal BM versus Leukemia
Figure 10a:	Principal Component Analysis
Figure 10b:	Hierarchical Cluster Analysis
Figure 10c:	
Figure 11a	Accurate diagnosis of leukemia is accomplished in a two-step approach. First, samples are assigned to one of the major leukemia types or normal BM, respectively. Then, if positive for ALL or AML, further subclassification based on cytogenetically

	defined characteristics is proposed. In total 111 samples were analyzed by gene expression profiling and implemented in the development of different class prediction models: normal BM (n=8), CLL (n=8), CML (n=10), ALL (n=18), and AML (n=59). 18 ALL samples can further be characterized by B-lineage ALL samples positive for t(8;14) (n=3), t(9;22) (n=7), or t(11q23)/MLL (n=4) and T-lineage ALL (n=3), respectively. Additionally, one B-ALL sample showed an aberrant karyotype. 59 AML samples were comprized of normal karyotype (n=3), complex aberrant karyotype (n=4), trisomy 8 as sole abnormality (n=3), t(8;21) (n=9), t(15;17) (n=16), inv(16) (n=10), and t(11q23)/MLL (n=10). The latter four AML entities were additionally represented by each of the following t(8;21),+8 (n=1), t(15;17),+8 (n=2), and inv(16),+8 (n=1). Furthermore, some expression profiles were excluded for development of the classifier but subsequently tested for performance in diagnostical class assignments: normal BM (n=1), CLL (n=2), CML (n=2), ALL with t(4;11) (n=1), and AML with t(15;17) (n=2), respectively.
Figure 11b:	Hierarchical clustering of 55 AML samples (rows) versus 25 informative genes (columns). In total, 15 comparisons within the 5 groups were performed (pairwise and one-versus-all). Genes were selected for maximal accuracy and confidence based on a modified signal-to-noise (S2N) algorithm. The scaled gene expression levels are coded by intensity and shown on a scale from black (no expression) to bright red (highest expression). The AML subgroups 'other' (n=10), t(11q23)/MLL (n=10), inv(16) (n=10), t(8;21) (n=9), and t(15;17) (n=16) are colored according to their chromosomal aberrations. The minimal set of informative genes is given by HGNC approved symbols (not yet approved genes are marked by asterisks).
Figure 11c	Hierarchical clustering of 17 ALL samples (rows) versus 19 informative genes (columns). In total, 10 pairwise or OVA comparisons within the 4 groups were performed. Genes were selected for maximal accuracy and confidence based on a modified S2N algorithm. The scaled gene expression levels are coded by intensity and shown on a scale from black (no

	expression) to bright red (highest expression). The ALL subgroups t(11q23)/MLL (n=4), t(9;22) (n=7), t(8;14) (n=3), and T-ALL (n=3) are colored according to their characteristical chromosomal aberrations or immunophenotype. The minimal set of informative genes is given by HGNC approved symbols (asterisks mark not yet approved genes).
Figure 12a – 12i	Bar graphs of gene expression intensities for distinct leukemia types and subtypes. A short description indicates the respective classes which can be distinguished at each case.
Figure 13a.	Dot plot of expression levels for a particular gene in two groups (e.g. group1= normal samples, group2 = disease samples). Golub's decision limit to distinguish between group1 and group2, which is defined as the mean of μ_1 and μ_2 (μ_a: mean expression in group a), is not optimal, because the standard deviations of gene expression levels within the two groups are very different. In this case, a lower limit (e.g. maximum level in group1) would have been more appropriate to separate the two groups by means of gene expression levels.
Figure 13b	Accuracy and confidence for all-pairs and one-versus-all comparisons in a dataset consisting of 103 samples from 5 classes (A,B,C,D,E) using Golub's method and *diffgenes*. Both accuracy and confidence are higher with *diffgenes*.
Figure 14	Detailed characteristics of the 37 AML cases representing three defined cytogenetic aberrations corresponding to four cytomorphological subtypes according to FAB classification: inv(16)(p13q22)/AML M4eo, t(8;21)(q22;q22)/AML M2, and t(15;17)(q22;q12)/AML M3 or M3v. Diagnosis was proven by a) karyotype analysis, b) interphase-FISH (*CBFB*, *AML1* and *ETO*, *PML* and *RARA*), c) RT-PCR (*CBFB-MYH11*, *AML1-ETO*, *PML-RARA*), and d) cytomorphology.
Figure 15	Figure 15: Three cytogenetically defined AML subtypes with t(15;17), t(8;21) or inv(16) can be separated based on their gene expression profiles of 1,000 preselected genes. The three

	different subgroups form distinct clusters. For visualization in a two-dimensional plot the first two principal components were chosen as they captured most of the variation in the original data set. The subgroups are coloured according to their chromosomal aberrations, respectively
Figure 16	Hierarchical cluster analysis of the gene expression pattern of the set of 13 predictor genes as identified according to the adapted class prediction methodology introduced by Golub et al. The three distinct cytogenetic AML subgroups can clearly be separated based on their gene expression profiles. Each row represents a leukemia sample and each column a gene. The gene accession numbers are shown on the top. Varying expression levels are shown on a scale from black (no gene expression) to bright red (highest expression). The subgroups are coloured according to their chromosomal aberrations, respectively.
Figure 17	Schematic representation of the 15 decision trees (a to o) used in the multiple-tree classifier. Arrows indicate high (arrow up) or low (arrow down) expression, "0" and "+" denote absence or presence of a gene, respectively (e.g., in (a) the low expression of X96719 indicates AML with t(15;17) whereas the high expression of X96719 indicates AML with inv(16) or AML with t(8;21); the latter two entities are distinguished by X53742: lack of expression identifies AML with inv(16) and positive expression predicts AML with t(8;21)). The GenBank accession numbers are given for genes the expression level of which are used for decision. Nodes are represented as ovals and leaves as rectangles. Classes are referred to as t(15;17), t(8;21) or inv(16).
Figure 18	Based on a preselection of 82 genes morphologically different but cytogenetically identical AML subtypes M3 with t(15;17) and M3v with t(15;17) can be separated based on their gene expression profile. AML M3 samples are shown as green dots, AML M3v samples as blue dots, respectively.

Figure 19:	Correlations between protein expression levels and mRNA abundance. Expression levels were compared by Pearson's correlation. Mean fluorescence intensity values obtained by flow cytometry were calculated for all events with fluorescence values higher than isotype controls using the CellQuest Pro software (Beckton Dickinson). Average fluorescence intensity values obtained by micorarray analyses were calculated by the Affymetrix software, Microarray Suite, Version 4.0.1.
Figure 20	Detailed characteristics of the 45 AML cases representing four defined recurrent cytogenetic abnormalities. Diagnosis was proven by a) karyo-type analysis, b) interphase-FISH, c) RT-PCR, and d) cytomorphology.
Fig. 21	Class separation by principal component analysis (PCA)
Fig. 22	Figure 3: PCA-Plot based on 39 informative genes. All leukemia samples could accurately be assigned to their corresponding cytogenetic subtype with 100% accuracies. To illustrate these results, a hierarchical clustering is shown (Fig. 4).
Fig. 23	Hierarchical clustering of 44 diagnostic AML samples and 8 normal BM samples (columns) versus 39 informative genes (rows). Gene expression levels are coded by intensity and represented on a scale from black (no expression) to bright red (highest expression).
Fig. 24 to 465	Bar graphs of gene expression intensities for distinct leukemia types and subtypes or normal bone marrow, respectively. Selected statistically significant genes are given by Affymetrix identification number and Human Gene Nomenclature Committee approved symbol (where available). A short description indicates the respective classes which can be distinguished at each case.

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The following examples, references, sequence listing and figures are provided to aid the understanding of the present invention, the true scope of which is set forth in the appended claims. It is understood that modifications can be made in the procedures set forth without departing from the spirit of the invention.

Examples

EXAMPLE 1

EXAMPLE 1 - General Methods

EXAMPLE 1 - (A) Selection and characterisation of Leukemia Samples

Bone marrow (BM) aspirates were taken at the time of the initial diagnostic biopsy and remaining material was immediately lysed in RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis. For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) was used. The targets for GeneChip analysis were prepared according to the current Expression Analysis. Briefly, frozen lysates of the leukemia samples were thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen).Normally 10 ug total RNA isolated from 1 x 107 cells was used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA was purified by phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug were fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) were chosen for monitoring of the integrity of the

cRNA. Only labeled cRNA-cocktails which showed a ratio of the messured intensity of the 3' to the 5' end of the GAPDH gene less than 3.0 were selected for subsequent hybridization on HG-U95Av2 probe arrays (Affymetrix). Washing and staining the Probe arrays was performed as described (siehe Affymetrix-Original-Literatur (LOCKHART und LIPSHUTZ). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the arrays as detected by confocal laser scanning according to the manufacturers recommendations.

EXAMPLE 1 - (B) Data analysis

Class separation by principal component analysis and hierarchical cluster analysis: In a first step we reduced the dimensionality of the number of genes. Therefore we scaled the data from each array to a target intensity value 50 (Affymetrix Microarray Suite) in order to be able to perform inter-array comparisons. Then all data was analyzed using Significance Analysis of Microarrays (Multiclass Response, Stanford University) and we selected a distinct number of genes based on a permutations test. This reduced set of genes which showed to be significant then was analyzed using the public available Java application J-Express analysis tool (download at www.molmine.com). Principal Component Analysis and Hierarchical Cluster Analysis (parameters Cluster method: single linkage and Distance metric: euclidean) showed a clear separation of analyzed groups of samples e.g. healthy bone marrow versus leukemia.

EXAMPLE 1 **- (C) Identification of differentially expressed genes according to Golub et al. (Science 1999 Oct 15;286(5439):531-7)**

A previously described (Science 1999 Oct 15;286(5439):531-7) was modified to reduce the number of candidate genes that could distinguish between our leukemic samples of interest. In a first step the raw data was scaled using Affymetrix software (target intensity 50 for all genes). To avoid division by zero or

negative numbers as occuring due to the current expression algorithm (Affymetrix) we set all average intensities of 20 or less to 20. Briefly, for a more detailed gene expression profiling we applied the data analysis method according to Golub et al. using weighted voting. In a first step gene expression levels were log-transformed with a cut-off value set at 20 units. To assess the significance of selected genes we performed a leave-one-out cross-validation. Only those genes were considered important which were contained in all cross validation classificators. To determine the association between genes by chance we performed a permutation test (100 cycles). Because the number of informative genes, which are able to discriminate between samples, is unknown, we applied the Golub method for different numbers of informative genes (range: 10-200). The minimal set of genes which provided optimal classification accuracy was selected to avoid overfitting.

EXAMPLE 2

EXAMPLE 2 - Identification of genes, the aberrant expression of which is associated with a particular leukemia subtype

Monitoring the gene expression level of thousands of mRNA transcripts simultaneously in one experiment is the key technology to find out the specific genes which allow the subsequent development of a class prediction model. We therefore used the Affymetrix oligonucleotide microarray technology (GeneChip® Instrument System) to obtain gene expression profiles of each individual clinical sample of interest. The HG-U95Av2 probe arrays gave us information about the relative mRNA abundance of about 12,000 full length human genes which are represented on these high-density oligonucleotide microarrays.

In total, 8 bone marrow samples of healthy volunteers and leukemia patients were investigated. Five different types of bioinformatic calculations were performed.

EXAMPLE 2 **(I) Three distinct genetic subtypes of AML**

Three defined cytogenetic aberrations t(8;21)(q22;q22) (n=9), t(15;17)(q22;q12) (n=16) and M4eo with inv(16) (p13q22) (n=10) corresponding to the 4 FAB-subtypes AML M2, M3 or M3v and M4eo, respectively. After we obtained bone marrow aspirates from 35 untreated patients with newly diagnosed AML, all cases were characterized by cytomorphology, cytogenetics and by molecular genetics (Fig. 1). AML subtypes M3 and M3v both carry the same chromosomal aberration but differ in morphological aspects like nuclear configuration, granulation and clinical aspects white blood cell count (WBC), respectively. In all cases, these balanced abnormalities were confirmed by fluorescence in-situ hybridization. The corresponding fusion transcript was detected by RT-PCR and/or quantitative real time PCR. The median age of the patients was 53 years (range, 19-82 years) and did not differ between the respective groups. The median WBC count was 17.0 G/l (range, 0.8-168.0 G/l) and was strikingly lower in patients with AML M3 as compared to all other patients.

EXAMPLE 2 - Methods used

EXAMPLE 2 - (A) Selection and characterisation of Leukemia Samples

We obtained bone marrow (BM) aspirates from 37 AML patients standing for four morphological and three underlying cytogenetic subgroups that were sent to the Laboratory of Leukemia Diagnostics (LFL) for central diagnosis within the German AMLCG study (Klinikum Grosshadern, Munich, Germany). They were selected for this study on the basis of several criteria. It was mandatory that none of the patients had been treated. All samples, exclusively newly diagnosed in our laboratory, had to be well characterized as de novo AML and diagnosis had been proven by cytomorphology, cytogenetics, flow cytometry and molecular genetics in every single case. All samples for gene expression analysis were taken at the time of the initial diagnostic biopsy when remaining material was immediately lysed in

RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis.

EXAMPLE 2 - (B) Microarray experiments

For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) was used. The targets for GeneChip analysis were prepared according to the current Expression Analysis Technical Manual. Briefly, frozen lysates of the leukemia samples were thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen). Normally 10 ug total RNA isolated from 1 x 107 cells was used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA was purified by phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug were fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) were chosen for monitoring of the integrity of the cRNA. Only labeled cRNA-cocktails which showed a ratio of the measured intensity of the 3' to the 5' end of the GAPDH gene less than 3 were selected for hybridization on HG-U95Av2 probe arrays (Affymetrix). Washing and staining the Probe arrays was performed as described. The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the arrays as detected by confocal laser scanning according to the manufacturers recommendations.

EXAMPLE 2 - (C) Class separation by principal component analysis and hierarchical cluster analysis

In a first step we reduced the dimensionality of the number of genes. Therefore we scaled the data from each array to a target intensity value 50 (Affymetrix Microarray Suite) in order to be able to perform inter-array comparisons. Then all data was analyzed using Significance Analysis of Microarrays (Multiclass Response, Stanford University) and we selected 580 genes based on a permutations test. This reduced set of genes which showed to be significant then was analyzed using the public available Java application J-Express analysis tool (download at www.molmine.com). Principal Component Analysis and Hierarchical Cluster Analysis (parameters Cluster method: single linkage and Distance metric: euclidean) showed a clear separation of analyzed groups of samples e.g. healthy bone marrow versus leukemia.

EXAMPLE 2 - (D) Identification of differentially expressed genes according to Golub

This analysis was carried cut as described in Example 1 (C) above. Briefly, classification of tumor samples was achieved by using a set of samples whose class had been already determined. This set was called training set. By using the oligonucleotide microarrays (Lockhart, D. J., et al., Nat Biotechnol 14 (1996) 1675-80), the, transcript levels in training set samples were measured for those genes that were represented on the microarray. The values for "transcriptien strength" were determined by averaging the values of a set of probes which were compared to a set of nearly identical probes containing a single mismatch. This was performed by using; methods provided by the oligonucleotide array of Affymetrix Inc.

EXAMPLE 2 - (E) Principle Components Analysis, Classifier and DecisionsTrees

In order to obtain comparable values between different samples, they had to be standardized first. The method followed that described (Lockhart, D. J., et al., Nat Biotechnol 14 (1996) 1675-80), except that correcting for (additive) background

had been omitted. In brief, the data from one of the samples were declared to serve as a "standard", and the values from all other samples were adapted to this standard. For every possible comparison to this standard, a set of "reliable" values was determined by calculating the correlation coefficient for a series of intervals of increasing length. The lower bound of reliability was the bound of the interval that had a correlation coefficient less than or equal to the smaller intervals. From all reliable values, 2 (logarithmized) correction factor was calculated by computing the median of the differences of the logarithmic values. Values that were zero or negative prior to taking the logarithm were not taken into account.

The obtained data matrix contained values from one sample per column. The gene expression profile across all samples for one gene or gene fragment represented on the oligonucleotide microarray was contained in a row of the matrix. To allow for rapid calculation of the classifier and to reduce memory usage, certain genes were pre-selected from the set of all genes represented on the array. The following criteria were applied:

Formula (1):

$$\sum_{i=1}^{k} |\mu_i - \overline{\mu}| - \sum_{i=1}^{k} \sigma_i > 0$$

Formula (2):

$$r < \frac{\sum_{i=1}^{k} |\mu_i - \overline{\mu}|}{\sum_{i=1}^{k} \sigma_i}$$

μ_1 refers to the average of the i-th class (i=l,...,k), μ to the total average, σ_i to the standard deviation of the i-th class and t to an arbitrary treshold ≤ 1. Selection by these methods resulted typically in a reduction in the number of genes by a factor of 10-30. To check the quality of the selection procedure, the first two principal components (Jolliffe, Principle Components Analysis (1986), Springer (New York)) for the samples were plotted. This allowed to judge whether or not a rigorous discrimination was possible between the different classes.

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For construction of the classifier, decision trees (Breiman et al., Classification and regression try, Wadsworth & Brooks/Cole (Monterey)) were used. Simple decision trees that discriminate between n classes by using only transcription levels for (n-l) genes were used. They were trained and the selected genes were the discarded from the original data set. A new tree was constructed by using the truncated data set and the entire procedure was iterated until a predetermined number of trees was reached. The optimal number of trees could be estimated by counting the number of misclassifications of classifiers built from different numbers of trees. For this, an independent data set of cross-validation had to be used. The final vote of the multi-classifier was obtained by applying a vote-by-majority rule to the predictions o f the contained trees. In the example of the present invention 15 decision trees had been used for the multi-classifier. This allowed perfect classification of 100% of the samples, discriminating between classes that were given by chromosomal aberrations. To estimate generalization properties, i.e. how accurate the classifier may perform on samples that have not been used for training, cross-validation had been used (Efron and Tibshirani, An introduction to the bootstrap (1993), Chapman & Hall (New York, London), pp. 237-247).

EXAMPLE 2 - Results (Golub Method)

From this point of view it was found that a set of 17 genes was sufficient to distinguish distinct AML subtypes from each other with high precision (Tables 1). The classification model was able to identify the 4 morphologically and 3 cytogenetically and molecular biological different subtypes AML with t(8;21), with t(15;17), and with inv(l6) (Figures la-b, 2).

In conclusion by comparison of gene expression profiles of AML samples (3 tested genetic subtypes t(8;21), t(15;17) and inv(16)) genes could be identified which allowed a differentiation between each individual AML subtype in detail could be shown for the first time that these distinct abnormalities on the genomic level relate to a specific gene expression pattern. In other words, in the experimental setting the knowledge of the expression status of' these designated genes was sufficient to predict the genetic abnormality and allows the diagnosis of specific genetically defined subtypes of AML (Table 1).

Results of methods described in I(E) are shown in Table 2 and Figures 3a + b, 1/2 and 4.

EXAMPLE 2 - **II) Pair-wise comparisons between normal bone marrow, AML, ALL, CML, and CLL**: By pair-wise comparisons gene expression profiles of 8 cases of normal bone marrow, 48 AML, 9 ALL, 8 CML, and 7 CLL were evaluated. These led to the identification of subtype-specific genes (Tables 3-12. Figs. 5a-c, 6a-c, 7a-c, 8a-c).

EXAMPLE 2 - **III) AML classified according to WHO proposal**

To allow classification of AML subtypes according to the new WHO proposal we used the gene expression profiles of four genetically defined AML subtypes (t(8;21) n= 9; t(15;17) n= 18; inv(16) n= 10; 11q23/MLL aberrations n= 11). This led to the identification of subtype-specific genes (Table 13, Figs. 9a-c).

EXAMPLE 2 - **IV) Normal bone marrow *versus* distinct genetic subtypes of AML:** We used the gene expression profiles of normal bone marrow (n=8) and of four genetically defined AML subtypes (t(8;21) n= 9; t(15;17) n= 18; inv(16) n= 10; 11q23/MLL aberrations n= 10). This led to the identification of genes that allow the distinction between normal bone marrow and each of the four AML subtypes (Table 14).

EXAMPLE 2 - **V) Identification of genes specifically separating normal bone marrow, AML, ALL, CML, and CLL:** : We used the gene expression profiles of normal bone marrow (n=8) and of AML (n=48), ALL (n = 9), CML (n = 8), and CLL (n =7). This led to the identification of xx genes that allow the distinction between normal bone marrow and each of the four leukemia subtypes (Table 15, Figures 10a-c).

Example 3: Gene expression profiling provides a global and robust diagnostic tool for leukemia

Example 3- Introduction

The expression profiles of 12,600 genes were analyzed in 103 patients suffering from chronic myeloid leukemia (CML), chronic lymphoid leukemia (CLL), acute lymphoblastic leukemia (ALL), and acute myeloid leukemia (AML). A set of 71 genes shown in table 16 to 19 was identified as the minimal set necessary to accurately diagnose prognostically relevant leukemia subtypes and to distinguish these from normal bone marrow (BM, n=8). Thus, microarray technology is a suitable method for diagnosis of leukemia.

Today, the classification of hematological malignancies according to the WHO criteria describes chronic myeloid leukemia (CML), chronic lymphoid (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within the latter two several prognostically relevant subtypes are established (see example 4). This subclassification is based on genetic abnormalities of the leukemic blasts associated with different prognoses and becomes increasingly important to guide therapy. Thus, the development of new, specific treatment approaches requires the precise identification of these subtypes that may benefit from individual therapeutic protocols. It has already been shown that the development of drugs targeting molecular aberrations can dramatically improve outcome. The introduction of all-trans retinoic acid (ATRA) into the treatment of AML with t(15;17)(q22;q11-12) has improved outcome from about 50% to 80% long-term survivors (1). In CML patients imatinib, a designed molecule that inhibits the t(9;22)(q34;q11) specific chimeric tyrosine kinase BCR-ABL, induces dramatically higher response rates as compared to conventional drugs (2). To fully take advantage of specific treatment options a precise identification of distinct leukemia subtypes is mandatory. However, standard diagnostics of leukemia using a combination of complementary methods is expensive, time-consuming, and requires experienced specialists.

Since its introduction, microarrays have been promising tools for basic research. With regard to leukemia, the pivotal discrimination of unselected ALL and AML samples based on their gene expression signatures inspired numerous studies (3). Recently, subtypes of childhood ALL could be correlated to specific gene

expression profiles leading to both marker genes suitable for initial diagnostics and canditates as predictors for outcome (Yeoh, Eng-Juh. pediadric ALL expression profiling *Cancer Cell*, 2002). Additionally, novel entities in hematological malignancies could be identified based on their distinct expression pattern as has been shown for multiple myeloma, large cell lymphoma, and childhood ALL (4-6). In example 4, it is demonstrated that cytogenetically defined AML subtypes can be correlated to specific gene expression profiles (see example 4). AML FAB M2 with t(8;21)(q22;q22), FAB M3/M3v with t(15;17)(q22;q11-12), or M4eo with inv(16)(p13q22) could be classified based on a minimal set of 13 genes. These genes belong to a large variety of different functional classes including members of signaling pathways, cell surface antigens, as well as plasma glycoproteins. Several genes are known to be involved in cytoskeletal structure, transcriptional processes, or have not yet further been functionally described.

Here, gene expression profiles of 103 leukemia patients were acquired representing 11 groups and eight normal BM donors to designate leukemia-specific genes which build up the basis for a novel diagnostic tool. Following the aims of Golub, who introduced the cancer class prediction methodology (3, 7), all four major leukemia types were analyzed and also included cytogenetically defined subgroups of AML and ALL as described in the WHO classification of leukemia, respectively (Fig. 11a). All patient samples were thoroughly characterized combining cytomorphology, cytogenetics, immunophenotyping, and molecular genetics. This was a prerequisite to obtain disease-specific gene expression profiles for each entity. We used Affymetrix expression probe arrays HG-U95Av2 to interrogate the mRNA abundance of approximately 12,600 transcripts. In order to identify genes suitable for a leukemia prediction classifier we applied a slightly modified prediction methodology as introduced by Golub [see (Note1_Golub method)]. A minimal set of candidate genes had to show both maximal classification accuracy and maximal confidence. Accuracy of the classifiers was determined by permutation-based neighborhood analysis [see (Note2_ leave-one-out crossvalidation)]. Additional information about the absolute differences of expression intensities and further descriptions of all candidate genes can be found in the supporting online material.

In a first step, based on 23 informative genes the samples were assigned to either normal BM, CLL, CML, ALL, or AML, respectively (Table 22; Description of Table 22: Classification scheme for 4 major leukemia types and normal BM. Matrices delineate distribution of actual leukemia types as compared with predicted types from pairwise comparisons. Class assignment can be based on the expression profiles of 23 genes. Except for pairwise comparison of AML versus ALL, all cases can be predicted accurately in leave-one-out cross validation with 100% accuracy and strong confidence. For each pairwise comparison the minimal set of informative genes is represented by approved HUGO Gene Nomenclature Committee (HGNC) symbols. Not yet approved genes are marked by asterisks.). In 9/10 pairwise comparisons all samples were classified correctly (335 individual assignments; 100% accuracy). In one comparison (AML versus ALL) 75/77 samples were classified correctly resulting in an accuracy of 97%. Two ALL samples were misclassified as AML. This may be due to the heterogenity of both groups (n=18 versus n=59) causing noise in the expression data.

For each pairwise comparison a set of discriminative genes is disclosed in table 20 whereby the gene names can be found in table 21. The most discriminative and informative genes are marked by asterisks in table 20 and are the 71 genes shown in table 16 to 19

In detail, we found phospholipidscramblase 1 (*PLSCR1*) to be lower expressed in AML and ALL as compared to normal BM. *PLSCR1* encodes for a plasma membrane protein and has been proposed to play a role in transbilayer migration of phospholipids and in recognition and phagocytic clearance of injured, aged, or apoptotic cells (8). The biologic effects of interferon-alpha may be mediated by *PLSCR1* which is markedly upregulated by interferon (9, 10). We also observed that *LEF-1* was absent in myeloid leukemias but highly expressed in lymphoid leukemias. *LEF-1* was shown to be mitogenic and important for cell survival in pro-B cells (11). The B-cell specific coactivator of octamer binding transcription factors, *POU2AF1*, plays an important role in the antigen-driven stages of B cell activation and maturation and discriminates between AML and CLL (12). *MSF* has been reported to be a translocation partner of the mixed-lineage leukemia gene (MLL) in AML and was able to separate AML from ALL (13). Likewise, *OS-9*, not yet further

functionally described except for amplification in osteosarcomas, was differentially expressed between AML and ALL (14). *HLA-DMB* plays a critical role in antigen presentation by catalyzing the release of class II HLA-associated invariant chain binding sites for acquisition of antigenic peptides (15). It is known that lymphocytes in CLL express high levels of class II antigens whereas mature myeloid leukemias are e.g. HLA-DR negative (16, 17). Therefore, the differential expression of *HLA-DMB* in CML as compared to CLL illustrates well the differential expression of cell surface MHC class II molecules. *NCOA1* plays a critical role in STAT3 and STAT6 pathways and was expressed higher in CLL as compared to ALL suggesting an inhibitory effect of STAT6-mediated transactivation in CLL (18). A member of the tumor necrosis factor receptor family, whose surface expression has already been reported in CLL (19), *CD27*, was identified to assign samples either ALL or CLL. We also detected *LCN2* that was shown to be a modulator of inflammation regulated by interleukin-9 with highest expression in CML samples (20). *IRF4*, an immune system-restricted interferon regulatory factor that is required for lymphocyte activation showed no expression in CML while it was expressed in normal BM. Recently, an increase of IRF4 levels in CML patients demonstrated an association with a good response to interferon-alpha therapy (21). Several other proteins (*DEFA3*, *SGP28*, *CAMP*, *CLC*) are known to be stored in the granules of neutrophils and allowed assignment of leukemic samples to the CML type if highly expressed (22-25).

The second step of our approach was to build up a classifier for the identification of AML subtypes genetically defined according to the WHO classification, i.e. AML with t(8;21), with t(15;17) with inv(16), and with 11q23-translocations involving the MLL gene, respectively. In addition, a category 'other' was analyzed comprizing AML with normal karyotype (n=3), AML with complex aberrant karyotype (n=4), and AML with trisomy 8 as sole abnormality (n=3), respectively. A set of 25 most informative genes was identified based on pairwise comparisons and one-versus-all (OVA) comparisons. None of these genes had already been identified for the classification of the four leukemia types and normal BM as described above. As shown in Figure 11b, distinct AML subgroups cluster together due to homogeneous expression profiles. This classification model showed 100% classification accuracies in 14/15 comparisons (440 individual assignments). In

one OVA comparison, 'other' versus all other AML, 54/55 samples were assigned correctly. The missclassification of one sample may also reflect the large heterogenity of both groups.

The following genes were identified in OVA comparisons and discriminate distinct AML subtypes. The gene most valuable for prediction of AML M4eo with inv(16) was *MYH11*. Its higher expression as compared to all other AML most probably is due to hybridization of the M4eo-specific fusion transcripts *CBFß-MYH11* to corresponding *MYH11*-oligonucleotides represented on the microarray (26). Likewise, the higher expression of *CBFA2T1* (formerly *ETO*) in AML with t(8;21) may be due to a similar effect of hybridization of the subtype-specific *AML1-ETO* fusion transcript (27). Another highly characteristic gene for t(8;21) positive AML was *POU4F1*, which has been described to play an important role in retinal ganglion cell differentiation and has recently been shown to confer an oncogenic potential when co-transfected with *H-RAS* (28). Furthermore, it was shown to be highly expressed in neuro-epithelioma and ewing sarcomas (29). Another member of this transcription factor family, *POU2F2*, was able to discriminate between t(11q23)/MLL versus group 'other'. A related gene, *POU2AF1*, has recently been reported to be underexpressed in acute leukemia with t(11q23)/MLL-rearrangement (5). The most informative genes in our approach discriminating AML with t(11q23)/MLL-rearrangement from all other AML subtypes were *SOCS-2* and *MBNL*. Generally, *SOCS-2* shows a higher expression level in AML with t(11q23)/MLL-rearrangement and is known to play a role in cytokine-induced signaling pathways (30). Similarly, *MBNL* shows a higher expression in AML with t(11q23)/MLL-rearrangement as compared to all other AML samples. Its encoded protein as well as other MBL family members are localized in the nucleus and share a Cys3His zinc finger motif (31). MBL proteins occur in several isoforms due to alternative splicing (32) and may have different functions as has been shown for *HOX* genes (33). *HOXA9* has been reported to be highly expressed in leukemia with MLL-rearrangements (5). In contrast, expression of *HOXB5* is characteristic of AML group 'other' as compared to all other AML subtypes in our data. The most important genes discriminating AML with t(15;17) from all other AML subtypes were *ARGHGAP4* and *CTSW*. ARGHGAP4 is predominantly expressed in hematopoietic cells but showed a lower expression level in AML with t(15;17) as

compared to all other AML subtypes. It encodes a member of signaling proteins involved in regulation of small GTP-binding proteins of the RAS-superfamily, which themselves play an important role in cell cycle and apoptosis (34). *CTSW* encodes for a recently described papain-like cysteine protease, which is predominantly expressed in NK cells and to a lesser extent in cytotoxic lymphocytes. It may represent a putative component of the endoplasmatic reticulum resident proteolytic machinery (35). A survey about the expression levels of genes in the AML subtypes can be found in Fig. 12a-d

Subclassification of ALL comprizing the three B-lineage groups ALL with t(9;22), with t(4;11), or with t(8;14) was analyzed next and compared with T-lineage ALL expression profiles. All samples were classified correctly on the basis of 19 genes (Fig. 11c). This set included *TRB*, which was already described to distinguish between CLL and CML (Table 22).

In detail, the genes encoding for the T cell receptor beta subunit and T cell surface CD3 delta chain (*TRB*, *CD3D*) were identified as highly indicative of T-ALL as compared to both ALL with t(9;22) and all other ALL subtypes. This is in line with standard diagnostics of T-ALL by immunophenotyping where these antigens comprize the most specific ones (36). Similarly, *MME* (formerly *CD10*) was highly expressed in ALL with t(9;22) only. This on the one hand may reflect that t(9;22) is observed in common-ALL and in pre-B ALL only. On the other hand, this data again demonstrates that the gene used for diagnostic purposes in flow cytometry, *MME*, may be highly indicative of these ALL subtypes in comparisons to the more immature B-lineage ALL, i.e. pro-B ALL, as well as the mature B-ALL and the T-ALL. Furthermore, the identification of connective tissue growth factor (*CTGF*) as a specific marker for ALL with t(4;11) adds to previous data demonstrating its increased gene expression in childhood ALL in general (37). The glucocorticoid receptor beta has been shown to be highly expressed in ALL with t(4;11) but not in t(9;22) positive ALL. This is in line with the particularly poor prognosis of the latter subtype since response to corticoid therapy is one of the most powerful prognostic factors in ALL (38, 39). In addition, we speculate that new treatment options may be realized for T-ALL based on the high expression of adenosine deaminase (*ADA*) in this subtype. Inhibitors of *ADA* have been shown to be effective in indolent T-cell lymphomas but have not yet been evaluated in T-ALL (40). One

cytokine differentially expressed between t(8;14) positive ALL and T-lineage ALL was *SCYA3*. We recommend testing the monitoring of its protein expression as a supplemental antigen useful for immunophenotypical identification of t(8;14) positive ALL. Finally, in ALL carrying t(4;11) *v-myb* is highly expressed and may thus be involved in the pathogenesis of this subtype. In general, a role of v-myb has been described for the transformation of myelomonocytic cells (41). A survey about the expression levels of genes in the AML subtypes can be found in Fig. 12e-12i.

At least, we intended to separate t(9;22) positive from t(9;22) negative ALL. Our data contained two genes encoding for *ADCY3* and the hypothetical protein *KIAA1013* which were sufficient for the 100% correct assignments of 18 analyzed cases. Both genes showed a higher expression in t(9;22) positive as compared to t(9;22) negative ALL. Additionally, distinguishing B-lineage from T-lineage ALL, *CD3D* and *TRB* repeatedly showed their usefulness as T-ALL marker genes as already described in Figure 11c (18/18 correct individual assignments).

Generally, chromosomal aberrations are strongly associated with morphological characteristics. However, there are two chromosomal aberrations which are observed in both myeloid and lymphatic neoplasms, i.e. t(11q23)/MLL and the t(9;22). The t(9;22) occurs in ALL and CML, and t(11q23)/MLL is observed in ALL and AML, respectively. Analyzing gene expression signatures of both t(9;22) positive ALL and CML we identified two genes, which allowed 17/17 correct lineage assignments. *CD74* plays a critical role in MHC class II antigen processing and demonstrated a lower expression in t(9;22) positive CML (42). This may also explain the relationship between the low MHC class II antigen presentation in CML in general and fits well to the recognized lower *HLA-DMB* expression in CML as compared to CLL (Table 1). *CAPN3* is a member of the papain superfamily and was higher expressed in CML discriminating them from t(9;22) positive ALL [see (Note_ 38894_g_at)].

In addition, our results indicate that the expression signatures of two genes, *CD24* and *CTGF*, are sufficient for 14/14 correct assignments of the t(11q23)/MLL positive leukemias either to ALL or to AML. Thus, in both scenarios lineage assignment can be accomplished based on specific gene expression signatures despite the same underlying chromosomal aberrations.

Taken together, these data demonstrate the utility of gene expression profiling using microarrays for diagnosis of leukemia. In total, 11 different leukemia entities could clearly be distinguished from each other and from normal BM, respectively. These leukemias are associated with highly differing prognoses and require specific treatment strategies. By performing these analyses on a single platform requiring basic molecular biological methods, this approach guarantees broad access to high-quality diagnosis of leukemia. The robust gene expression analysis with high diagnostic accuracy can substitute the combination of cytomorphology, cytogenetics, immunophenotyping, and molecular biological methods used today. Compared to the combination of methods used so far, this approach also reduces costs. In order to introduce diagnostical genomics into routine clinical practice, prospective trials in parallel to conventional methods are necessary to prove the reliability in a large cohort of patients. Furthermore, gene expression patterns will allow the additional subclassification of leukemia especially in subtypes with no specific cytogenetic markers and the identification of deregulated master genes within distinct leukemia entities can guide the way to new therapeutic approaches.

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Notes of Example 3

[see (Note1_Golub method)]

When comparing two groups of microarray experiments, Golub's method sorts the genes with respect to the signal-to-noise ratio of gene x: $S_x = (\mu_1-\mu_2)/(\sigma_1+\sigma_2)$, where μ_k and σ_k denote the mean expression and standard deviation of gene x in group k. According to a specified number of "informative" genes (e.g. 20) the best discriminating genes are selected. For each informative gene a decision limit is calculated as $b_x = (\mu_1+\mu_2)/2$. To classify a new sample of an independent test set, the gene expression levels of informative genes are taken and for each gene x and sample y a so-called vote is calculated as $V_x = S_x (g_x^y - b_x)$, where g_x^y denotes expression level of gene x in sample y. The votes of all informative genes are summed up ("weighted voting") and depending upon the sign of this sum the new sample is classified as group 1 or group 2. The *confidence* in the prediction is calculated as $|\Sigma V_x / \Sigma |V_x| |$.

However, the decision limit proposed by Golub does not provide optimal classification accuracy in all situations. Importantly, when the standard deviation of expression levels within the two groups are very different, the decision limit is biased towards the group with the higher standard deviation. A decision limit for a particular gene can be considered optimal, if it achieves maximum classification accuracy for a given dataset. By determining systematically classification accuracies for a set of possible decision limits, an optimal decision limit can be

calculated. We selected an optimal decision limit from the following set of decision limits L_x: $L_x = \{ (g_x^y + g_x^{y-1})/2 \mid 1 < y <= n \}$ where g_x^y denotes expression level of gene x in sample y, n denotes the total number of samples in the training set.

Additionally, we applied an heuristic approach to select a minimal set of discriminative genes, which provides maximum classification accuracy in leave-one-out-crossvalidation. We applied for a given set of 20 informative genes weighted voting as described above and the classification accuracy was calculated by crossvalidation. Therefore, our algorithm consists of the following steps: (i) Calculate the top 20 discriminating genes according to the signal-to-noise ratio. (ii) Calculate classification accuracy and confidence based on optimal decision limits for each of the top 20 genes (iii) Select the gene which provides best classification accuracy and confidence out of step 2. (iv) Test for each of the remaining 19 genes, whether adding this gene to the model improves accuracy and confidence; if the gene improves accuracy and confidence, it is added to the weighted voting model, otherwise it is discarded.

In detail, this method can be described as follows:
Example 3 - Subheading to Note1_Golub method: Abstracts

Differentially expressed genes can potentially be used in medical diagnostics, if the gene expression patterns are reliable and specific for a particular disease. *diffgenes* is a program to identify differentially expressed genes in microarray experiments. Its algorithm is based on the method proposed by Golub, but contains two improvements: an optimized decision limit per gene and a minimal set of discriminative genes.

The new method was applied to a human dataset from the domain of cancer research consisting of 103 microarrays with 12625 genes each. *diffgenes* outperforms Golub's method clearly both in terms of accuracy and confidence of classifications. The biological validation of the results is facilitated, because *diffgenes* identifies a very small number of candidate genes (typically < 5). Microarray datasets can be analyzed with *diffgenes* on the Internet at http://martin-dugas.de/diffgenes/

Example 3 - <u>Subheading to Note1_Golub method: Introduction</u>

Microarrays are used in ongoing research to characterize disease processes on a molecular level. Gene expression analysis enables to identify new subtypes within known diseases with prognostic relevance for the patients [Alizadeh 2000].

For interpretation of the wealth of data - more than 10.000 parameters per experiment - it is advisable to integrate microarray data with detailed clinical information. For applications in medical diagnostics, significant associations between gene expression profiles and sample groups resulting in classification accuracies in the range of 70 - 80% are not sufficient; for diagnostic purposes at least 95% classification accuracy is required.

If a certain disease is characterized by a specific gene product, e.g. a pathologic fusion gene, a precise measurement of the expression of this particular gene should be a reliable marker for the disease. Therefore in a diagnostic setting, very few and specific genes would be desirable.

However, for many diseases the precise molecular pathogenesis is not yet known. In addition, the function of many genes on currently available microarrays like Affymetrix GeneChip^R is still unclear.

Therefore microarray data should be analyzed and interpreted carefully. By integration of data from different diagnostic modalities (morphology, PCR, FISH, clinical data) the biological plausibility and consistency of microarray data can be verified.

Example 3 - **Subheading to Note1_Golub method: Methods**
Example 3 - **Subheading to Note1_Golub method: Golub's method**

When comparing two groups of microarray experiments, Golub's method sorts the genes with respect to the signal-to-noise ratio of gene x: $S_x = (\mu_1-\mu_2)/(\sigma_1+\sigma_2)$, where μ_k and σ_k denote the mean expression and standard deviation of gene x in group k.

According to a specified number of "informative" genes (e.g. 20) the best discriminating genes are selected. For each informative gene a decision limit is calculated as $b_x = (\mu_1+\mu_2)/2$. To classify a new sample of an independent test set,

the gene expression levels of informative genes are taken and for each gene x and sample y a so-called vote is calculated as $V_x = S_x (g_x^y - b_x)$, where g_x^y denotes expression level of gene x in sample y. The votes of all informative genes are summed up ("weighted voting") and depending upon the sign of this sum the new sample is classified as group 1 or group 2. The *confidence* in the prediction is calculated as $|\Sigma V_x / \Sigma |V_x| |$ .To assess the significance of each gene, a permutation test is performed, which determines signal-to-noise ratios when class labels are permuted randomly. To assess the robustness of the classifier, a leave-one-out crossvalidation is performed. *Accuracy* is the rate of correctly classified test samples. Further details are contained in [Golub 1999], [Pomeroy 2002, Supplement].

Example 3 - <u>Subheading to Note1 Golub method: An optimized decision limit</u>

The decision limit proposed by Golub does not provide optimal classification accuracy in all situations. As can be seen in Figure 13a, when the standard deviation of expression levels within the two groups are very different, the decision limit is biased towards the group with the higher standard deviation.

A decision limit for a particular gene can be considered optimal, if it achieves maximum classification accuracy for a given dataset. By determining systematically classification accuracies for a set of possible decision limits, an optimal decision limit can be calculated. The *diffgenes* program selects an optimal decision limit from the following set of decision limits L_x:

$$L_x = \{ (g_x^y + g_x^{y-1})/2 \mid 1 < y <= n \}$$

where g_x^y denotes expression level of gene x in sample y, n denotes the total number of samples in the training set.

Example 3 - Subheading to Note1_Golub method: A minimal set of discriminative genes

Golubs method selects an arbitrary number of "informative" genes to discriminate between two classes of samples according to their signal-to-noise ratio, typically in the range of 10 to 50 genes. Choosing too many genes carries the risk of overfitting, which causes poor generalization features of the model. Therefore *diffgenes* applies an heuristic approach to select a minimal set of discriminative genes, which provides maximum classification accuracy in leave-one-out-crossvalidation. I.e. for a given set of genes weighted voting as described by Golub is applied and the classification accuracy is calculated by crossvalidation.

The *diffgenes* algorithm consists of the following steps:

1. Calculate the top 20 discriminating genes according to the signal-to-noise ratio

2. Calculate classification accuracy and confidence based on optimal decision limits for each of the top 20 genes

3. Select the gene which provides best classification accuracy and confidence out of step 2.

4. Test for each of the remaining 19 genes, whether adding this gene to the model improves accuracy and confidence; if the gene improves accuracy and confidence, it is added to the weighted voting model, otherwise it is discarded.

Example 3 - Subheading to Note1 Golub method: Results

The method was applied to a new human dataset from the domain of cancer research consisting of 103 Affymetrix Genechip(R) microarrays with 12625 genes each. Table 23 presents an analysis of 18 samples class A versus 85 samples class non-A (Description of Table 23: Analysis of 18 samples class A versus 85 samples class non-A. On the left the analysis according to Golub is presented for 20 informative genes. The crossvalidation accuracy is 0,87, confidence 0,77. Samples, where crossvalidation failed, are listed. For each gene signal to noise ratio, p-value (significance obtained from permutation test) and decision limit are provided. On the right the same data set is analyzed using *diffgenes*. By selection

of 3 genes (marked with asterisks) out of the top 20 genes and selecting optimized decision limits, the crossvalidation accuracy reaches 0,96, confidence 0,88.). Based on 20 informative genes Golub's method results in a crossvalidation accuracy of 0,87 (confidence 0,77); *diffgenes* achieves with three genes out of the top 20 set a crossvalidation accuracy of 0,96 (confidence 0,88). The same analysis was performed for one versus all (OVA) and all pairs (AP) comparisons in this dataset consisting of 5 different classes. Figure 13b presents accuracy and confidence obtained by both methods: *diffgenes* outperforms Golub's method clearly both in terms of accuracy and confidence of classifications. The same comparative approach was applied to two datasets in cardiology and cell biology consisting of 44 and 67 microarrays. The results concerning Golub's method and *diffgenes* were very similar (data not shown).

Example 3 - Subheading to Note1 Golub method: **Discussion**

There are two major challenges in the analysis of microarray data: the number of variables (genes) is much higher than the number of individual samples and the correlation structure of the parameters is widely unknown.

Golub's method to analyse microarray data has been applied to important medical datasets [Armstrong 2002]. Recently many different approaches have been applied to microarray data: Classical statistical techniques like ANOVA with adjustment for multiple testing, significance analysis of microarrays (SAM) [Tusher 2001] , selection of discriminative genes with support vector machines (SVM), neural networks and many more. This indicates that the underlying problem is important and non-trivial; a comparison of different methods is needed. Robustness of the generated mathematical models is an important issue, therefore bootstrap procedures and permutation tests are applied.

For medical diagnostics differentially expressed genes are of interest, but the sensitivity and specificity for particular diseases must be validated prospectively in larger patient cohorts. *diffgenes* is an extension of Golub's method to improve classification accuracy, which is very relevant in a diagnostic setting. The optimized decision limit plays an important role, because the situation presented in Figure 13a is quite common in biological contexts: group 1 represents samples, where the expression of gene x is repressed while gene x is activated in group 2. The biological validation of the results is facilitated, because *diffgenes* identifies a very small number of candidate genes (typically < 5).

Emphasis must be placed on verification of results by other diagnostic procedures, because the selected "important" genes are not only dependent on the statistics procedure, but also on the preprocessing of data. In our setting by integration of microarray analysis with other laboratory modalities (morphology, cytogenetics, molecular genetics, immunphenotyping) and clinical data the plausibility and consistency of results could be evaluated, therefore we are optimistic, that the demanding requirements for medical diagnostics can be fulfilled with microarray technology in the near future.

Example 3 - Subheading to Note1 Golub method: References

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EXAMPLE 3 - [see (Note2_ leave-one-out crossvalidation)]

To assess the significance of each gene, a permutation test is performed, which determines signal-to-noise ratios when class labels are permuted randomly. To assess the robustness of the classifier, a leave-one-out crossvalidation is performed. *Accuracy* is the rate of correctly classified test samples.

EXAMPLE 3 - [see (Note_ 38894_g_at)]

The second top-ranked gene was represented by the Affymetrix probe set identifier: 38894_g_a. However, no clear gene assignment was possible for this informative prove set. Therefore, CAPN3 was chosen.

Example 4: PNAS

EXAMPLE 4 - ABSTRACT

Acute myeloid leukemia (AML) is a heterogeneous group of genetically defined diseases. Their classification is important with regard to prognosis and treatment. We performed microarray analyses for gene expression profiling on bone marrow samples of 37 patients with newly diagnosed AML. All cases had either of the distinct subtypes AML M2 with t(8;21), AML M3 or M3v with t(15;17), or AML M4eo with inv(16). Diagnosis was established by cytomorphology, cytogenetics, fluorescence-in-situ hybridization, and RT-PCR in every sample. By using two different strategies for microarray data analyses, this study for the first time revealed a unique correlation between AML-specific cytogenetic aberrations and gene expression profiles.

EXAMPLE 4 - INTRODUCTION

Acute myeloid leukemia (AML) is a heterogeneous group of diseases with respect to biology and clinical course. Since the introduction of the FAB-classification in 1976 diagnosis and classification have been based on cytomorphology and cytochemistry(1). As other techniques like immunophenotyping, cytogenetics, and molecular genetics contributed to the definition of AML subtypes the FAB-classification was updated. In 1999 the WHO classification for tumors of hematopoietic and lymphoid tissues was proposed. In an attempt to define biologically homogeneous entities which have clinical relevance morphologic, immunophenotypic, genetic and clinical features were incorporated(2, 3).

For optimal treatment approaches both a precise diagnosis and prognostic parameters that determine response to therapy and survival are needed. So far, the karyotype of the AML blasts is the most important independent prognostic factor. A favorable outcome under currently used treatment regimens with cure rates from 50% up to 85% was observed in several studies in patients with a) t(8;21)(q22;q22) occuring mostly in FAB subtype AML M2, b) inv(16)(p13q22) associated with AML M4eo and c) t(15;17)(q22;q11-12) associated with AML M3 and AML M3v(4-6). In contrast, chromosome aberrations with an unfavorable clinical course are -5/del(5q), -7/del(7q), inv(3)/t(3;3) and complex aberrant

karyotypes with cure rates of less than 10%(7, 8). The remainder AML patients are assigned to a prognostically intermediate group. This latter group is very heterogeneous because it includes patients with a normal karyotype as well as those with rare chromosome aberrations and yet unknown prognostic impact.

Besides their prognostic impact genetic aberrations are involved in the pathogenesis of leukemia. While for unbalanced cytogenetic aberrations the heterogeneous pathogenetic mechanisms have not yet conclusively been determined, several studies provide strong evidence for the central pathogenetic role of leukemia-specific fusion genes that are generated by the above mentioned balanced abnormalities(9-12). Therefore it can be postulated that AML with balanced abnormalities most probably display a homogeneous gene expression profile and thus are promising candidates for microarray analyses.

In a pivotal study, gene expression profiles were analyzed in bone marrow samples of 27 ALL and 11 AML. A set of 50 genes out of 6,817 analyzed genes was sufficient to discriminate ALL and AML. By leave-one-out cross-validation it was possible to correctly classify 36 out of 38 acute leukemia cases. A class predictor could automatically determine new leukemia cases out of an independent test set as belonging to the myeloid or the lymphoid lineage. Thus, these results demonstrated the possibility of cancer classification based on gene expression profiling(13). In a further approach comparing AML with trisomy 8 and AML with normal karyotype expression profiling revealed fundamental biological differences in AML with isolated trisomy 8 and normal cytogenetics(14). More recently, acute lymphoblastic leukemias (ALL) with translocations involving the *MLL* gene could be separated from ALL cases without MLL translocations and from cases with AML by gene expression profiling(15).

The aim of our investigation was to answer the question whether a leukemia specific genotype is associated with a distinct gene expression profile. Therefore, we analyzed three distinct genetic subtypes of acute myeloid leukemia: t(8;21)(q22;q22), inv(16)(p13q22) and t(15;17)(q22;q12) which lead to subtype specific fusion genes *AML1-ETO*, *CBFB-MYH11* and *PML-RARA*, respectively. They are specifically associated with four distinct morphological subtypes according to the FAB-classification: AML M2, AML M4eo, AML M3 and AML M3v(16-18). We performed microarray analyses on a cohort of leukemia samples (n=37) and applied several methodologies to evaluate genes which allowed an assignment to the corresponding type of cytogenetic aberration for classification.

This is the first time that AML-specific cytogenetic aberrations can be correlated with corresponding gene expression profiles and vice versa.

EXAMPLE 4- METHODS

Example 4- Selection and characterization of leukemia samples

For this investigation we selected bone marrow (BM) samples from 37 AML patients representing four morphological and three underlying cytogenetic subgroups. All cases were sent for reference diagnostics to our laboratory and registered in our leukemia database(19). Samples were received either locally or by overnight mail. All samples were newly diagnosed *de novo* AML and were characterized by cytomorphology, cytogenetics, FISH, and molecular genetics in each case. Gene expression analyses were performed on cells remaining from the diagnostic samples. Samples had been lysed immediately, frozen and were stored at -80°C from one to 34 months until preparation for gene expression analysis.

Example 4- Cytomorphology

Analysis was based on May-Grünwald-Giemsa stain, myeloperoxidase reaction, and non-specific esterase reaction using alpha-naphthyl-acetate. All staining from bone marrow and blood was performed routinely according to standard procedures(20). The cytomorphologic diagnosis followed the criteria of the FAB classification and the new WHO classification(1, 3, 18).

Example 4- Cytogenetics

Chromosome analyses were performed on bone marrow or peripheral blood samples according to standard protocols(21). Metaphases were analyzed for G-bands using a modified GAG-banding technique as described elsewhere(22). Twenty to 25 metaphase cells were analyzed. The chromosomes were interpreted according to the International System for Human Cytogenetic Nomenclature(23).

Example 4- Fluorescence in situ hybridization (FISH) on interphase nuclei

FISH was performed on interphase nuclei on bone marrow smears or on slides prepared for cytogenetic analysis. For interphase-FISH at least 100 interphase nuclei were evaluated. FISH was carried out using commercially available *AML1-ETO*, *PML-RARA* and *CBFB* probes (VYSIS, Downers Grove, Il, USA). The signals were evaluated with an Axioskop^R (Zeiss, Jena, Germany). For documentation the analyzing system ISIS^R (MetaSystems, Altlussheim, Germany) was used.

Example 4- RNA isolation and Reverse-transcription-polymerase-chain-reaction (RT-PCR)

Mononuclear cells were isolated by a Ficoll gradient separation. $1x10^7$ cells were lysed in RLT-buffer (Qiagen, Hilden, Germany) and total RNA was extracted with a RNeasy-kit (Qiagen) according to the manufacturers instructions. RNA was eluted in 50 μl of elution buffer.

Five μl of the total RNA, an equivalent quantity of $1x10^6$ cells or about 1 μg of RNA were reversely transcribed in a 40 μl reaction using 300 U of Superscript^R (LifeTechnologies, Karlsruhe, Germany) and random hexamers (Pharmacia, Freiburg, Germany).

PCR for the specific *AML1-ETO*, *CBFB-MYH11*, or *PML-RARA* fusion transcripts were performed as has been described(24). For each sample an *ABL* specific RT-PCR was performed to control the integrity of RNA using primers ABL5´: 5´-GGCCAGTAGCATCTGACTTTG-3´ and ABL3´: 5´-ATGGTACCAGGAGTGTTTCTCC-3´. Strict precautions were taken to prevent contamination. Water instead of cDNA was included as a blank sample in each experiment. Amplification products were analyzed on 1.5% agarose gels stained with ethidium bromide.

Example 4- Microarray experiments

For microarray analysis the GeneChip® System (Affymetrix, Santa Clara, California) was used. The targets for GeneChip® analysis were prepared

according to the current Expression Analysis Technical Manual. Briefly, lysates of the leukemia samples were homogenized (QIAshredder, Qiagen, Hilden, Germany) and total RNA extracted (RNeasy Mini Kit, Qiagen). Normally, 10 μg total RNA isolated from $1x10^7$ cells was used as starting material in the subsequent cDNA-synthesis using oligo$[(dT)_{24}T7promotor]_{65}$ primer (cDNA Synthesis System, Roche Diagnostics, Mannheim, Germany). The cDNA was purified by phenol:chlorophorm:IAA extraction (Ambion, Austin, Texas) and acetate/ethanol precipitated over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the *in vitro* transcription (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO, Farmingdale, USA). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 μg was fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip® microarrays. Before hybridization onto U95Av2, Test3 microarrays (Affymetrix) were chosen for monitoring of the integrity of the cRNA. Washing and staining of the probe arrays were performed according to the current protocols (Micro_1v1, EukGE-WS2v2). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the microarrays as detected by confocal laser scanning according to the manufacturers recommendations. Thirty-two out of 37 hybridization cocktails demonstrated high quality cRNA characteristics (Test3 probe arrays: 3'/5' ratio of *GAPDH* probe sets ≤3.0) and were selected for building up class prediction models.

Example 4- Class separation by principal component analysis

Potential clusters corresponding to the genetic subgroups were visualized applying a two-step approach. The data were scaled from each array to a target intensity value 50 (Affymetrix Microarray Suite 4.0.1) in order to be able to perform inter-array comparisons. All data were permutated 100 cycles using the multiclass response parameter of the Significance Analysis of Microarrays algorithm (SAM)(25) (http://www-stat.stanford.edu/~tibs/SAM/index.html). The total set of 12,600 genes was reduced to the significant differentially expressed genes. In a second step, the reduced set of genes was prepared for principal component analysis (PCA) and analyzed with J-Express(26) (http://www.molmine.com/). For

visualization in a two-dimensional plot we chose the first two principal components as they captured most of the variation in the original data set.

Example 4- Class prediction by weighted voting(13)

We adapted a previously described method to reduce the number of candidate genes that could distinguish between the three different cytogenetic AML subgroups(13). Briefly, to avoid division by zero or negative numbers as occurs due to the expression algorithm (Affymetrix Microarray Suite 4.0.1) we set all average fluorescence intensities of 1 or less to 1. Then, gene expression levels were log-transformed. Performing pairwise comparisons (A vs. B), for each gene g P(g,c) values and votes (defined by: P(g,c)=(m1(g)-m2(g))/(s1(g)+s2(g))) were calculated based on mean expression levels (m) and standard deviations (s) in the respective cytogenetic subgroup. Subsequently, votes were summed and prediction strength (PS) values reflected the margin of victory in the direction of either cytogenetic group A or B of the pairwise comparison. PS values range between 0 and 1, values >0.45 demonstrate significance (according to the permutation test). The relevance of selected genes was assessed by performing leave-one-out cross-validation. Only those genes that were contained in all cross validation classifiers were considered important. To determine a random association between genes we performed a permutation test (100 cycles). Because the number of informative genes, which are required to discriminate between samples, is unknown, we applied this method for different numbers of informative genes (range: 2 to 200). The minimal set of genes which provided optimal classification accuracy together with the highest prediction strength was selected to avoid overfitting. To visualize the identified genes and check their suitability for class separation a hierarchical cluster analysis was performed utilizing J-Express(26) (cluster method: average linkage; distance metric: euclidean). The accuracy of this class prediction model was validated on an independent test set of five cases of AML not fulfilling the cRNA high quality criterion as outlined above.

Example 4- Multiple-tree classifier

As basic units in this classifier, classification trees are used(27-29). The optimal number of trees has been determined to be 15 (data not shown). Class votes of these trees are aggregated by a vote-by-majority rule. The classifier was fed with gene expression intensity values from a set of 973 genes that had been chosen based on their r statistic:

$$r = \frac{\sum_{i=1}^{k} |\mu_i - \overline{\mu}|}{\sum_{i=1}^{k} \sigma_i}$$

where μ_i refers to the class averages, $\overline{\mu}$ to the overall average, σ_i to the within-class standard deviation, and summation is carried out over all k classes. The threshold was set to $r > 0.75$. Classification trees were constructed as follows: tree building was performed while restricting trees to contain no more than *n*-1 nodes to discriminate between n classes. The C5.0 algorithm was used(28). The variables (gene expression intensities) used for tree construction were eliminated from the data set, and a new tree was calculated based on the truncated data set. This procedure was iterated until the predetermined number of trees had been reached. The accuracy of the multiple-tree classifier was estimated by 10-fold cross validation(30) and on an independent test set of data from 5 bone marrow aspirates, where the quality of the corresponding cRNA preparation was slightly lower than the high quality standards required for the training set.

EXAMPLE 4 - RESULTS

Example 4- Characterization of leukemia samples

We investigated 37 AML cases representing three defined cytogenetic aberrations corresponding to four FAB subtypes: t(8;21)(q22;q22)/AML M2 (*n*=9), t(15;17)(q22;q12)/AML M3 or AML M3v (*n*=10, *n*=8), and inv(16)(p13q22)/AML M4eo (*n*=10). All cases were characterized by cytomorphology, cytogenetics, FISH, and RT-PCR (Fig. 14). All cases with AML and t(8;21) had AML M2, all with AML and inv(16) had AML M4eo, ten cases with AML and t(15;17) had AML M3, and eight cases with AML and t(15;17) had AML M3v. All patients showed these balanced abnormalities as the sole karyotype change. Using FISH analysis, more than 65% of cells demonstrated the specific signal constellation. The respective fusion transcripts were detected by RT-PCR in all samples. The median age of all

patients was 53 years (range, 19-82 years; male:female=15:22) and did not differ between the respective groups. AML subtypes M3 and M3v both carry the same chromosomal aberration but differ in morphological aspects like nuclear configuration, granulation, and clinical aspects like white blood cell count (WBC). The median WBC count was 20,000/μl (range, 800-168,000/μl) and was strikingly lower in patients with AML M3 as compared to all other patients (median, 6,200 vs. 36,500/μl, P=0.0002).

Example 4- Microarray analyses

The gene expression profiles of 37 AML samples were evaluated. Thirty-two hybridization cocktails demonstrated high quality cRNA characteristics (Test3 probe arrays: 3'/5' ratio of GAPDH probe sets ≤3.0) and were selected for building class prediction models: t(8;21)/AML M2 (n=7), t(15;17)/AML M3 or M3v (n=9, n=7), and inv(16)/AML M4eo (n=9). Five cases were primarily excluded (3'/5' ratios ranging between 3.9 and 5.4, see Methods) and were used for subsequent validations of the class prediction models: t(8;21)/AML M2 (n=2), t(15;17)/AML M3 or M3v (n=1, n=1), and inv(16)/AML M4eo (n=1).

Example 4- Class separation by principal component analysis

In order to visualize clusters corresponding to the three underlying genetic subgroups we applied a two-step approach. Based on a permutation test (100 permutations) we correlated our expression data to the three different cytogenetic parameters(25). We obtained 1000 significant genes. By principal component analysis we were able to clearly separate the three distinct chromosomal aberrations t(8;21), t(15;17), and inv(16) (Fig. 15)(26). These data suggest that genetically defined AML subtypes can be specified and identified based on their gene expression profiles.

Example 4- Class prediction by weighted voting(13)

In order to identify the genes which enable the accurate discrimination of these subgroups, we applied the data analysis methodology introduced by Golub et al.(13). We selected the minimal set of genes which provided optimal classification accuracy together with the highest prediction strength to avoid overfitting. Thirteen genes were sufficient to separate these AML subtypes with high precision (Table 24; Table 24 shows that a minimal set of 13 genes (GenBank accession numbers are given) is sufficient for accurate class prediction with optimal classification accuracy and highest prediction strength. Comparisons (A vs. B) were performed either between two distinct subtypes or between one distinct subtype and all other subtypes (=remainder), respectively. As calculated from pairwise comparisons, positive P(g,c) values indicate a higher expression in first class listed, negative P(g,c) values a higher expression in second class listed, respectively). GenBank accession numbers and detailed descriptions of the genes are given in table 25 (Table 25: Thirty-six genes separate accurately three distinct cytogenetic AML subtypes. GenBank accession numbers, approved human gene nomenclature symbol (*=not approved) and description of the function are presented. Six genes are included in the minimal set of both weighted voting according to Golub et al.(13) (total=13) and multiple-tree classifiers (total=29).

All 32 clinical samples could be assigned to their corresponding cytogenetic subtype with best accuracy in leave-one-out cross-validation (1.0). Prediction strength values ranged from 0.91 to 0.98 (Table 24). To illustrate these results we applied hierarchical clustering(31). The resulting dendrogram clearly demonstrates the capacity of this subset of genes to separate all AML cases according to their cytogenetic aberration (Fig. 16). This demonstrates that class prediction of a chromosomal aberration in AML is feasable solely based on gene expression data.

For external validation, we tested whether primarily excluded samples could also be accurately assigned to their specific cytogenetic category. Despite their non-optimal cRNA quality, all 5 cases were correctly classified with high prediction strength (0.76,1.00,1.00,1.00,1.00).

Example 4- Class prediction by multiple-tree models

As a second and independent methodological approach we developed a multiple-tree classifier to separate the three genetically defined subtypes based on the expression level of a minimal set of genes. In short, we computed classification trees to discriminate between the different AML subclasses. To avoid overfitting of a singular tree model, we computed a multiple-tree model using an iteratively reduced set of genes. For each tree, we used only those genes that have not been used by the previously computed classification tree. The procedure is stopped when a predetermined number of trees has been reached. For this study, the optimal number of trees was calculated to be 15. The votes of the 15 trees were aggregated by a vote-by-majority rule. Equal votes for two of the three classes were counted as misclassification.

The classifier utilized the expression values of 29 genes (*MYH11* was identified twice by two different probe sets; Table 25) to discriminate between three classes, namely samples displaying t(15;17), t(8;21), and inv(16) (Fig. 17). The accuracy on the training set (n=32) was 100%, and on the independent test set (n=5) 100%. The average accuracy in ten-fold cross validation was 94%.

In summary, we identified 36 genes using two independent methodologies for class prediction in AML (Table 25). Six genes were described in both calculations, seven were found exclusively in the minimal set according to Golub et al.(13), and another 23 genes using multiple-tree classifiers.

Example 4- Correlation of phenotype and gene expression profile

We were able to demonstrate striking correlations between genotype and gene expression profiles in three genetically defined subgroups of AML. In addition, we answered the question, whether the cytogenetically identical AML with t(15;17) but appearing with two different phenotypes, AML M3 or AML M3v (Fig. 14), can also be separated by different gene expression patterns. We used 100-fold permutation of M3 (n=10) and M3v (n=8) data followed by principal component analysis and hierarchical cluster analysis based on 82 informative genes (data not shown). Separation into the corresponding two morphologically defined FAB subtypes M3 and M3v was possible in all cases (Fig. 18) and suggests also a close correlation between phenotype and gene expression profile.

EXAMPLE 4 - DISCUSSION

This is the first study to demonstrate an unequivocal association between disease-specific genetic alterations and distinct gene expression profiles. For each of the three analyzed clearly defined subtypes of AML (t(8;21), t(15;17), inv(16)) patterns of gene expression were identified that were homogeneous within all samples of the respective subgroups but clearly differed between these three subgroups. The analyzed samples represent disease subtypes that are specifically defined on the genetic and the phenotypic level by conventional diagnostics including cytomorphology, cytogenetics, and molecular genetics.

By applying two independent approaches for the analysis of microarray data, the present study demonstrates that AML samples from previously defined subtypes(3) can be classified adequately on the basis of gene expression profiles. It is intriguing that there is both sufficient coherence in gene expression within and difference between these subtypes to classify them with high accuracy even though the samples derive from the same myeloid cell lineage.

In order to correlate gene expression with cytogenetics Virtaneva et al. compared the expression status of 6,606 genes of AML blasts with normal cytogenetics and trisomy 8 as the sole abnormality. While in this study normal CD34+ cells clustered into a distinct group, AML with trisomy 8 and AML with normal karyotype intercalated with each other. Microarray analyses showed an overall increased gene expression of genes located on chromosome 8 suggesting a gene-dosage effect(14). AML with trisomy 8 is heterogeneous on the phenotypic level as it occurs in different FAB subtypes. In contrast, AML with t(15;17), inv(16) and t(8;21) show a very close correlation to distinct morphological subtypes. Furthermore, trisomy 8 is probably not a primary, disease-defining aberration leading to AML as it also occurs in addition to a variety of different cytogenetic and molecular genetic abnormalities(32, 33). In contrast to this study, Armstrong et al. compared samples of the more homogeneous group of ALL with *MLL* translocations to ALL without *MLL* translocations and to AML(15). They demonstrated that ALL with *MLL* translocations comprizes a distinct disease which can be classified robustly by gene expression profiling.

The main focus of the present analyses was the assessment of the differences between three highly characterized subgroups of AML defined by specific primary

chromosome aberrations. As anticipated, it was shown that AML with t(8;21) and AML with inv(16), which both involve alterations of the core binding factor-complex, are more related to each other as compared to AML with t(15;17)(34). Both phenotypically different subtypes of AML with t(15;17), AML M3 and AML M3v, cluster within one area. In an additional analysis, also the latter two subtypes were separated from each other based on their gene expression profiles. This data suggests the existence of further genetic and not yet identified alterations leading to the different phenotypes of AML M3 and AML M3v. One possible candidate gene is *FLT3* which is mutated more frequently in AML M3v than in AML M3 (67% vs. 19%, *P*=0.001)(35).

Several studies confirmed that gene expression profiles can be used for class prediction. This has been shown for acute leukemias, round blue cell tumors, and malignant melanomas(13, 36-38) as well as for different types of solid tumors using multi-class cancer classification(39). While the selection of different subgroups in these studies was performed using exclusively phenotypic criteria, other studies were based on genetically defined entities(40, 41). In the present study not only the discrimination of the three genetically defined AML subgroups was accomplished but also all these cases of AML were separated from normal bone marrow (data not shown)(42).

To develop a classifier two independent approaches were applied. While classification by weighted voting according to Golub et al.(13) allows the discrimination between the three classes based on a minimal set of 13 genes, the multiple-tree classifier utilizes 30 genes. As indicated by cross-validation, generalization properties are excellent for the multiple-tree classifier, i.e. it is likely to perform equally well on new, unseen samples. Furthermore, it can be easily extended to more than the three subclasses described in the present study.

Our classifiers contained genes already known to be primarily involved in the pathogenesis of the respective entities, namely *MYH11*(43) and *ETO*(44). Presumably, the detection of overexpression of *MYH11* in inv(16) cases and of *ETO* in t(8;21) cases relates to the detection of the fusion gene transcripts rather than of the wild type transcripts. The other genes identified belong to various functional categories. Their potential pathogenetic significance in AML has to be clarified yet.

It is expected that the extension of the present analyses to currently less well-defined AML will identify additional subgroups of AML with clinical relevance based on their gene expression profiles. The feasibility of such an approach has been demonstrated for the first time for diffuse large B-cell lymphoma(45). Alizadeh et al. have subdivided an entity previously considered homogeneous by various pathological methods into two not only new but also prognostically highly relevant subgroups. In two recent studies, gene expression profiling also in breast cancer revealed subgroups significantly differing in their prognosis(46, 47). With regard to AML, this approach may be most promising in AML with normal karyotype. This subgroup cannot be further defined on the cytogenetic level and is characterized by an intermediate prognosis possibly masking poor and favorable subgroups.

In addition, the current data may have major implications with regard to delineating aberrant gene expression pathways underlying the pathogenesis of AML. As has been shown in mantle cell lymphoma and medulloblastoma(48, 49) the extension of our analyses to all subgroups of AML should enable us to define the deregulated genes important for the initiation and the progression of AML. Finally, these analyses will promote the identification of new targets for specific treatment approaches.

EXAMPLE 4 - REFERENCES

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Example 6: Correlation of Protein Expression and Gene Expression in Acute Myeloid Leukemia

INTRODUCTION

The determination of the surface and cytoplasmic expression of characteristic proteins by flow cytometry (FC) is a common method applied to the diagosis and the subclassification of acute myeloid leukemias (AML)[1]. The oligonucleotide microarray analysis (MA) represents a novel technology for the simultaneous detection of the mRNA abundance of large numbers of genes[2,3]. Based on specific gene-expression patterns distinct disease entities have been identified[4-6]. Therefore MA may become of major importance as a diagnostic tool for AML in the near future[7,8]. However, up to now data on the correlation between protein expression levels and mRNA abundance are limited[9-12]. To analyze the relation of protein expression and mRNA abundance in AML we performed 450 individual comparisons of 29 genes in 25 patients with AML at diagnosis analyzed by FC and MA in parallel[13].

METHODS

Samples

Bone marrow samples from highly characterized patients with newly diagnosed and untreated AML were used. Samples had been analyzed by cytomorphology, cytochemistry, cytogenetics and molecular genetics in all cases and were characterized by either of the balanced chromosomal aberrations t(8;21), t(15;17), or inv(16) and the respective molecular and morphologic features[7]. The studies abide by the rules of the local Internal Review Board and the tenets of the revised Helsinki protocol.

Flow cytometry

The studies were performed on cells isolated from bone marrow by Ficoll-Hypaque density gradient centrifugation as described previously[14]. Applying triple-stainings and isotype controls monoclonal antibodies against 29 antigens were used in the following combinations as designed for diagnostic purposes (conjugated with the fluorochromes FITC, PE, and PC-5, respectively): CD34/CD2/CD33, CD7/CD33/CD34, CD34/CD56/CD33, CD11b/CD33/CD34, CD64*/CD4/CD45, CD15*/CD13/CD33, HLA-DR/CD33/CD34, CD34/CD135/CD33,

CD34/CD116/CD33, CD34/NG2/CD33, CD38/CD133**/CD34, CD61/CD14/CD45, CD36/CD235a/CD45, CD34/CD10/CD19, MPO***/LF***/cyCD15, TdT/cyCD22/cyCD3, TdT/cyCD79a/cyCD3. All antibodies were purchased from Immunotech (Marseilles, France), except for: * = Medarex (Annandale, NJ); ** = Milteny Biotech (Bergisch Gladbach, Germany); *** = Caltag (Burlingame, CA). The respective combinations of antibodies were added to $1x10^6$ cells (volume, 100 μl) and incubated for ten minutes at room temperature. The samples were then washed twice in phosphate-buffered saline (PBS) and resuspended in 0.5 ml PBS. FC analysis was performed using a FACSCalibur flow cytometer (Becton Dickinson, San Jose, CA). Analysis of list-mode files was performed by means of the CellQuest Pro Software (Becton Dickinson). Antigen expression was rated positive at a cut-off level of 20% of the cells within the mononuclear gate for membrane proteins and at a cut-off level of 10% for cytoplasmic antigens. Mean fluorescence intensity values were calculated for all events with fluorescence values higher than isotype controls.

Microarray experiments

For microarray analysis the GeneChip® System (Affymetrix, Santa Clara, California) was used. The targets for GeneChip® analysis were prepared according to the current Expression Analysis Technical Manual. Briefly, lysates of the leukemia samples were homogenized (QIAshredder, Qiagen, Hilden, Germany) and total RNA extracted (RNeasy Mini Kit, Qiagen). Normally, 10 μg total RNA isolated from $1x10^7$ cells were used as starting material in the subsequent cDNA-synthesis using oligo$[(dT)_{24}$T7promotor$]_{65}$ primer (cDNA Synthesis System, Roche Diagnostics, Mannheim, Germany). The cDNA was purified by phenol:chlorophorm:isoamylalcohol extraction (Ambion, Austin, Texas) and acetate/ethanol precipitated overnight. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the *in vitro* transcription (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO, Farmingdale, USA). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 μg were fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip®

microarrays. Before hybridization onto U95Av2, Test3 microarrays (Affymetrix) were chosen for monitoring of labelling efficiency and the integrity of the cRNA. Washing and staining of the probe arrays was performed according to the current protocols (Micro_1v1, EukGE-WS2v4). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the microarrays as detected by confocal laser scanning according to the manufacturers recommendations. In order to be able to compare different experiments the global
microarray intensities were scaled to a common target intensity. Furthermore, the mRNA abundance of the genes was qualitatively rated as a) present, b) marginal, and c) absent calls, respectively.

Statistics-

A total of 29 genes were analyzed in 25 patients with AML. The congruence of positivity and negativity of the expression of the respective genes as determined by FC and MA was analyzed for each gene in each individual patient. Comparisons of microarray intensities were performed by Mann-Whitney *U*-test. Analyses for bivariate correlations of mRNA and protein expression levels were performed by Pearson´s correlation using SPSS, Version 10.0.7.

RESULTS AND DISCUSSION

Twenty-five cases of AML were analyzed in parallel by FC and MA for the expression of 29 genes. Seven had AML M2 with t(8;21), 5 had AML M3 with t(15;17), 7 had AML M3v with t(15;17), and 6 had AML M4Eo with inv(16). A total of 450 comparisons of individual expression data obtained by both methods were performed. Of these, 399 (88.7%) revealed congruent results for protein expression and mRNA abundance (230 cases (51.1%) with positive expression and 169 cases (37.6%) with negative expression, respectively; table 26). In 30 comparisons (6.7%) MA detected positivity for mRNA expression (call: present) while the results of FC indicated negativity. In 21 cases (4.7%) protein expression was demonstrated by FC while no mRNA expression was detected by MA (call: absent).

Focussing on the genes most specific for the diagnosis of AML, i.e. myeloperoxidase, CD13, and CD33, a high correlation between protein expression and mRNA abundance was observed (congruence in 73 of 75 comparisons (97%)). In detail, all cases were rated positive for expression of myeloperoxidase and all but one were positive for both CD13 and CD33, respectively, by both methods. Furthermore, for most other genes essential for the subclassification of AML as well as for the distinction of AML from acute lymphoblastic leukemia and chronic leukemias the results obtained by both methods were always congruent (i.e., for CD10, CD22, CD7, CD133, CD116, CD11b, CD61, CD45, HLA-DR, NG2) or were congruent in the majority (117/140, 84%) of cases (CD79a, CD19, CD2, CD3, CD15, Lactoferrin, CD14, CD235a, CD135, CD34; Table 26).

Furthermore, the high correlations between protein expression and mRNA abundance were not limited to congruence in positivity but were significantly correlated also quantitatively. To proof this, the protein expression levels and mRNA abundance were compared by Pearson´s correlation in genes expressed in the majority of the analyzed cases. These comparisons revealed significant correlations for the fluorescence intensities as assessed by FC and MA for CD13 ($p=0.001$), CD33 ($p=0.034$), CD34 ($p=0.003$), CD45 ($p=0.015$), CD15 ($p=0.016$), and CD7 ($p=0.033$) and thus further underline the high coherence of expression patterns for both protein and mRNA (figure 19).

Thirty comparisons displayed mRNA expression and no protein expression. Due to the ongoing process of maturation (CD14, CD15) and due to the cross-lineage expression of the genes (CD3, CD19) the levels of mRNA abundance may have been to low to result in detectable protein expression levels using the described cut-off levels of 20% and 10%, respectively. This suggestion is supported by a quantitative analysis of mRNA expression data which shows relatively low albeit positive levels for the respective cases and genes (mean average fluorescence intensity, 46.7±54.5 in cases positive for CD14, CD15, CD3, or CD19 versus 389.4±831.0 in all positive cases, Mann-Whitney *U*-test: $p<0.001$) while at the same time protein expression amounts to a mean of 5±4%.

Twenty-one comparisons displayed positivity by FC and negativity of MA, which comprize 4.7% of all individual comparisons performed. These discrepancies most probably are due to: a) erythrocytic debris positive for CD36 interfering with the

acquisition of CD36 negative cells during flow cytometric analysis; b) differences between both methods in the selected DNA sequences and antigen epitopes, respectively, detected (i.e. CD38, CD4, CD56); and c) differences in the stability of mRNA and protein of the respective genes.

Overall, these results demonstrate for the first time that there is a significant correlation between protein expression and gene expression in AML and that the antigens so far identified essential for the diagnosis and subclassification of AML by flow cytometry may represent additional candidate genes when using MA as a diagnostic tool for molecular cancer class prediction[15,16]. Furthermore, it is anticipated that the present analyses represent a prime example and will be reproduced for a variety of other entities like lymphoid malignancies. Due to their high potential to assess the expression patterns of high numbers of genes and due to their excellent reproducibility features microarrays are a promising future diagnostic tool. As a consequence, they may replace the more time and resource consuming diagnostic methods currently used for diagnosing leukemias like cytomorphology, cytogenetics, and FC.

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Example 6: Gene Expression Profiles of Distinct Cytogenetic AML Subtypes as Defined by the New WHO Classification: A Study of 45 Patients

Example 6: Introduction

Since their introduction, microarrays have been promising tools for basic research. With regard to leukemia, the pivotal discrimination of unselected acute lymphoblastic (ALL), and acute myeloid leukemia (AML) samples based on their gene expression signatures inspired numerous studies (Golub et al., 1999). We performed gene expression analyses to designate candidate genes for discriminating specific AML samples from normal bone marrow (BM) of healthy volunteers. With regard to the classification of hematological malignancies according to the WHO, distinct AML subtypes have been established based on genetic abnormalities of the leukemic blasts. Here, we demonstrate gene expression analyses of 8 healthy BM donors and 45 leukemia patients representing four cytogenetic subtypes of AML: t(8;21)(q22;q22), inv(16)(p13q22), t(15;17)(q22;q12), and t(11q23)/MLL. Combining different approaches for data analysis a minimal set of genes was identified to designate a reliable class prediction model. Based on the expression pattern of 39 genes, cytogenetically defined AML subtypes could accurately be predicted and separated from healthy BM. Taken together, gene expression signatures of AML cases with recurrent genetic abnormalities demonstrate a very close correlation between genotype and gene expression. Therefore, introducing a set of candidate genes, expression profiling may serve for diagnosis of AML subtypes defined by the new WHO classification.

Example 6 Material and Methods

We analyzed BM aspirates from 8 healthy volunteers and the following 45 untreated AML patients:

- t(8;21)(q22;q22)/AML M2 (n=9),
- t(15;17)(q22;q12)/AML M3/M3v (n=16),

- inv(16)(p13q22)/AML M4eo (n=10), and
- t(11q23)/MLL-aberrations (n=10)

Example 6- Microarray experiments. Gene expression analyses were performed from cells remaining from the diagnostic sample. They had immediately been lysed, frozen and were stored at -80°C from 1 to 34 months until preparation for gene expression profiling. The targets for U95Av2 microarrays were prepared according to current protocols (Affymetrix). Before expression profiling, Test3 Probe Arrays were chosen for monitoring the integrity of the cRNA.

Example 6 - Results I: Characterization of leukemia samples

AML samples were thoroughly characterized by a combination of cytomorphology, cytogenetics, FISH, RT-PCR and quantitative real-time PCR (Fig. 20). All patients showed the above mentioned balanced abnormalities as the sole karyotype change. Using FISH analysis, more than 90% of cells demonstrated the specific signal constellation. The respective fusion transcripts AML1-ETO in t(8;21), CBF□-MYH11 in inv(16), PML-RAR□ in t(15;17) and various MLL-fusion partners in t(11q23) were detected by PCR techniques in all samples. These subtypes are specifically associated with five cytomorphological subtypes according to FAB classification: inv(16)(p13q22)/AML M4eo, t(8;21)(q22;q22)/AML M2, t(15;17)(q22;q12)/AML M3/M3v, and t(11q23)/MLL in FAB M5a/b, respectively. AML subtypes M3 and M3v both carry the same chromosome aberration but differ in morphological and clinical aspects.

Example 6 - Results II: Class separation

For data analysis we combined different approaches. First, a reduced subset of 200 genes obtained by permutation-based neighborhood analysis (SAM, Tusher et al., 2001) was visualized for corresponding clusters using principal component analysis (J-Express, Dysvik et al., 2001)(Fig.21). Samples from healthy donors cluster into a distinct group, likewise all AML samples demonstrate homogenity by forming a second cluster.

Example 6 - Results III: Class prediction

Next, we adapted the signal-to-noise/weighted voting algorithm (Golub et al., 1999) to identify discriminative genes. A minimal set of 39 genes, which provided both optimal classification accuracy and highest prediction strength, was selected to avoid overfitting. The significance of each gene was tested by permutation-based neighborhood analysis. The robustness of the classifier was assessed by leave-one-out crossvalidation. These expression signatures were sufficient to distinguish AML samples with high accuracies from normal bone marrow and to predict the recurrent chromosome aberration, respectively (Table 27, Fig. 22). Table 28a shows for which comparison a gene was important including its statistical significance.

A set of 39 genes is sufficient for class prediction. *Accuracy* denotes the rate of correctly classified test samples. P(g,c) indicates the signal-to-noise ratio of gene x: $S_x = (\mu_1-\mu_2)/(ó_1+ó_2)$, where μ_k and $ó_k$ denote the mean expression and standard deviation of gene x in group k. As calculated from pairwise comparisons (class A vs. B), positive P(g,c) values indicate a higher gene expression in class A, negative P(g,c) values a higher gene expression in class B, respectively. HGNC symbols are given in column 1.

All leukemia samples could accurately be assigned to their corresponding cytogenetic subtype with 100% accuracies. To illustrate these results, a hierarchical clustering is shown (Fig. 23).

Example 6 – Conclusions

- The expression pattern of 39 genes allowed precise class assignments of four cytogenetically defined AML subtypes according to the WHO classification of hematological malignancies, and normal BM, respectively.
- Thus, we introduce candidate genes suitable for diagnosis of AML subgroups based on gene expression profiling.
- Potentially, gene expression patterns will allow the additional subclassification of AML, especially in subtypes with no specific cytogenetic markers (e.g. normal karyotype).

Example 7: Gene Expression Profiles of Distinct Leukemia Types and Subtypes: A Study of 280 Patients using high-density microarrays

Example 7: Introduction

Here, we demonstrate gene expression analyses of 9 healthy BM donors and 271 leukemia patients representing:

AML: 4 distinct cytogenetic subtypes t(8;21)(q22;q22) (AML t(8;21)), inv(16)(p13q22) (AML inv(16)), t(15;17)(q22;q12) (AML t(15;17)), and t(11q23)/MLL (AML MLL). In addition, we analyzed AML samples characterized by normal karyotypes (AML normal), complex aberrant karyotypes (AML complex), trisomy 8 as sole aberration (AML +8), and other chromosomal changes (AML other).

ALL: 3 distinct genetically defined subtypes: t(4;11)(q21;q23) (ALL t(4;11)), t(8;14)(q24;q32) (ALL t(8;14)), t(9;22)(q34;q11) (ALL Ph) and 2 subtypes defined by their immunophenotype: ALL of the B-lineage not carrying the t(9;22) (ALL B not Ph) and T-ALL (T-ALL)

CLL: 5 genetically defined subtypes: trisomy 12 (tri 12), deletion 11q (11q-), deletion 13q (13q-), deletion 17p (17p-) and none of these aberrations (normal)

CML (CML) without any further subdivison and

Normal bone marrow from healthy volunteers (normal BM).

We used the Affymetrix oligonucleotide microarray technology (GeneChip® Instrument System) to obtain gene expression profiles of each individual clinical sample of interest. The commercially available HG-U133 probe arrays gave information about the relative mRNA abundance of about 33,000 human genes which are represented on these high-density DNA-oligonucleotide microarrays.

Chip Information (as provided by manufacturer):

The GeneChip® Human Genome U133 Set (HG-U133A and HG-U133B) is comprised of two microarrays containing over 1,000,000 unique oligonucleotide features covering more than 39,000 transcript variants, which in turn represent greater than 33,000 of the best characterized human genes. This powerful set allows to reproducibly examine the quantitative and qualitative expression of most genes in the human genome, and was designed using the recently published and publicly available draft of the human genome sequence. Sequences used in the design of the array were selected from GenBank, dbEST, and RefSeq. Sequence clusters were created from Build 133 of UniGene (April 20, 2001) and refined by analysis and comparison with a number of other publicly available databases including the Washington University EST trace repository and the University of California, Santa Cruz golden-path human genome database (April 2001 release). In addition, ESTs were analyzed for untrimmed low-quality sequence information, correct orientation, false priming, false clustering, alternative splicing and alternative polyadenylation.

Combining different approaches for data analysis, a set of genes was identified to designate a reliable class prediction model. Based on the expression pattern of those genes, defined leukemia types and subtypes could accurately be predicted and separated from healthy BM. Taken together, gene expression signatures demonstrate a very close correlation between genotype and gene expression. Therefore, introducing a set of candidate genes, measurements of mRNA abundancies by gene expression profiling serves for diagnosis of leukemia types and subtypes.

Example 7 Material and Methods

We analyzed BM aspirates from 9 healthy volunteers and the following 280 leukemia patients:

Acute myeloid leukemia (AML)

t(8;21)(q22;q22)/AML M2 (n=13),

t(15;17)(q22;q12)/AML M3/M3v (n=20),

inv(16)(p13q22)/AML M4eo (n=12),

t(11q23)/MLL-aberrations (n=15)

trisomy 8 (n=10)

normal karyotype (n=62)

complex aberrant karyotype (n=36)

other aberrations (n=5)

Acute lymphoblastic leukemia (ALL)

t(4;11)(q21;q23) (n=9)

t(8;14)(q24;q32) (n=4)

t(9;22)(q34;q11) (ALL Ph) (n=15)

ALL B lineage without t(9;22) (ALL B not Ph) (n=9)

T-ALL (n=9)

Chronic lymphocytic leukemia (CLL)

trisomy 12 (tri 12) (n=5)

deletion 11q (11q-) (n=4)

deletion 13q (13q-) (n=10)

deletion 17p (17p-) (n=4)

none of these aberrations (normal) (n=9)

Chronic myeloid leukemia (n=14)

Normal bone marrow (normal BM) (n=9)

Example 7 - Results I: Characterization of leukemia samples

We selected bone marrow (BM) samples from 271 leukemia patients at diagnosis representing 18 different disease entities or subentities and from 9 healthy volunteers, respectively. All cases were sent for reference diagnostics to our laboratory, registered in our leukemia database and were treated within prospective randomized multi-center trials. The studies abide by the rules of the local internal review board and the tenets of the revised Helsinki protocol. Samples were received either locally or by overnight mail. Diagnosis was performed by an individual combination of cytomorphology, cytogenetics, FISH, immunophenotyping and molecular genetics. Mononuclear cells were isolated by a Ficoll gradient, lysed, frozen and were stored at -80°C from one to 34 months until sample preparation for gene expression analysis. All leukemia samples were thoroughly characterized by a individual combination of cytomorphology, cytogenetics, immunophenotyping, fluorescence in situ hybridisation (FISH), polymerase chain reaction based methods both qualitative RT-PCR and quantitative real-time PCR. Using FISH analysis, more than 90% of cells demonstrated the specific signal constellation. The respective fusion transcripts BCR-ABL in t(9;22) positive CML (Schoch et al. 2002a) and in t(9;22) positive ALL, AML1-ETO in AML with t(8;21), CBFbeta-MYH11 in AML with inv(16), PML-RARalpha in AML with t(15;17) (Schoch et al. 2002b) and various MLL-fusion partners in both AML and ALL with t(11q23) were detected by FISH and PCR techniques in all samples.

In t(8;14) positive ALL the IGH-C-MYC rearrangement was confirmed by FISH. In all cases with AML and complex aberrant karyotype 24 color FISH was performed in addition to chromosome banding analysis (Schoch et al. 2002c).

Genetic subtyping of CLL was carried out using interphase FISH with the following probes (Buhmann et al. 2002):

- for the detection of trisomy 12 a centromere specific probe for chromosome 12
- for the detection of 11q deletions probes for the ATM as well as for the RDX gene
- for the detection of 13q deletions probes for the retinoblastoma gene (Rb), and the anonymous loci D13S25 and D13S319
- for the detection of 17p deletion a probe for the p53 gene
- cases with none of the above mentioned aberrations were assigned to the group normal

References:

Buhmann R, Kurzeder C, Rehklau J, Westhaus D, Bursch S, Hiddemann W, Haferlach T, Hallek M, Schoch C.

CD40L stimulation enhances the ability of conventional metaphase cytogenetics to detect chromosome aberrations in B-cell chronic lymphocytic leukaemia cells.

Br J Haematol 2002 Sep;118(4):968-75

Schoch C, Schnittger S, Kern W, Lengfelder E, Löffler H, Hiddemann W, Haferlach T.

Rapid diagnostic approach to PML-RARalpha-positive acute promyelocytic leukemia.
Hematol J 2002a;3(5):259-63

Schoch C, Schnittger S, Bursch S, Gerstner D, Hochhaus A, Berger U, Hehlmann R, Hiddemann W, Haferlach T.

Comparison of chromosome banding analysis, interphase- and hypermetaphase-FISH, qualitative and quantitative PCR for diagnosis and for follow-up in chronic myeloid leukemia: a study on 350 cases, Leukemia 2002b Jan;16(1):53-9

Schoch C, Haferlach T, Bursch S, Gerstner D, Schnittger S, Dugas M, Kern W, Löffler H, Hiddemann W.

Loss of genetic material is more common than gain in acute myeloid leukemia with complex aberrant karyotype: A detailed analysis of 125 cases using conventional chromosome analysis and fluorescence in situ hybridization including 24-color FISH.
Genes Chromosomes Cancer 2002 Sep;35(1):20-9

Example 7 - Results II: Sample preparation and microarray hybridisation

Microarray analyses were performed utilising the GeneChip® System (Affymetrix, Santa Clara, USA). The targets for GeneChip® analyses were prepared according to the current Expression Analysis Technical Manual. Briefly, lysates of the leukemia samples were homogenised (QIAshredder, Qiagen, Hilden, Germany) and total RNA extracted (RNeasy Mini Kit, Qiagen). Normally, 5 μg total RNA isolated from $1x10^7$ cells were used as starting material in the subsequent cDNA-synthesis using oligo[$(dT)_{24}$T7promotor]$_{65}$ primer (cDNA Synthesis System, Roche Applied Science, Mannheim, Germany). The cDNA was purified by phenol:chloroform:isoamyl alcohol (25:24:1) extraction (Ambion, Austin, USA) and acetate/ethanol precipitated over night. For detection of the hybridised target nucleic acid biotin-labeled ribonucleotides were incorporated during the in vitro transcription (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO, Farmingdale, USA). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 μg labeled cRNA were fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridisation cocktail sufficient for 5 hybridisations on standard

format GeneChip® microarrays. Before hybridisation to HG-U133 microarrays, Test3 microarrays (Affymetrix) were chosen in some cases for monitoring the integrity of the cRNA. Washing and staining of the probe arrays was performed according to the current protocols of the manufacturer (Fluidics Station, Micro_1v1, EukGE-WS2v4). The Affymetrix software (Microarray Suite, Version 5.0) extracted fluorescence intensities from each feature on the microarrays as detected by confocal laser scanning according to the manufacturers recommendations. Some of the hybridization cocktails had previously been hybridized to U95Av2 arrays. Hybridization cocktails can be used for up to 5 distinct array analyses.

All hybridisation cocktails demonstrated high quality cRNA characteristics. We considered both low 3'/5' ratio (e.g., lower than about 3) of housekeeping controls and the total number of present called genes (> about 30% on U133A), along with the average signal intensity of a present called gene. Expression profiles which fulfilled all quality control criteria were selected for subsequent supervised selection of informative genes.

Example 7 - Results III: Statistical Analyses

For data analysis we combined different approaches. First, the expression data was preprocessed. Raw expression intensities were scaled using the Affymetrix Microarray Suite software scaling parameter (target intensity: 5000). This preprocessing is based on a mask file which compares expression intensities of a set of 100 genes which code for ubiquitous housekeeping cellular proteins. This set of genes for normalisation of expression intensities is represented on both U133A and U133B arrays. The step of data preprocessing assures that array experiments can be compared properly using further statistical algorithms and methods. Subsequently, the data was analyzed according to two different established methods from as described below. The results from the two analyses were systematically compared to validate the list of differentially expressed genes.

1. Selection of differentially expressed genes

a) Analysis according to example 3.

The top 20 differentially expressed genes were calculated for all disease entities and normal bone marrow, respectively, as described in example 3. Expression data were analyzed in order to select a minimal set of discriminative genes, which provides, as described hereinabove (Example 3), maximum classification accuracy in leave-one-out-crossvalidation.

One-versus-all (OVA) and all-pairs comparisons (AP) were systematically applied. Genes were ranked according to signal-to-noise ratio (STN). For each OVA and AP comparison a set of discriminative genes is disclosed in tables 29, 32, 35, 38 and 41 whereby the gene names can be found in tables 43a,b. The most discriminative and informative genes are marked by asterisks in tables 29, 32, 35, 38 and 41. Classification accuracy was estimated by means of leave-one-out-crossvalidation and weighted voting.

References:

Golub TR, Slonim DK, Tamayo P, Huard C, Gaasenbeek M, Mesirov JP, Coller H, Loh ML, Downing JR, Caligiuri MA, Bloomfield CD, Lander ES. Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. Science 1999; 286(5439):531-7

Pomeroy SL, Tamayo P, Gaasenbeek M, Sturla LM, Angelo M, McLaughlin ME, KimJY, Goumnerova LC, Black PM, Lau C, Allen JC, Zagzag D, Olson JM, Curran T,Wetmore C, Biegel JA, Poggio T, Mukherjee S, Rifkin R, Califano A, StolovitzkyG, Louis DN, Mesirov JP, Lander ES, Golub TR. Prediction of central nervous system embryonal tumour outcome based on geneexpression. Nature 2002; 415(6870):436-42.

2. Estimation of classification accuracy

A set of 20 top-ranked genes, which provided both optimal classification accuracy and highest prediction strength, was selected to avoid overfitting. The significance

of each gene was tested by permutation-based neighborhood analysis. The robustness of the classifier was assessed by leave-one-out crossvalidation. These expression signatures were sufficient to distinguish leukemia samples with high accuracies from normal bone marrow and also to predict the recurrent chromosome aberration, respectively (Tables 29, 32, 35, 38, 41). *Accuracy* denotes the rate of correctly classified test samples. P(g,c) indicates the signal-to-noise ratio of gene x: $S_x = (\mu_1-\mu_2)/(ó_1+ó_2)$, where μ_k and $ó_k$ denote the mean expression and standard deviation of gene x in group k. As calculated from pairwise comparisons (class A vs. B), positive P(g,c) values indicate a higher gene expression in class A, negative P(g,c) values a higher gene expression in class B, respectively.

b) Analysis according to Westfall & Young the same data set was analysed according to Westfall & Young to identify significantly differentially expressed genes with adjustment of the p-values for multiple testing.

Step-down maxT and minP multiple testing procedures were applied, which compute permutation adjusted p-values for the step-down maxT and minP multiple testing procedures, which provide strong control of the family-wise Type I error rate (FWER). The multitest package (version 1.0) from Bioconductor was applied, which is based on the R statistical language. These methods outperform other methods (see Dudoit, JASA 2002).

References:

Westfall PH, Young SS (1993) Resampling-based multiple testing: Examples and methods for p-value adjustment. John Wiley & Sons. ISBN 0-471-55761-7

Dudoit S, Fridlyand J, Speed TP.

Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data. JASA 2002; 97:77-87

Package multtest (version 1.0)

from Bioconductor http://www.bioconductor.org

R statistical language: http://www.r-project.org/

c) Comparison of gene lists

The list of differentially expressed genes obtained from 1a) and 1b) were systematically compared using PERL scripts in order to identify genes that occurred in both list, versus genes occurring in one list only.

Expression intensities (expression levels) derived from the above-mentioned MicroArray Suite program were plotted as bar graphs showing gene expression profiles using a Perl script (Figures 24 to 464).

References:

PERL: http://www.perl.com

Sensitivities for the detection of leukemia types and subtypes were calculated as the number of positive samples predicted divided by the number of true positives.

Specificities for the detection of leukemia types and subtypes were calculated as the number of negative samples predicted divided by the number of true negatives.

Example 7 - Results IV: Analysis of 14 leukemia subtypes and normal bone marrow

Here we analyzed in total 14 distinct leukemia types and subtypes as well a cohort of healthy volunteers for normal bone marrow characteristics. We applied the described two different statistical methods for identification of genes which allow accurate class assignments to the respective groups.

ALL t(4;11) (n=9)

ALL t(8;14) (n=4)

ALL B not Ph (n=9)

ALL Ph (n=15)

T-ALL (n=9)

AML +8 (n=10)

AML complex (n=36)

AML normal (n=62)

AML t(8;21) (n=13)

AML t(15;17) (n=20)

AML inv(16) (n=12)

AML MLL (n=15)

CLL (n=32)

CML (n=14)

normal BM (n=9)

total: 269 samples

First, expression data were analyzed according to example 3, as described hereinabove.

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A set of 20 top-ranked genes, which provided both optimal classification accuracy and highest prediction strength for all pairwise (all pairs) and one-versus-all comparisons is given as table 29. Within this set of genes, optimal classification accuracy can be obtained with genes marked by asterisks. Gene expression intensities, plotted as bar graphs are given in Figures 24 to 188. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in tables 43a,b.

In total 269 cases with leukemia or normal bone marrow (BM) were analyzed. 248 of 269 (92.2%) cases were assigned to the correct leukemia type in all pairwise comparisons (table 28 b). The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons (range 60% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 85.3% to 100%).

In total 3766 individual assignments of leukemia and normal bone marrow were analyzed. 3745 of 3766 assignments (99.4%) were correct (table 28c). The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. (range 97.1% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 98.4% to 100%).

In a second approach significant genes were identified according to Westfall & Young. Table 30 represents all genes found to be significant after p-value adjustment. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

Furthermore, we provide information about genes which were found to be rated significant independently by both methodologies (Table 30). Top-significant genes

according to the method of example 3 are marked by asterisks. Genes which were included in any of the top-20 lists are marked by positive signs.

In addition, selected gene profiles were chosen to demonstrate their capability of discriminating different leukemia types, subtypes and normal bone marrow, respectively. Gene expression profiles were generated by means of PERL-programs, evaluated and plotted as bar graphs. Each of the analyzed groups are accordingly outlined. The following genes were selected and are given as Figures 189 to 233:

GeneID	gene symbol	feature
201162_at	IGFBP7	CLL low
201163_s_at	IGFBP7	CLL low
201362_at	NS1-BP	CML high
201496_x_at	MYH11	AML inv(16) high
201497_x_at	MYH11	AML inv(16) high
201998_at	SIAT1	CLL high
202095_s_at	BIRC5	CLL low
203074_at	ANXA8	AML t(15;17) high
204150_at	STAB1	AML t(15;17) high
204511_at	KIAA0793	CLL high
205528_s_at	CBFA2T1	AML t(8;21) high
205529_s_at	CBFA2T1	AML t(8;21) high

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205805_s_at	ROR1	CLL high
206940_s_at	POU4F1	AML t(8;21) high
207819_s_at	ABCB4	CLL high
208091_s_at	DKFZP564K0822	CLL high
208456_s_at	RRAS2	CLL high
209061_at	NCOA3	CLL high
209101_at	CTGF	ALL t(4;11) high, ALL Ph high, T-ALL high
209374_s_at	IGHM	CLL high
209616_s_at	CES1	AML MLL high
210997_at	HGF	AML t(15;17) high
212285_s_at	AGRN	AML t(15;17) high
213539_at	CD3D	T-ALL high
214450_at	CTSW	AML t(15;17) high
215925_s_at		ALL t(4;11) high
218223_s_at	LOC51177	CML low
222166_at		AML +8 high
224520_s_at	MGC13168	ALL t(8;14) high
224794_s_at	LOC51148	AML t(15;17) high
225660_at	SEMA6A	ALL B not Ph high, ALL Ph high

226496_at	Homo sapiens, Similar to hypothetical protein FLJ22611, clone MGC:24716 IMAGE:4277726, mRNA, complete cds	ALL high, CLL high
228827_at	Homo sapiens clone 25023 mRNA sequence	AML t(8;21) high
228904_at	ESTs	AML normal high, AML +8 high, AML complex high
236301_at	Homo sapiens, clone IMAGE:3866403, mRNA	CLL high
236892_s_at	HOXB6	AML normal high, AML +8 high, AML complex high
239214_at	ESTs	ALL t(4;11) high
239393_at	ESTs	ALL t(4;11) high
239791_at	HOXB6	AML normal high, AML +8 high
240581_at	ESTs	ALL t(4;11) high
241464_s_at	ESTs	AML MLL high, AML normal high, AML +8 high, AML complex high
241525_at	ESTs	AML inv(16) high
243362_s_at	LEF1	ALL high, CLL high
36566_at	CTNS	T-ALL low
38487_at	FLJ12442	AML t(15;17) high

Generally, chromosomal aberrations are strongly associated with morphological characteristics. However, there are two chromosomal aberrations which are observed in both myeloid and lymphatic neoplasms, i.e. t(11q23)/MLL and the t(9;22). The t(9;22) occurs in ALL (ALL Ph) and CML, and t(11q23)/MLL is observed in ALL (ALL t(4;11)) and AML (AML MLL), respectively. Analysing gene expression signatures of both t(9;22) positive ALL and CML we identified genes, which allowed correct lineage assignments (table 29). In addition, our results indicate that the distinct expression signatures are also sufficient for correct assignments of the t(11q23)/MLL positive leukemias either to ALL or to AML (table 29). Thus, in both scenarios lineage assignment (lymphoid or myeloid), and even subtype classification can be accomplished based on the methods and markers described herein, despite of the fact that e.g., in the above-noted t(11q23) and t(9;22) chromosomal aberrations, the same chromosomal aberration is associated with different kinds of leukemia.

Example 7 - Results V: Analysis of 5 ALL subtypes defined by genetics and immunophenotype

Here we analyzed in 5 distinct ALL subtypes. We applied the described two different statistical methods for identification of genes which allow accurate class assignments to the respective groups.

ALL t(4;11)	(n=9)
ALL t(8;14)	(n=4)
ALL B not Ph	(n=9)
ALL Ph	(n=15)
T-ALL	(n=9)

First, expression data were analyzed according to example 3, as described hereinabove.

A set of 20 top-ranked genes, which provided both optimal classification accuracy and highest prediction strength for all pairwise (all pairs) and one-versus-all comparisons is given in table 32. Within this set of genes, optimal classification accuracy can be obtained with genes marked by asterisks. Gene expression intensities, plotted as bar graphs are given in Figures 234 to 252. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

In total 46 cases of ALL were analyzed. 44 of 46 cases (95.7%) were assigned to the correct ALL subtype in all pairwise comparisons (table 31a). The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons (range 88.9% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 88.9% to 100%).

In total 184 individual assignments of ALL were analyzed. 182 of 184 assignments (98.9%) were correct (table 31b). The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. (range 97.2% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 97.2% to 100%).

In a second approach significant genes were identified according to Westfall & Young. Table 33 represents all genes found to be significant after p-value adjustment. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

Furthermore, we provide information about genes which were found to be rated significant independently by both methodologies (Table 33). Top-significant genes according to the method of example 3 hereinabove are marked by asterisks. Genes which were included in any of the top-20 lists are marked by positive signs.

In addition, selected gene profiles were chosen to demonstrate their capability of discriminating different leukemia types, subtypes and normal bone marrow, respectively. Gene expression profiles were generated by means of PERL-programs, evaluated and plotted as bar graphs. Each of the analyzed groups are accordingly outlined. The following genes were selected and are given as Figures 253 to 271:

GeneID	gene symbol	feature
201105_at	LGALS1	ALL t(4;11) high
204044_at	QPRT	ALL t(4;11) high
205899_at	CCNA1	ALL t(4;11) high
209168_at	GPM6B	ALL t(4;11) high
213539_at	CD3D	T-ALL high
213894_at	KIAA0960	ALL t(4;11) high
215925_s_at		ALL t(4;11) high
218224_at	PNMA1	T-ALL high
219463_at	C20orf103	ALL t(4;11) high
219631_at	FLJ12929	T-ALL high
225563_at	ESTs	ALL t(4;11) high

225592_at	NRM	ALL t(4;11) high
228083_at	Homo sapiens mRNA; cDNA DKFZp434I1216 (from clone DKFZp434I1216)	ALL t(4;11) high
228988_at	ZNF6	T-ALL high
235749_at		ALL t(8;14) high
242414_at	ESTs	ALL t(4;11) high
243756_at	ESTs	ALL t(4;11) high

Example 7 - Results VI: Analysis of 8 AML subtypes

Here we analyzed in total 8 distinct AML subtypes. We applied the described two different statistical methods for identification of genes which allow accurate class assignments to the respective groups.

trisomy 8	(n=10)
other aberrant	(n=5)
complex	(n=36)
normal	(n=62)
t(8;21)	(n=13)
t(15;17)	(n=20)
inv(16)	(n=12)
MLL	(n=15)

First, expression data were analyzed according to example 3 as described hereinabove.

A set of 20 top-ranked genes, which provided both optimal classification accuracy and highest prediction strength for all pairwise (all pairs) and one-versus-all comparisons is given as table 35. Within this set of genes, optimal classification accuracy can be obtained with genes marked by asterisks. Gene expression intensities, plotted as bar graphs are given in Figures 272 to 336. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

In total 173 cases of AML were analyzed. 160 of 174 cases (92.5%) were assigned to the correct AML subtype in all pairwise comparisons (table 34a). The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons (range 60% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 85.5% to 100%).

In total 1211 individual assignments of AML were analyzed. 1198 of 1211 assignments (98.9%) were correct (table 34b). The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons (range 94.3% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 97.7% to 100%).

In a second approach significant genes were identified according to Westfall & Young. Table 36 represents all genes found to be significant after p-value adjustment. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

Furthermore, we provide information about genes which were found to be rated significant independently by both methodologies (Table 36). Top-significant genes according to the method of example 3 are marked by asterisks. Genes which were included in any of the top-20 lists are marked by positive signs.

In addition, selected gene profiles were chosen to demonstrate their capability of discriminating different leukemia types, subtypes and normal bone marrow, respectively. Gene expression profiles were generated by means of PERL-programs, evaluated and plotted as bar graphs. Each of the analyzed groups are accordingly outlined. The following genes were selected and are given as Figures 337 to 370:

GeneID	gene symbol	feature
201497_x_at	MYH11	AML inv(16) high
228827_at	Homo sapiens clone 25023 mRNA sequence	AML t(8;21) high
38487_at	FLJ12442	AML t(15;17) high
203074_at	ANXA8	AML t(15;17) high
205528_s_at	CBFA2T1	AML t(8;21) high
205529_s_at	CBFA2T1	AML t(8;21) high
206940_s_at	POU4F1	AML t(8;21) high
211341_at	POU4F1	AML t(8;21) high
201496_x_at	MYH11	AML inv(16) high
228660_x_at	SEMA4F	other high
202718_at	IGFBP2	AML t(15;17) high

205380_at	PDZK1	other high
202746_at		AML MLL low
201596_x_at	KRT18	AML t(8;21) low
34210_at	CDW52	AML t(15;17) low
212850_s_at	LRP4	AML inv(16) high
228904_at	ESTs	AML t(8;21) low, AML t(15;17) low, AML inv(16) low, AML MLL low
203151_at	MAP1A	AML t(8;21) low
201137_s_at	HLA-DPB1	AML t(15;17) low
200675_at	CD81	AML inv(16) low
201425_at	ALDH2	AML t(8;21) low
202085_at	TJP2	AML inv(16) low
202619_s_at	PLOD2	AML MLL low
203092_at	TIMM44	AML inv(16) low
204425_at	ARHGAP4	AML t(15;17) low
205366_s_at	HOXB6	AML t(8;21) low, AML t(15;17) low, AML inv(16) low, AML MLL low
205472_s_at	DACH	AML MLL high
206761_at	TACTILE	AML MLL low

222166_at		AML +8 low
222335_at	ESTs	AML MLL low
223318_s_at	MGC10974	AML complex low
225330_at	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds	AML inv(16) low
231277_x_at	ESTs	AML complex low
635_s_at	PPP2R5B	other low

Example 7 - Results VII: Analysis of 5 genetically defined CLL subtypes

Here we analyzed in total 5 genetically defined CLL subtypes. We applied the described two different statistical methods for identification of genes which allow accurate class assignments to the respective groups.

trisomy 12 (n=5)

11q- (n=4)

13q- (n=10)

17p- (n=4)

normal (n=9)

First, expression data were analyzed according to example 3 as described hereinabove.

A set of 20 top-ranked genes, which provided both optimal classification accuracy and highest prediction strength for all pairwise (all pairs) and one-versus-all comparisons is given as table 38. Within this set of genes, optimal classification accuracy can be obtained with genes marked by asterisks. Gene expression

intensities, plotted as bar graphs are given in Figures 371 to 404. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

In total 32 cases of CLL were analyzed. 31 of 32 cases (96.9%) were assigned to the correct CLL subtype in all pairwise comparisons (table 37a). The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons (range 90% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 90% to 100%).

In total 128 individual assignments of CLL were analyzed. 127 of 128 assignments (99.2%) were correct (table 37b). The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons (range 97.5% to 100%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 97.3% to 100%).

In a second approach significant genes were identified according to Westfall & Young. Table 39 represents all genes found to be significant after p-value adjustment. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

Furthermore, we provide information about genes which were found to be rated significant independently by both methodologies (Table 39). Top-significant genes according to the method of example 3 are marked by asterisks. Genes which were included in any of the top-20 lists are marked by positive signs.

Example 7 - Results VIII: Analysis of the four major leukemia types (ALL, AML, CLL, CML) and normal bone marrow

Here we analyzed in total 4 major leukemia types as well a cohort of healthy volunteers for normal bone marrow characteristics. We applied the described two different statistical methods for identification of genes which allow accurate class assignments to the respective groups.

ALL (n=47)

AML (n=175)

CLL (n=35)

CML (n=14)

Normal bone marrow (n=9)

First, expression data were analyzed according to example 3 as described hereinabove.

A set of 20 top-ranked genes, which provided both optimal classification accuracy and highest prediction strength for all pairwise (all pairs) and one-versus-all comparisons is given as table 41. Within this set of genes, optimal classification accuracy can be obtained with genes marked by asterisks. Gene expression intensities, plotted as bar graphs are given in Figures 405 to 431. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

In total 280 cases of leukemia and normal bone marrow (BM) were analyzed. 263 of 280 cases (93.9%) were assigned to the correct leukemia subtype or normal bone marrow in all pairwise comparisons (table 40a). The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons (range 76.6% to 98.3%). The

specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 88.9% to 97.1%).

In total 1120 individual assignments of leukemia subtype or normal bone marrow were analyzed. 1103 of 1120 assignments (98.5%) were correct (table 40b). The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons (range 94.2% to 99.3%). The specificity indicates for each subgroup the percentage of correct assignments to this subgroup (range 97.2% to 99.3%).

In a second approach significant genes were identified according to Westfall & Young. Table 42 represents all genes found to be significant after p-value adjustment. Genes are depicted as unique Affymetrix identifier (for example 201497_x_at) and, where available, approved HGNC symbols (HUGO Gene Nomenclature Committee). More detailed, the complete annotation and sequence information about this set of genes is listed in table 43a,b.

Furthermore, we provide information about genes which were found to be rated significant independently by both methodologies (Table 42). Top-significant genes according to the method of example 3 are marked by asterisks. Genes which were included in any of the top-20 lists are marked by positive signs.

In addition, selected gene profiles were chosen to demonstrate their capability of discriminating different leukemia types, subtypes and normal bone marrow, respectively. Gene expression profiles were generated by means of PERL-programs, evaluated and plotted as bar graphs. Each of the analyzed groups are accordingly outlined. The following genes were selected and are given as Figures 432 to 464:

GeneID	gene symbol	feature
202503_s_at	KIAA0101	CLL low

202580_x_at	FOXM1	CLL low
202709_at	FMOD	CLL high
204882_at	KIAA0053	CLL high
205049_s_at	CD79A	ALL high, CLL high
205051_s_at	KIT	AML high
205382_s_at	DF	AML high
205599_at	TRAF1	CML low CLL high
206255_at	BLK	ALL high, CLL high
206398_s_at	CD19	ALL high, CLL high
210487_at	DNTT	ALL high
210948_s_at	LEF1	ALL high, CLL high
211352_s_at	NCOA3	CLL high
211404_s_at	APLP2	AML high
214761_at	OAZ	ALL high
217950_at	NOSIP	CLL high
218090_s_at		CLL high
218516_s_at	FLJ20421	normal BM low
218916_at	FLJ23436	normal BM low

219753_at	STAG3	ALL high
221969_at	PAX5	ALL high, CLL high
223703_at	CDA017	AML high, CML high, normal BM high
226147_s_at	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385	CLL high
228471_at	ESTs	CLL high
229487_at	ESTs	ALL high
229790_at	TERF2	CML low, BM low
231736_x_at	MGST1	AML high, CML high, normal BM high
231854_at	Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391	CML low
239287_at	ESTs	CLL high
243362_s_at	LEF1	ALL high
243363_at	LEF1	ALL high, CLL high
41577_at	PPP1R16B	CML low

Tables 43a, b: functional gene annotation for genes identified to be differentially expressed between different types of leukemia, or between healthy bone marrow and leukemia, respectively.

As described by the GeneChip manufacturer, for each probeset (for example 200093_s_at_HG-U133A), a GenBank or RefSeq accession number was chosen

to represent the target sequence. Using this accession number, a UniGene cluster (in current release) was identified where the accession number was used. If there is a link to LocusLink in the UniGene record, then annotations were retrieved from LocusLink. Those annotations include gene symbol, location, OMIM, EC, Gene Ontology (GO), description and RefSeq sequence accession. The RefSeq accession was linked to the protein annotations, which include domain identification (Pfam and BLOCKS), similarity search (blastp nr) and family classification (SCOP, EC and GPCR HMM searches).

Target sequence information for all the probes which were identified to be able to distinguish between different types and subtypes of leukemia and normal bone marrow, respectively, are given in Table 44.

As further described by the GeneChip manufacturer, the HG-U133 Target Databank is a compilation of probe set annotations and target sequence information for all the probes represented on the HG-U133 A and B arrays. Target sequences are the relatively short (typically around 300-600 bp) sequences against which probes have been designed on a GeneChip® array. These target sequences can be thought of as a subsequence of the Consensus/Exemplar sequence.

The Consensus/Exemplar sequences (i.e., the coding or full cDNA sequences corresponding to the markers described herein as being able to distinguish between different types and subtypes of leukemia and normal bone marrow) for most markers are given in Table 45.

Example 7 Conclusions

The expression pattern of genes allowed precise class assignments of defined leukemia types and subtypes according to the WHO classification of hematological malignancies, and normal BM, respectively.

Thus, we introduce candidate genes suitable for diagnosis of leukemia types and subtypes based on gene expression profiling.

These data demonstrate the utility of gene expression profiling for the discrimination of all leukemia major entities and most subentities. In total, up to 14 different leukemia types and subtypes could clearly be distinguished from each other and from normal BM, respectively. These leukemias are associated with highly differing prognoses and require specific treatment strategies. By performing these analyses on a single platform requiring basic molecular biological methods, this approach provides a broad access to high-quality diagnosis of leukemia.

Golub				invention			
A -	samples: 18 / 85			A -	samples: 18 / 85		
accuracy	0,87			accuracy	0,96		
confidence	0,77			confidence	0,88		
failed	6,19,22,26,78,79,80,81,82,83,84,85,99			failed	5,6,19,22		
gene	signal-to-noise	p	decision limit	gene	signal-to-noise	p	decision limit
g1	-1,14	0*	482,01	g1	-1,14	0	
g2	-1,06	0*	192,17	g2	-1,06	0*	98,50
g3	-0,97	0*	207,67	g3	-0,97	0	
g4	0,94	0*	205,05	g4	0,94	0	
g5	-0,93	0*	1818,11	g5	-0,93	0	
g6	0,93	0*	451,74	g6	0,93	0	
g7	-0,91	0*	23,84	g7	-0,91	0	
g8	-0,90	0*	225,72	g8	-0,90	0	
g9	0,90	0*	43,85	g9	0,90	0	
g10	0,89	0*	210,78	g10	0,89	0	
g11	-0,88	0*	118,63	g11	-0,88	0	
g12	0,87	0*	55,39	g12	0,87	0*	67,80

g13	0,87	0*	127,15	g13	0,87	0*	164,10
g14	0,86	0*	222,04	g14	0,86	0	
g15	0,85	0*	68,52	g15	0,85	0	
g16	-0,85	0*	546,97	g16	-0,85	0	
g17	0,84	0*	1242,77	g17	0,84	0	
g18	-0,84	0*	162,61	g18	-0,84	0	
g19	-0,83	0*	385,39	g19	-0,83	0	
g20	0,46	0*	105,38	g20	0,46	0	

Table A. Analysis of 18 samples class A versus 85 samples class non-A. On the left the analysis according to Golub is presented for 20 informative genes. The crossvalidation accuracy is 0,87, confidence 0,77. Samples, where crossvalidation failed, are listed. For each gene signal to noise ratio, p-value (significance obtained from permutation test) and decision limit are provided. On the right the same data set is analyzed using the protocol of the invention. By selection of 3 genes (marked with asterisks) out of the top 20 genes and selecting optimized decision limits, the crossvalidation accuracy reaches 0,96, confidence 0,88.

Table 1

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	34210_at
GAS2-related on chromosome 22	Y07846	Hs.322852	NM_006478	22q11.2	Cluster Incl. Y07846:H.sapiens mRNA for GAR22 protein /cds=(132,1145) /gb=Y07846 /gi=1666070 /ug=Hs.15346 /len=2238	31874_at
HLA-DPA1	X00457	Hs.914		6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	38833_at
ADRA2C (adrenergic, alpha-2C-, receptor)	J03853	Hs.123022	NM_000683	4p16	Cluster Incl. J03853:Human kidney alpha-2-adrenergic receptor mRNA, complete cds /cds=(38,1423) /gb=J03853 /gi=178193 /ug=Hs.123022 /len=1491	34512_at

POU4F1 (POU domain, class 4, transcription factor 1)	X64624	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492	35940_at
CLECSF2 (C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced))	X96719	Hs.85201	NM_005127	12p13-p12	Cluster Incl. X96719:H.sapiens mRNA for AICL (activation-induced C-type lectin) /cds=(132,581) /gb=X96719 /gi=1632815 /ug=Hs.85201 /len=739	40698_at
PTGDS (prostaglandin D2 synthase (21kD, brain))	AI207842	Hs.8272	NM_000954	9q34.2-q34.3	Cluster Incl. AI207842:ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1953089 /clone_end=3 /gb=AI207842 /gi=3769784 /ug=Hs.8272 /len=771	38407_r_at
TRH (thyrotropin-releasing hormone)	M63582	Hs.182231	NM_007117	3q13.3-q21	Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cds=(8,736) /gb=M63582 /gi=190297 /ug=Hs.182231 /len=1457	32323_at
DKFZP586N1922	N99340	Hs.7357		19	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074	36095_at

					/gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110	
PTGDS (prostaglandin D2 synthase	M98539	Hs.8272	NM_000954	9q34.2-q34.3	M98539 /FEATURE=exon /DEFINITION=HUMPDS03 Human prostaglandin D2 synthase gene, exon 7	216_at
HLA-DQB1	M81141	Hs.73931	NM_002123	6p21.3	Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171	36773_f_at
CTSW (cathepsin W (lymphopain))	AF013611	Hs.87450	NM_001335	11q13.1	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	40718_at
KIAA0246	D87433	Hs.301989	NM_015136	3	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777	38487_at

MYH11	AF013570	Hs.78344	NM_002474, NM_022844, NM_022870	16p13.13-p13.12	Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	37407_s_at
KRT18 (keratin 18)	M26326	Hs.65114	NM_000224	12q13	Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343) /gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412	35766_at
POU4F1 (POU domain, class 4, transcription factor 1)	L20433	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. L20433:Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588 /len=3824	35939_s_at
CRA	U78556	Hs.166066	NM_006697	1	U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds	1230_g_at

MYH11	AF001548	Hs.78344	NM_002474	16p13.13-p13.12	AF001548 /FEATURE=mRNA /DEFINITION=HUAF001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence	767_at

Table 2:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	
HOXB2 (homeo box B2)	X16665	Hs.2733	NM_002145	17q21-q22	Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520	39610_at
CTSW (cathepsin W (lymphopain))	AF013611	Hs.87450	NM_001335	11q13.1	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	40718_at
C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)/ug=Hs.85201 /len=739	X96719	Hs.85201	NM_005127	12p13-p12	Cluster Incl. X96719:H.sapiens mRNA for AICL (activation-induced C-type lectin) /cds=(132,581) /gb=X96719 /gi=1632815 /ug=Hs.85201 /len=739	40698_at

myosin, heavy polypeptide 11, smooth muscle	AF001548	Hs.78344	NM_002474	16p13.13-p13.12	AF001548 /FEATURE=mRNA /DEFINITION=HUAF001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence	767_at
Human mRNA for SB classII histocompatibility antigen alpha-chain	X00457	Hs.914	NM_033554	6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405/ug=Hs.914 /len=1048	38833_at
	AF013570	Hs.78344	NM_002474	16p13.13-p13.12	Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	37407_s_at
ARHGAP4 (Rho GTPase activating protein 4)	X78817	Hs.3109	NM_001666	xq28	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236	39649_at
Homo sapiens mRNA for KIAA0246 protein, partial	D87433	Hs.84753			Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639)	38487_at

cdsgi|1665760|dbj|D87433.1|D87433[1665760]					/gb=D87433 /gi=1665760 /ug=Hs.84753/len=6777	
major histocompatibility complex, class II, DM alpha	X62744	Hs.77522	NM_006120	6p21.3	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079	37344_at
voltage-dependent anion channel 1	L06132	Hs.149155	NM_003374	Xq13-q21	Cluster Incl. L06132:Human voltage-dependent anion channel isoform 1 (VDAC) mRNA, complete cds /cds=(99,950) /gb=L06132 /gi=340198 /ug=Hs.149155 /len=1806	40198_at
ITGB2 (integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen ; macrophageantigen 1 (mac-1) beta subunit))	M15395	Hs.83968	NM_000211	21q22.3	Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA /cds=(72,2381 /gb=M15395 /gi=186933 /ug=Hs.83968 /len=2776	37918_at
SERPING1 (serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1,	X54486	Hs.151242	NM_000062	11q12-q13.1	Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486	39775_at

(angioedema, hereditary))					/gi=29534 /ug=Hs.151242 /len=1827	
Homo sapiens mRNA; cDNA DKFZp564K0822 (from clone DKFZp564K0822)	W25986	Hs.4750		6	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
CBFA2T1 (core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related)	D43638	Hs.31551	NM_004349	8q22	Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	35638_at
DKFZP586N1922 protein	N99340	Hs.7357		19	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110	36095_at
ADP-ribosylation factor related protein	X91504	Hs.64904	NM_003224	20q13	Cluster Incl. X91504:H.sapiens mRNA for ARP1 protein/cds=(11,616) /gb=X91504 /gi=1103581 /ug=Hs.64904 /len=1541	35765_at

HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38096_f_at
ADP-RIBOSYLATION FACTOR-RELATED PROTEIN 1; ARFRP1	X91504	Hs.64904	NM_003224	20q13.3	Cluster Incl. X91504:H.sapiens mRNA for ARP1 protein/cds=(11,616) /gb=X91504 /gi=1103581 /ug=Hs.64904 /len=1541	36142_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38095_i_at
annexin V	U05770	Hs.79274		4q26-q28	Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126/gb=U05770 /gi=2182176 /ug=Hs.79274 /len=1597	37747_at
CD74 (CD74 antigen (invariant polypeptide of major histocompatibility complex, class II	M13560	Hs.84298	NM_004355	5q32	Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene	35016_at

antigen-associated))						/cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080	
interleukin 13 receptor, alpha 1	Y10659	Hs.285115	NM_001560	X		Y10659 /FEATURE=cds /DEFINITION=HSIL13RA_ H.sapiens IL-13Ra mRNA	359_at
meningioma (disrupted in balanced translocation) 1	X82209	Hs.79085	NM_002430	22q12.1		Cluster Incl. X82209:H.sapiens MN1 mRNA /cds=(887,4915)/gb=X82209 /gi=804991 /ug=Hs.79085 /len=7554	37283_at
CDw52, cell surface	N90866	Hs.276770	NM_001803	1p36		Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at
transforming growth factor, beta-induced, 68kD	M77349	Hs.118787	NM_000358	5q31		M77349 /FEATURE= /DEFINITION=HUMTGFBIG Human transforming growth factor-beta induced gene product (BIGH3) mRNAcomplete cd	1385_at

MGC2747(hypothetical protein MGC2747	AL046940	Hs.250723	NM_024104	19	Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /clone_end=5 /gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695	41273_at
major histocompatibility complex, class II, DR alpha	J00194	Hs.76807	NM_019111	6p21.3	Cluster Incl. J00194:human hla-dr antigen alpha-chainmrna & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231/ug=Hs.76807 /len=1199	37039_at
bone gamma-carboxyglutamate (gla) protein (osteocalc	AI131030	Hs.2558	NM_000711	1q25-q31	Cluster Incl. AI131030:qb82f10.x1 Homo sapiens cDNA3' end /clone=IMAGE-1706635 /clone_end=3' /gb=AI131030/gi=3601046 /ug=Hs.2558 /len=565	36253_at
NPR3 (natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C))	M59305	Hs.123655	NM_000908	5p14-p13	Cluster Incl. M59305:Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, complete cds /cds=(362,1987) /gb=M59305 /gi=178651	34519_at

aldehyde dehydrogenase 2, mitochondrial	X05409	Hs.195432	NM_000690	12q24.2	/ug=Hs.123655 /len=2081		
					Cluster Incl. X05409:Human RNA for mitochondrial aldehyde dehydrogenase I ALDH I (EC 1.2.1.3) /cds=(36,1586) /gb=X0540/gi=28605 /ug=Hs.195432 /len=1989		32747_at

Table 3:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
CAMP (cathelicidin antimicrobial peptide)	Z38026	Hs.51120	NM_004345	3p21.3	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	36710_at
SYNE-1B(synaptic nuclear envelope 1)]	AB018339	Hs.8182		6	Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
ALDH1A1 (aldehyde dehydrogenase 1 family, member A1)	K03000	Hs.76392	NM_000689	9q21	Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560	37015_at

LIG1 (ligase I, DNA, ATP-dependent)	AL039458	Hs.4193		3p14	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N0910 /clone_end=3 /gb=AL039458 /gi=5408506 /ug=Hs.4193 /len=849	34800_at
SGP28(specific granule protein (28 kDa); cysteine-rich secretory protein-3)	X94323	Hs.54431	NM_006061	6	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	36464_at
CBX7 (chromobox homolog 7)	AL031846			22q13.1	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39209_r_at

KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2)	AF052728	Hs.188021	NM_000238	7q35-q36	Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively spliced, partial cds /cds=(0,284) /gb=AF052728 /gi=3549258 /ug=Hs.165664 /len=767	38225_at
PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39208_i_at
PF4 (platelet factor 4)	M25897	Hs.81564	NM_002619	4q12-q21	M25897 /FEATURE=mRNA /DEFINITION=HUMPF4A Human platelet factor 4 (PF4) mRNA, complete cds	1115_at
PLSCR1 (phospholipid scramblase 1)	AB006746	Hs.198282	NM_021105	3q23	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077	32775_r_at
LCN2 (lipocalin 2 (oncogene 24p3))	AI762213	Hs.204238	NM_005564	9q34	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-	32821_at

					2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	41796_at
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase))	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at
TRB@ (T cell receptor beta locus)	M12886	Hs.303157		7q35	M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	1105_s_at
SPTA1 (spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	M61877	Hs.1985	NM_003126	1q21	Cluster Incl. M61877:Human erythroid alpha-spectrin (SPTA1) mRNA, complete cds /cds=(186,7475) /gb=M61877	38906_at

					/gi=338437 /ug=Hs.1985 /len=8001	
SYNE-2(synaptic nuclei expressed gene 2)	AL080133	Hs.57749	NM_015180	14	Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	41815_at
HLA-F (major histocompatibility complex, class I, F)	AL022723	Hs.110309	NM_018950	6p21.3	Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, class I, F (CDA12)) /cds=(97,1185) /gb=AL022723 /gi=5002624 /ug=Hs.110309 /len=1303	37420_i_at
SLU7(step II splicing factor SLU7)	AI660656	Hs.76325	NM_006425	5	Cluster Incl. AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2351436 /clone_end=3 /gb=AI660656 /gi=4764239 /ug=Hs.76325 /len=522	37006_at
CTSE (cathepsin E)	J05036	Hs.1355	NM_001910	1q31	J05036 /FEATURE=mRNA /DEFINITION=HUMCTSE Human cathepsin E mRNA, complete cds	271_s_at

CPO (coproporphyrinogen oxidase (coproporphyria, harderoporphyria))	D16611	Hs.89866	NM_000097	3q12	Cluster Incl. D16611:Human mRNA for coproporphyrinogen oxidase, complete cds /cds=(93,1157) /gb=D16611 /gi=469488 /ug=Hs.89866 /len=2333	37999_at
LEF1 (lymphoid enhancer-binding factor 1)	AL049409	Hs.44865	NM_016269	4q23-q25	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	36021_at
TFDP1 (transcription factor Dp-1)	L23959	Hs.79353	NM_007111	13q34	Cluster Incl. L23959:Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds /cds=(37,1269) /gb=L23959 /gi=414316 /ug=Hs.79353 /len=1440	37757_at
	S67247				Cluster Incl. S67247:smooth muscle myosin heavy chain isoform SMemb [human, umbilical cord, fetal aorta, mRNA Partial, 971 nt] /cds=(0,681) /gb=S67247 /gi=452986 /ug=Hs.2094 /len=971	32838_at

MMP8 (matrix metalloproteinase 8 (neutrophil collagenase))	J05556	Hs.73862	NM_002424	11q22.3	J05556 /FEATURE=mRNA /DEFINITION=HUMCLGNA Homo sapiens collagenase mRNA, complete cds	681_at
MINPP1 (multiple inositol polyphosphate histidine phosphatase, 1)	AL050356	Hs.95907	NM_004897	10q23	Cluster Incl. AL050356:Homo sapiens mRNA; cDNA DKFZp564L2016 (from clone DKFZp564L2016) /cds=UNKNOWN /gb=AL050356 /gi=4914568 /ug=Hs.95907 /len=2396	38325_at
TCF7 (transcription factor 7 (T-cell specific, HMG-box))	X59871	Hs.169294	NM_003202	5q31.1	Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form C) /cds=(79,885) /gb=X59871 /gi=36789 /ug=Hs.169294 /len=2910	32649_at
NS1-BP(NS1-binding protein)	AB020657	Hs.197298	NM_006469	1	Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete cds /cds=(630,2558) /gb=AB020657 /gi=4240188 /ug=Hs.197298 /len=3682	33752_at

CCR2 (chemokine (C-C motif) receptor 2)	U95626	Hs.395	NM_000647	3p21	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at
TRB@ (T cell receptor beta locus)	X00437	Hs.303157		7q35	Cluster Incl. X00437:Human mRNA for T-cell specific protein /cds=(37,975) /gb=X00437 /gi=36748 /ug=Hs.2003 /len=1151	32794_g_at
ADD2 (adducin 2 (beta))	U43959	Hs.247423	NM_001617	2p14-p13	Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145 /ug=Hs.4852 /len=1284	36052_at
CD59 (CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32	M84349	Hs.119663	NM_000611	11p13	Cluster Incl. M84349:Human transmembrane protein (CD59) gene /cds=(18,404) /gb=M84349 /gi=180150 /ug=Hs.119663 /len=1840	39351_at

TPM1 (tropomyosin 1 (alpha))	M19267	Hs.77899	NM_000366	15q22.1	Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	36791_g_at
TNFRSF7 (tumor necrosis factor receptor superfamily, member 7)	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	38578_at
TRB@ (T cell receptor beta locus)	X00437	Hs.303157		7q35	Cluster Incl. X00437:Human mRNA for T-cell specific protein /cds=(37,975) /gb=X00437 /gi=36748 /ug=Hs.2003 /len=1151	32793_at
PRKWNK1 (protein kinase, lysine deficient 1)	U00946	Hs.184592	NM_018979	12p13.3	Cluster Incl. U00946:Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA /cds=UNKNOWN /gb=U00946 /gi=405048 /ug=Hs.184592 /len=1971	32185_at

PLXNC1 (plexin C1)	AF030339	Hs.286229	NM_005761	12	Cluster Incl. AF030339:Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds /cds=(249,4955) /gb=AF030339 /gi=3176761 /ug=Hs.184697 /len=5121	32193_at
TRA@ (T cell receptor alpha locus)	M12959	Hs.74647		14q11.2	M12959 /FEATURE= /DEFINITION=HUMTCAXB Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds	1106_s_at
CPNE3 (copine III)	AB014536	Hs.14158	NM_003909	8p22-q21.3	Cluster Incl. AB014536:Homo sapiens mRNA for KIAA0636 protein, complete cds /cds=(120,1733) /gb=AB014536 /gi=3327085 /ug=Hs.14158 /len=4737	39706_at
MGEA5 (meningioma expressed antigen 5 (hyaluronidase))	AB014579	Hs.5734	NM_012215	10q24.1-q24.3	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303	35317_at

NELL2 (nel (chicken)-like 2)	D83018	Hs.79389	NM_006159	12q13.11-q13.12	Cluster Incl. D83018:Homo sapiens mRNA for nel-related protein 2, complete cds /cds=(96,2546) /gb=D83018 /gi=1827484 /ug=Hs.79389 /len=3198	32598_at
MECP2 (methyl CpG binding protein 2 (Rett syndrome))	AJ132917	Hs.3239	NM_004992	Xq28	Cluster Incl. AJ132917:Homo sapiens mRNA for methyl-CpG-binding protein 2 /cds=(75,1535) /gb=AJ132917 /gi=5419676 /ug=Hs.3239 /len=10091	34355_at
TRA@ (T cell receptor alpha locus)	X02883	Hs.74647		14q11.2	X02883 /FEATURE=cds /DEFINITION=HSTCRAC Human gene for T-cell receptor alpha chain C region	432_s_at
BLVRB (biliverdin reductase B (flavin reductase (NADPH)))	D32143	Hs.76289	NM_000713	19q13.1-q13.2	Cluster Incl. D32143:Human mRNA for biliverdin-IXbeta reductase I /cds=(109,729) /gb=D32143 /gi=699602 /ug=Hs.76289 /len=824	37002_at
PRDX2 (peroxiredoxin 2)	L19185	Hs.146354	NM_005809	13q12	Cluster Incl. L19185:Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds /cds=(124,720) /gb=L19185	39729_at

						/gi=440307 /ug=Hs.146354 /len=980	
AIF1 (allograft inflammatory factor 1)	Y14768	Hs.76364	NM_001623	6p21.3		Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /cds=(10,744) /gb=Y14768 /gi=3805800 /ug=Hs.890 /len=896	40729_s_at
TPM1 (tropomyosin 1 (alpha))	M19267	Hs.77899	NM_000366	15q22.1		Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	36790_at
AMPD3 (adenosine monophosphate deaminase (isoform E))	U29926	Hs.83918	NM_000480	11p15		Cluster Incl. U29926:Human AMP deaminase (AMPD3) gene, promoter 1a region /cds=(453,2777) /gb=U29926 /gi=1002661 /ug=Hs.83918 /len=4018	38463_s_at
	AF035315					Cluster Incl. AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence /cds=UNKNOWN /gb=AF035315 /gi=2661077 /ug=Hs.180737 /len=1331	33267_at

CDC2 (cell division cycle 2, G1 to S and G2 to M)	X05360	Hs.184572	NM_001786	10q21.1	X05360 /FEATURE=cds /DEFINITION=HSCDC2 Human CDC2 gene involved in cell cycle control	1803_at
GCLM (glutamate-cysteine ligase, modifier subunit)	L35546	Hs.89709	NM_002061	1p22.1	Cluster Incl. L35546:Homo sapiens gamma-glutamylcysteine synthetase light subunit mRNA, complete cds /cds=(253,1077) /gb=L35546 /gi=530136 /ug=Hs.89709 /len=1610	33163_r_at
NPAT (nuclear protein, ataxia-telangiectasia locus)	D83243	Hs.89385	NM_002519	11q22-q23	Cluster Incl. D83243:Human NPAT mRNA, complete cds /cds=(66,4349) /gb=D83243 /gi=1304113 /ug=Hs.89385 /len=5900	40732_at
KIAA0471(KIAA0471 gene product)	AB007940				Cluster Incl. AB007940:Homo sapiens mRNA for KIAA0471 protein, complete cds /cds=(412,1524) /gb=AB007940 /gi=3413903 /ug=Hs.107325 /len=6834	34445_at
ITK (IL2-inducible T-cell kinase)	L10717	Hs.211576	NM_005546	5q31-q32	L10717 /FEATURE= /DEFINITION=HUMTKTCS Homo sapiens T cell-specific tyrosine kinase mRNA,	1478_at

					complete cds	
TAL1 (T-cell acute lymphocytic leukemia 1 (NOTE: redefinition of symbol))	M63589	Hs.73828	NM_003189	1p32	M63589 /FEATURE=mRNA#5 /DEFINITION=HUMSCL7 Human stem cell leukemia gene product, exon 6	560_s_at
OLR1 (oxidised low density lipoprotein (lectin-like) receptor 1)	AF079167	Hs.77729	NM_002543	12p13.2-p12.3	Cluster Incl. AF079167:untitled /cds=(61,882) /gb=AF079167 /gi=4050003 /ug=Hs.77729 /len=2468	37233_at
	AL080216				Cluster Incl. AL080216:Homo sapiens mRNA; cDNA DKFZp586K1123 (from clone DKFZp586K1123) /cds=UNKNOWN /gb=AL080216 /gi=5262707 /ug=Hs.26837 /len=2204	35187_at
KIAA0922(KIAA0922 protein)	AB023139	Hs.37892	NM_015196		Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505	39929_at

GZMK (granzyme K (serine protease, granzyme 3; tryptase II))	U26174	Hs.3066	NM_002104	5q11-q12	Cluster Incl. U26174:Human pre-granzyme 3 mRNA, complete cds /cds=(40,834) /gb=U26174 /gi=829637 /ug=Hs.3066 /len=1040	36280_at
	U23852				Cluster Incl. U23852:Human T-lymphocyte specific protein tyrosine kinase p56lck (lck) abberant mRNA, complete cds /cds=(59,1150) /gb=U23852 /gi=775207 /ug=Hs.1765 /len=2129	33238_at
	L47276				L47276 /FEATURE=UTR#1 /DEFINITION=HUMTOPATR Homo sapiens (cell line HL-60) alpha topoisomerase truncated-form mRNA, 3 UTR	904_s_at
TOSO(regulator of Fas-induced apoptosis)	AF057557	Hs.58831	NM_005449	1	Cluster Incl. AF057557:Homo sapiens anti-Fas-induced apoptosis (TOSO) mRNA, complete cds /cds=(19,1191) /gb=AF057557 /gi=3169292	32967_at

						/ug=Hs.238857 /len=1339	
FCN1 (ficolin (collagen/fibrinogen domain-containing) 1)	S80990	Hs.252136	NM_002003	9q34	Cluster Incl. S80990:ficolin [human, uterus, mRNA, 1736 nt] /cds=(532,1512) /gb=S80990 /gi=1911529 /ug=Hs.169237 /len=1723	36447_at
CD3Z (CD3Z antigen, zeta polypeptide (TiT3 complex))	J04132	Hs.97087	NM_000734	1q22-q23	Cluster Incl. J04132:Human T cell receptor zeta-chain mRNA, complete cds /cds=(74,565) /gb=J04132 /gi=623041 /ug=Hs.97087 /len=1472	37078_at
CEACAM1 (carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein))	S71326	Hs.50964	NM_001712	19q13.2	Cluster Incl. S71326:BGPc=biliary glycoprotein adhesion molecule {alternatively spliced} [human, HT29 colon carcinoma cell line, mRNA Partial, 1473 nt] /cds=(0,1394) /gb=S71326 /gi=550030 /ug=Hs.50964 /len=1473	36082_at
DEFA4 (defensin, alpha 4, corticostatin)	AI250799	Hs.2582	NM_001925	8p23	Cluster Incl. AI250799:qi36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-	34546_at

GCA (grancalcin, EF-hand calcium-binding protein)	M81637	Hs.79381	NM_012198	2p14-q14.3	1858620 /clone_end=3 /gb=AI250799 /gi=3847328 /ug=Hs.2582 /len=542	
					Cluster Incl. M81637:Human grancalcin mRNA, complete cds /cds=(119,772) /gb=M81637 /gi=183030 /ug=Hs.79381 /len=1652	37556_at
KIAA0275(KIAA0275 gene product)	D87465	Hs.74583	NM_014767	10	Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(316,1590) /gb=D87465 /gi=1665814 /ug=Hs.74583 /len=5316	36155_at
IL2RB (interleukin 2 receptor, beta)	M26062	Hs.75596	NM_000878	22q13.1	M26062 /FEATURE= /DEFINITION=HUMIL2RBC Human interleukin 2 receptor beta chain (p70-75) mRNA, complete cds	1365_at
KIAA0513(KIAA0513 gene product)	AB011085	Hs.301658	NM_014732	16	Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete cds /cds=(631,1866) /gb=AB011085	38735_at

					/gi=3043549 /ug=Hs.85053 /len=7758	
RHAG (Rhesus blood group-associated glycoprotein)	X64594	Hs.169536	NM_000324	6p21.1-p11	Cluster Incl. X64594:H.sapiens mRNA for 50 kDa erythrocyte plasma membrane glycoprotein /cds=(27,1256) /gb=X64594 /gi=31194 /ug=Hs.169536 /len=1891	32663_at
IGF2R (insulin-like growth factor 2 receptor)	Y00285	Hs.76473	NM_000876	6q26	Y00285 /FEATURE=cds /DEFINITION=HSIGFIIR Human mRNA for insuline-like growth factor II receptor /NOTE=replacement of probe set 972_s_at	160027_s_at
PPP2R5C (protein phosphatase 2, regulatory subunit B (B56), gamma isoform)	U37352	Hs.171734	NM_002719	3p21	U37352 /FEATURE= /DEFINITION=HSU37352 Human protein phosphatase 2A B alpha1 regulatory subunit mRNA, complete cds	176_at
CCR7 (chemokine (C-C motif) receptor 7)	L31584	Hs.1652	NM_001838	17q12-q21.2	L31584 /FEATURE=exon /DEFINITION=HUMEBI103 Human G protein-coupled receptor (EBI 1) gene	1097_s_at

					exon 3, complete cds	
LCK (lymphocyte-specific protein tyrosine kinase)	M36881	Hs.1765	NM_005356	1p35-p34.3	M36881 /FEATURE=mRNA /DEFINITION=HUMLCKAA Human lymphocyte-specific protein tyrosine kinase (lck) mRNA, complete cds	2059_s_at
ALS2CR3 (amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3)	AB011121	Hs.154248	NM_015049	2q33	Cluster Incl. AB011121:Homo sapiens mRNA for KIAA0549 protein, partial cds /cds=(0,1409) /gb=AB011121 /gi=3043621 /ug=Hs.154248 /len=4745	40064_at
	AF055029				Cluster Incl. AF055029:Homo sapiens clone 24711 mRNA sequence /cds=UNKNOWN /gb=AF055029 /gi=3005759 /ug=Hs.4988 /len=1816	34866_at
GG2-1(TNF-induced protein)	AF099935	Hs.17839	NM_014350	5	Cluster Incl. AF099935:Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds /cds=(84,680) /gb=AF099935 /gi=3860092 /ug=Hs.17839 /len=1897	33243_at

EPOR (erythropoietin receptor)	M60459	Hs.89548	NM_000121	19p13.3-p13.2	Cluster Incl. M60459:Human erythropoietin receptor mRNA, complete cds /cds=(105,1631) /gb=M60459 /gi=182244 /ug=Hs.89548 /len=1818	37986_at
CDC25B (cell division cycle 25B)	S78187	Hs.153752	NM_004358	20p13	S78187 /FEATURE= /DEFINITION=S78187 CDC25Hu2=cdc25+ homolog [human, mRNA, 3118 nt]	1347_at
KLRB1 (killer cell lectin-like receptor subfamily B, member 1)	U11276	Hs.169824	NM_002258	12p13	Cluster Incl. U11276:Human hNKR-P1a protein (NKR-P1A) mRNA, complete cds /cds=(60,737) /gb=U11276 /gi=538270 /ug=Hs.169824 /len=738	35449_at
KIAA0349(KIAA0349 protein)	AB002347			6	Cluster Incl. AB002347:Human mRNA for KIAA0349 gene, partial cds /cds=(0,3827) /gb=AB002347 /gi=2224638 /ug=Hs.15303 /len=6158	39797_at
GYPB (glycophorin B (includes Ss blood group))	U05255	Hs.250653	NM_002100	4q28-q31	Cluster Incl. U05255:Human glycophorin HeP2 mRNA, partial cds /cds=(0,302)	41026_f_at

					/gb=U05255 /gi=454085 /ug=Hs.93223 /len=338	
CREME9(cytokine receptor-like molecule 9)	AF046059	Hs.7120	NM_015986	17	Cluster Incl. AF046059:Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA, complete cds /cds=(22,1350) /gb=AF046059 /gi=4105471 /ug=Hs.119410 /len=2848	37509_at
DGKA (diacylglycerol kinase, alpha (80kD))	X62535	Hs.172690	NM_001345	12q13.3	Cluster Incl. X62535:H.sapiens mRNA for diacylglycerol kinase /cds=(103,2310) /gb=X62535 /gi=30822 /ug=Hs.172690 /len=2564	32716_at
KIAA0008(KIAA0008 gene product)	D13633	Hs.77695	NM_014750	14	Cluster Incl. D13633:Human mRNA for KIAA0008 gene, complete cds /cds=(121,2418) /gb=D13633 /gi=286012 /ug=Hs.77695 /len=2640	37231_at
MAF (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene homolog)	AF055376	Hs.30250	NM_005360	16q22-q23	Cluster Incl. AF055376:Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds	41504_s_at

					/cds=(807,1928) /gb=AF055376 /gi=3335147 /ug=Hs.30250 /len=4246	
CEACAM1 (carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein))	X16354	Hs.50964	NM_001712	19q13.2	X16354 /FEATURE= /DEFINITION=HSTM1CEA Human mRNA for transmembrane carcinoembryonic antigen BGPa (formerly TM1-CEA)	988_at
GCLC (glutamate-cysteine ligase, catalytic subunit)	M90656	Hs.151393	NM_001498	6p12	Cluster Incl. M90656:Human gamma-glutamylcysteine synthetase (GCS) mRNA, complete cds /cds=(92,2005) /gb=M90656 /gi=183038 /ug=Hs.151393 /len=2615	31850_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. :H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
HIRA (HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A)	X89887	Hs.172350	NM_003325	22q11.21	Cluster Incl. X89887:Homo sapiens mRNA for WD repeat protein (HIRA) /cds=(220,3273) /gb=X89887 /gi=3928218	32706_at

					/ug=Hs.172350 /len=4018		
EPOR (erythropoietin receptor)	M60459	Hs.89548	NM_000121	19p13.3-p13.2	M60459 /FEATURE= /DEFINITION=HUMERYTH Human erythropoietin receptor mRNA, complete cds	1087_at	
LILRB2 (leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member	AF004231	Hs.22405	NM_005874	19q13.4	Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds /cds=(208,2001) /gb=AF004231 /gi=2343110 /ug=Hs.22405 /len=2863	39221_at	
KLF5 (Kruppel-like factor 5 (intestinal))	D14520	Hs.84728	NM_001730	13q21.2-13q22.2	Cluster Incl. D14520:Human mRNA for GC-Box binding protein BTEB2, complete cds /cds=(558,1217) /gb=D14520 /gi=303596 /ug=Hs.84728 /len=1301	37926_at	
MTMR1 (myotubularin related protein 1)	AJ224979	Hs.23200		Xq28	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200	34654_at	

					/len=2582	
KEL (Kell blood group)	M64934	Hs.157	NM_000420	7q33	Cluster Incl. M64934:Human kell blood group protein mRNA /cds=(123,2321) /gb=M64934 /gi=413776 /ug=Hs.157 /len=2458	38197_at
MAL (mal, T-cell differentiation protein)	X76220	Hs.80395	NM_002371	2cen-q13	Cluster Incl. X76220:H.sapiens MAL gene exon 1 (and joined CDS) /cds=(59,520) /gb=X76220 /gi=433225 /ug=Hs.80395 /len=1056	38051_at
CDC2 (cell division cycle 2, G1 to S and G2 to M)	D88357	Hs.184572	NM_001786	10q21.1	Cluster Incl. D88357:Homo sapiens mRNA for CDC2 delta T, complete cds /cds=(27,749) /gb=D88357 /gi=3126638 /ug=Hs.184572 /len=780	33324_s_at
IGLL3 (immunoglobulin lambda-like polypeptide 3)	AI932613	Hs.296552		22q11.23	Cluster Incl. AI932613:wo05c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2454434 /clone_end=3 /gb=AI932613 /gi=5671350 /ug=Hs.62036 /len=570	41827_f_at

IL7R (interleukin 7 receptor)	M29696	Hs.237868	NM_002185	5p13	M29696 /FEATURE= /DEFINITION=HUMIL7AA Human interleukin-7 receptor (IL-7) mRNA, complete cds	1370_at
EGFL5 (EGF-like-domain, multiple 5)	AB011542	Hs.5599		9q32-q33.3	Cluster Incl. AB011542:Homo sapiens mRNA for MEGF9, partial cds /cds=(0,1129) /gb=AB011542 /gi=3449309 /ug=Hs.5599 /len=5507	36488_at
GW112(differentially expressed in hematopoietic lineages)	AF097021	Hs.273321	NM_006418	13	Cluster Incl. AF097021:Homo sapiens GW112 protein (GW112) mRNA, complete cds /cds=(508,1071) /gb=AF097021 /gi=3860076 /ug=Hs.100347 /len=2830	38615_at
NME2 (non-metastatic cells 2, protein (NM23B) expressed in)	X58965	Hs.275163	NM_002512	17q21.3	X58965 /FEATURE= /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2 gene	1980_s_at
SET (SET translocation (myeloid leukemia-associated))	M93651	Hs.145279	NM_003011	9q34	Cluster Incl. M93651:Human set gene, complete cds /cds=(3,836) /gb=M93651 /gi=338038 /ug=Hs.145279 /len=2562	40189_at

					/gi=338038 /ug=Hs.145279 /len=2562	
KDELR1 (KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1)	X55885	Hs.78040	NM_006801	19q13.3	Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=(146,784) /gb=X55885 /gi=34030 /ug=Hs.78040 /len=1086	37386_i_at
NME2 (non-metastatic cells 2, protein (NM23B) expressed in)	X58965	Hs.275163	NM_002512	17q21.3	Cluster Incl. X58965:H.sapiens RNA for nm23-H2 gene /cds=(72,530) /gb=X58965 /gi=35069 /ug=Hs.227823 /len=670	33415_at
KARS (lysyl-tRNA synthetase)	D32053	Hs.3100	NM_005548	16q23-q24	Cluster Incl. D32053:Homo sapiens mRNA for Lysyl tRNA Synthetase, complete cds /cds=(40,1833) /gb=D32053 /gi=2366751 /ug=Hs.3100 /len=1997	34336_at
(NOT approved by the HUGO/GDB nomenclature commitee)	U41635	Hs.76228	NM_006812	12	Cluster Incl. U41635:Human OS-9 precurosor mRNA, complete cds /cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736	36996_at

PLOD3 (procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3)	AF046889	Hs.153357	NM_001084	7q22	Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735	39801_at
(NOT approved by the HUGO/GDB nomenclature commitee)	AC004410	Hs.284161		19	Cluster Incl. AC004410:Homo sapiens chromosome 19, fosmid 39554 /cds=(0,1196) /gb=AC004410 /gi=2959558 /ug=Hs.167352 /len=1197	35426_at
P2RX4 (purinergic receptor P2X, ligand-gated ion channel, 4)	U83993	Hs.321709	NM_002560	12q24.32	Cluster Incl. U83993:Human P2X4 purinoreceptor mRNA, complete cds /cds=(309,1475) /gb=U83993 /gi=4099120 /ug=Hs.9610 /len=2031	38332_at
COMT (catechol-O-methyltransferase)	M58525	Hs.240013	NM_000754	22q11.21	Cluster Incl. M58525:Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds /cds=(204,1019) /gb=M58525 /gi=179954 /ug=Hs.78534 /len=1206	34651_at

UQCRC2 (ubiquinol-cytochrome c reductase core protein II)	J04973	Hs.173554	NM_003366	16p12	Cluster Incl. J04973:Human cytochrome bc-1 complex core protein II mRNA, complete cds /cds=(53,1414) /gb=J04973 /gi=180927 /ug=Hs.173554 /len=1588	40854_at
EIF4A1 (eukaryotic translation initiation factor 4A, isoform 1)	D13748	Hs.129673	NM_001416	17p13	D13748 /FEATURE= /DEFINITION=HUM4AI Human mRNA for eukaryotic initiation factor 4AI	1199_at
(NOT approved by the HUGO/GDB nomenclature commitee)	AI582831	Hs.102419	NM_015871	1	Cluster Incl. AI582831:tn36c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2169706 /clone_end=3 /gb=AI582831 /gi=4568728 /ug=Hs.102419 /len=555	38640_at
NFIL3 (nuclear factor, interleukin 3 regulated)	X64318	Hs.79334	NM_005384	9q22	Cluster Incl. X64318:H.sapiens E4BP4 gene /cds=(213,1601) /gb=X64318 /gi=30955 /ug=Hs.79334 /len=1904	37544_at

(NOT approved by the HUGO/GDB nomenclature commitee)	AL022328	Hs.33026	NM_025204	22	Cluster Incl. AL022328:Human DNA sequence from clone 402G11 on chromosome 22q13.31-13.33 Contains genes for SAPK3 (stress-activated protein kinase 3), PRKM11 (protein kinase mitogen-activated 11), KIAA0315, ESTs, GSSs and CpG islands /cds=(11,1105) /gb=AL	40033_at
GSTP1 (glutathione S-transferase pi)	U12472	Hs.226795	NM_000852	11q13	Cluster Incl. U12472:Human glutathione S-transferase (GST phi) gene, complete cds /cds=(0,632) /gb=U12472 /gi=763404 /ug=Hs.226795 /len=757	33396_at
GRHPR (glyoxylate reductase/hydroxypyruvate reductase)	W28944	Hs.155742	NM_012203	9q12	Cluster Incl. W28944:54h12 Homo sapiens cDNA /gb=W28944 /gi=1308955 /ug=Hs.155742 /len=748	40133_s_at
HSPCB (heat shock 90kD protein 1, beta)	M16660	Hs.74335	NM_007355	6p12	Cluster Incl. M16660:Human 90-kDa heat-shock protein gene, cDNA, complete cds /cds=UNKNOWN /gb=M16660 /gi=184420	33984_at

					/ug=Hs.74335 /len=2543	
(NOT approved by the HUGO/GDB nomenclature commitee)	U70671	Hs.43509	NM_007245	7	Cluster Incl. U70671:Human ataxin-2 related protein mRNA, partial cds /cds=(0,1044) /gb=U70671 /gi=1679685 /ug=Hs.43509 /len=1206	34817_s_at
ARHGDIA (Rho GDP dissociation inhibitor (GDI) alpha)	X69550	Hs.159161	NM_004309	17q25.3	Cluster Incl. X69550:H.sapiens mRNA for rho GDP-dissociation Inhibitor 1 /cds=(53,667) /gb=X69550 /gi=456190 /ug=Hs.159161 /len=1819	40164_at
(NOT approved by the HUGO/GDB nomenclature commitee)	S82470	Hs.78768	NM_024298	19	S82470 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	181_g_at
DF (D component of complement (adipsin))	M84526	Hs.155597	NM_001928	19	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526	40282_s_at

					/gi=178625 /ug=Hs.155597 /len=1071	
CLN3 (ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease))	AC002544	Hs.194660	NM_000086	16p12.1	Cluster Incl. AC002544:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5 /cds=(85,2826) /gb=AC002544 /gi=3337382 /ug=Hs.4835 /len=3027	34841_at
DAP (death-associated protein)	X76105	Hs.75189	NM_004394	5p15.2	Cluster Incl. X76105:H.sapiens DAP-1 mRNA /cds=(159,467) /gb=X76105 /gi=434844 /ug=Hs.75189 /len=2232	36199_at
NACA (nascent-polypeptide-associated complex alpha polypeptide)	AF054187	Hs.32916	NM_005594	12q23-q24.1	Cluster Incl. AF054187:Homo sapiens alpha NAC mRNA, complete cds /cds=(309,956) /gb=AF054187 /gi=4092059 /ug=Hs.146763 /len=1059	39740_g_at

Table 4:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
KIAA0842(KIAA0842 protein)	AB020649	Hs.74569		1	Cluster Incl. AB020649:Homo sapiens mRNA for KIAA0842 protein, partial cds /cds=(0,3062) /gb=AB020649 /gi=4240172 /ug=Hs.74569 /len=3896	36150_at
H1FX (H1 histone family, member X)	D64142	Hs.109804	NM_006026		D64142 /FEATURE=mRNA /DEFINITION=D64142 Human mRNA for histone H1x, complete cds	319_g_at
NUFIP1 (nuclear fragile X mental retardation protein interacting protein 1)	AL049842	Hs.120247	NM_012345	13q14	Cluster Incl. AL049842:Human DNA sequence from clone 129L7 on chromosome 6q12-13. Contains the gene for a PUTATIVE novel protein, ESTs, an STS, GSSs and a taga repeat polymorphism /cds=(9,749) /gb=AL049842	37518_at

						/gi=5419788 /ug=Hs.120247 /len=1679	
PPP6C (protein phosphatase 6, catalytic subunit)	X92972	Hs.80324	NM_002721		xq22.3	Cluster Incl. X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21,938) /gb=X92972 /gi=5701862 /ug=Hs.80324 /len=1292	37581_at
SUI1(putative translation initiation factor)	AJ012375	Hs.150580	NM_005801		19	Cluster Incl. AJ012375:Homo sapiens mRNA for SUI1 protein translation initiation factor /cds=UNKNOWN /gb=AJ012375 /gi=4468342 /ug=Hs.150580 /len=1350	40203_at
UNRIP(unr-interacting protein)	AB024327	Hs.3727	NM_007178		12	Cluster Incl. AB024327:Homo sapiens pt-wd mRNA for WD-40 repeat protein, complete cds /cds=(300,1352) /gb=AB024327 /gi=4519416 /ug=Hs.3727 /len=1850	34402_at

ATF4 (activating transcription factor 4 (tax-responsive enhancer element B67))	AL022312	Hs.181243	NM_001675	22q13.1	Cluster Incl. AL022312:dJ1104E15.2 (activating transcription factor 4 (tax-responsive enhancer element B67)) /cds=(882,1937) /gb=AL022312 /gi=4914501 /ug=Hs.181243 /len=2016	41235_at
WBSCR1 (Williams-Beuren syndrome chromosome region 1)	D26068	Hs.180900	NM_022170	7q11.23	Cluster Incl. D26068:Human mRNA for KIAA0038 gene, partial cds /cds=(0,694) /gb=D26068 /gi=436225 /ug=Hs.180900 /len=2477	41212_r_at
RNPS1 (RNA-binding protein S1, serine-rich domain)	L37368	Hs.75104	NM_006711	16p13.3	Cluster Incl. L37368:Human (clone E5.1) RNA-binding protein mRNA, complete cds /cds=(549,1466) /gb=L37368 /gi=1236282 /ug=Hs.75104 /len=2438	36186_at
C6orf5 (chromosome 6 open reading frame 5)	AL050289	Hs.7446	NM_015524	6q21	Cluster Incl. AL050289:Homo sapiens mRNA; cDNA DKFZp586G0522 (from clone DKFZp586G0522) /cds=(179,1876) /gb=AL050289 /gi=4886510 /ug=Hs.7446 /len=2364	36139_at

	W28807				Cluster Incl. W28807:52a3 Homo sapiens cDNA /gb=W28807 /gi=1308755 /ug=Hs.121849 /len=819	39370_at
POLB (polymerase (DNA directed), beta)	D29013	Hs.180107	NM_002690	8p11.2	D29013 - /FEATURE= /DEFINITION=HUMLNCAP Human mRNA for DNA polymerase beta, complete cds	1696_at
DKFZP434D1335(DKFZP434D1335 protein)	AI920820	Hs.8258		19	Cluster Incl. AI920820:wn82e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2452362 /clone_end=3 /gb=AI920820 /gi=5656784 /ug=Hs.8258 /len=519	38400_at
PRCC (papillary renal cell carcinoma (translocation-associated))	X99720	Hs.9629	NM_005973	1q21.1	Cluster Incl. X99720:H.sapiens TPRC gene /cds=(212,1687) /gb=X99720 /gi=1869817 /ug=Hs.9629 /len=2053	39149_at
GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))	M63904	Hs.73797	NM_002068	19p13.3	Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	40365_at

RBM4 (RNA binding motif protein 4)	U89505	Hs.6106	NM_002896	11q13	Cluster Incl. U89505:Human Hlark mRNA, complete cds /cds=(55,1155) /gb=U89505 /gi=2078528 /ug=Hs.6106 /len=1598	35351_at
TCEB3 (transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A))	L47345	Hs.155202	NM_003198	1p36.1	L47345 /FEATURE= /DEFINITION=HUMELONA Homo sapiens elongin A mRNA, complete cds	639_s_at
BLCAP (bladder cancer associated protein)	AL049288	Hs.5300	NM_006698	20q11.2-q12	Cluster Incl. AL049288:Homo sapiens mRNA; cDNA DKFZp564M053 (from clone DKFZp564M053) /cds=UNKNOWN /gb=AL049288 /gi=4500049 /ug=Hs.5300 /len=2018	35267_g_at
SNRPA1 (small nuclear ribonucleoprotein polypeptide A')	X13482	Hs.80506	NM_003090	22q	Cluster Incl. X13482:Human mRNA for U2 snRNP-specific A protein /cds=(56,823) /gb=X13482 /gi=37546 /ug=Hs.80506 /len=1033	37585_at
ZNF207 (zinc finger protein 207)	AF046001	Hs.62112	NM_003457	17p13.2	Cluster Incl. AF046001:Homo sapiens zinc finger transcription factor (ZNF207) mRNA, complete cds /cds=(202,1638)	35368_at

					/gb=AF046001 /gi=2895869 /ug=Hs.62112 /len=2331	
KIAA0174(KIAA0174 gene product)	D79996	Hs.75824	NM_014761	19	Cluster Incl. D79996:Human mRNA for KIAA0174 gene, complete cds /cds=(63,1157) /gb=D79996 /gi=1136407 /ug=Hs.75824 /len=2348	36942_at
UBE2D3 (ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	U39318	Hs.118797	NM_003340	4q24-q26	Cluster Incl. U39318:Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds /cds=(45,488) /gb=U39318 /gi=1145690 /ug=Hs.118797 /len=724	39083_at
H1FX (H1 histone family, member X)	D64142	Hs.109804	NM_006026		D64142 /FEATURE=mRNA /DEFINITION=D64142 Human mRNA for histone H1x, complete cds	318_at
KIF5A (kinesin family member 5A)	U06698	Hs.192760	NM_004984	12q13	Cluster Incl. U06698:Human neuronal kinesin heavy chain mRNA, complete cds /cds=(148,3246) /gb=U06698 /gi=497123	35880_at

					/ug=Hs.192760 /len=3840	
ELF1 (E74-like factor 1 (ets domain transcription factor)	M82882	Hs.154365		13q13	Cluster Incl. M82882:Human cis-acting sequence /cds=UNKNOWN /gb=M82882 /gi=180551 /ug=Hs.154365 /len=3564	40067_at
ZNF278 (zinc finger protein 278)	AI352450	Hs.27801	NM_014323	22q12.2	Cluster Incl. AI352450:qt16g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1947812 /clone_end=3 /gb=AI352450 /gi=4089656 /ug=Hs.27801 /len=508	34300_at
TCF7L2 (transcription factor 7-like 2 (T-cell specific, HMG-box))	Y11306	Hs.173638	NM_030756	10q25.3	Cluster Incl. Y11306:Homo sapiens mRNA for hTCF-4 /cds=(307,2097) /gb=Y11306 /gi=4469251 /ug=Hs.154485 /len=2444	32025_at
RNF10 (ring finger protein 10)	D87451	Hs.5094	NM_014868	12	Cluster Incl. D87451:Human mRNA for KIAA0262 gene, complete cds /cds=(698,2983) /gb=D87451 /gi=1665790 /ug=Hs.5094 /len=3205	34883_at

TACC1 (transforming, acidic coiled-coil containing protein 1)	AF049910	Hs.173159	NM_006283	8p11	Cluster Incl. AF049910:Homo sapiens TACC1 (TACC1) mRNA, complete cds /cds=(320,2737) /gb=AF049910 /gi=3435156 /ug=Hs.173159 /len=7735	40841_at
PTS (6-pyruvoyltetrahydropterin synthase)	L76259	Hs.366	NM_000317	11q22.3-q23.3	Cluster Incl. L76259:Homo sapiens PTS gene, complete cds /cds=(68,505) /gb=L76259 /gi=2276403 /ug=Hs.366 /len=921	35697_at
MT1A (metallothionein 1A (functional))	K01383	Hs.173451		16q13	Cluster Incl. K01383:Human metallothionein-I-A gene, complete coding sequence /cds=(0,185) /gb=K01383 /gi=187536 /ug=Hs.203967 /len=186	31623_f_at
CAMK2G (calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma)	U81554	Hs.250857		10q22	Cluster Incl. U81554:Homo sapiens CaM kinase II isoform mRNA, complete cds /cds=(212,931) /gb=U81554 /gi=2275253 /ug=Hs.231812 /len=972	31670_s_at
SFPQ (splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-	W27050	Hs.180610	NM_005066	1pter-p32.3	Cluster Incl. W27050:19f7 Homo sapiens cDNA /gb=W27050 /gi=1306422	41199_s_at

associated))					/ug=Hs.180610 /len=699	
PPP2CA (protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform)	M60483	Hs.91773	NM_002715	5q23-q31	M60483 /FEATURE=mRNA /DEFINITION=HUMPP2AA Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds	237_s_at
KIAA0105(Wilms' tumour 1-associating protein	D14661	Hs.119	NM_004906	6	Cluster Incl. D14661:Human mRNA for KIAA0105 gene, complete cds /cds=(124,579) /gb=D14661 /gi=285946 /ug=Hs.119 /len=1622	41635_at
GNA13 (guanine nucleotide binding protein (G protein), alpha 13)	L22075	Hs.1666	NM_006572	17q22-q24	Cluster Incl. L22075:Human guanine nucleotide regulatory protein (G13) mRNA, complete cds /cds=(41,1174) /gb=L22075 /gi=404721 /ug=Hs.1666 /len=1402	33635_at
UGTREL7(UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter)	D87449	Hs.82635	NM_015139	1	Cluster Incl. D87449:Human mRNA for KIAA0260 gene, partial cds /cds=(0,1153) /gb=D87449 /gi=1665786 /ug=Hs.82635 /len=5918	37888_at

BRAP (BRCA1 associated protein)	AL042733	Hs.122764	NM_006768	12q24	Cluster Incl. AL042733:DKFZp434B2222_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434B2222 /clone_end=3 /gb=AL042733 /gi=5422182 /ug=Hs.30982 /len=782	41512_at
PMAIP1 (phorbol-12-myristate-13-acetate-induced protein 1)	D90070	Hs.96	NM_021127	18q22	Cluster Incl. D90070:Human ATL-derived PMA-responsive (APR) peptide mRNA /cds=(173,337) /gb=D90070 /gi=219475 /ug=Hs.96 /len=1885	41048_at
KIAA1116(KIAA1116 protein)	AB029039	Hs.227602	NM_014892	6	Cluster Incl. AB029039:Homo sapiens mRNA for KIAA1116 protein, complete cds /cds=(185,4000) /gb=AB029039 /gi=5689568 /ug=Hs.227602 /len=4664	34274_at
ERF (Ets2 repressor factor)	U15655	Hs.333069	NM_006494	19q13	U15655 /FEATURE= /DEFINITION=HSU15655 Human ets domain protein ERF mRNA, complete cds	1242_at

ZNF161 (zinc finger protein 161)	D28118	Hs.6557	NM_007146	3q26.2	D28118 /FEATURE= /DEFINITION=HUMDB1 Human mRNA for DB1, complete cds	350_at
MAPK3 (mitogen-activated protein kinase 3)	X60188	Hs.861		16p12-p11.2	X60188 /FEATURE=mRNA /DEFINITION=HSERK1 Human ERK1 mRNA for protein serine/threonine kinase	1000_at
	AI659108				Cluster Incl. AI659108:tu08c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2250448 /clone_end=3 /gb=AI659108 /gi=4762678 /ug=Hs.99093 /len=492	41084_at
SYPL (synaptophysin-like protein)	X68194	Hs.80919	NM_006754	7q22.1-7q31.33	Cluster Incl. X68194:H.sapiens h-Sp1 mRNA /cds=(33,812) /gb=X68194 /gi=32473 /ug=Hs.80919 /len=2108	38075_at
SUPT5H (suppressor of Ty (S.cerevisiae) 5 homolog)	AF040253	Hs.70186	NM_003169	19q13	Cluster Incl. AF040253:Homo sapiens transcription factor Tat-CT1 mRNA, complete cds /cds=(207,3470) /gb=AF040253 /gi=4104823 /ug=Hs.70186	35826_at

					/len=3738	
D13S106E(highly charged protein)	X59131	Hs.151236	NM_005800	13	Cluster Incl. X59131:Homo sapiens D13S106 mRNA for a highly charged amino acid sequence /cds=(177,3455) /gb=X59131 /gi=3776087 /ug=Hs.151236 /len=3650	31847_at
WHN (winged-helix nude)	Y11739	Hs.198313	NM_003593	7q11-q12	Cluster Incl. Y11739:H.sapiens mRNA for whn transcription factor /cds=(29,1975) /gb=Y11739 /gi=2315191 /ug=Hs.198313 /len=2697	31980_at
ARHA (ras homolog gene family, member A)	L25080	Hs.77273	NM_001664	3p21.3	L25080 /FEATURE= /DEFINITION=HUMRHOAA Homo sapiens GTP-binding protein (rhoA) mRNA, complete cds	1394_at
ERF (Ets2 repressor factor)	U15655	Hs.333069	NM_006494	19q13	Cluster Incl. U15655:Human ets domain protein ERF mRNA, complete cds /cds=(122,1768) /gb=U15655 /gi=1015336	38996_at

					/ug=Hs.110906 /len=2667	
MAX (MAX protein)	X60287	Hs.42712	NM_002382	14q23	X60287 /FEATURE=cds /DEFINITION=HSMAXM H.sapiens max mRNA	1981_s_at
RAB14(GTPase Rab14)	AF052113	Hs.5807	NM_016322	9	Cluster Incl. AF052113:Homo sapiens clone 23675 mRNA sequence /cds=UNKNOWN /gb=AF052113 /gi=3360420 /ug=Hs.5807 /len=1652	35325_at
EIF3S5 (eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD))	U94855	Hs.7811	NM_003754	2p16.1	Cluster Incl. U94855:Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, compl U94855 cds /cds=(6,1079) /gb=U94855 /gi=2055430 /ug=Hs.7811 /len=1231	32576_at
DNAJA1 (DnaJ (Hsp40) homolog, subfamily A, member 1)	L08069	Hs.94	NM_001539	9p13-p12	Cluster Incl. L08069:Human heat shock protein, E. coli DnaJ homologue mRNA, complete cds /cds=(82,1275) /gb=L08069 /gi=306713 /ug=Hs.94 /len=1438	39118_at

SLBP (stem-loop (histone) binding protein)	U75679	Hs.75257	NM_006527	4p16.3	Cluster Incl. U75679:Human histone stem-loop binding protein (SLBP) mRNA, complete cds /cds=(115,927) /gb=U75679 /gi=1732076 /ug=Hs.75257 /len=1725	36913_at
CCNI (cyclin I)	D50310	Hs.79933	NM_006835	4	D50310 /FEATURE= /DEFINITION=HUMCYI Human mRNA for cyclin I, complete cds	1836_at
	L10910				Cluster Incl. L10910:Homo sapiens splicing factor (CC1.3) mRNA, complete cds /cds=(149,1723) /gb=L10910 /gi=405191 /ug=Hs.145696 /len=2595	39725_at
SSH3BP1 (spectrin SH3 domain binding protein 1)	AF001628	Hs.24752	NM_005470	10p11.2	Cluster Incl. AF001628:Homo sapiens interactor protein AblBP4 (AblBP4) mRNA, complete cds /cds=(48,1403) /gb=AF001628 /gi=4100618 /ug=Hs.204036 /len=2175	38924_s_at
DYRK1A (dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	D86550	Hs.75842	NM_001396	21q22.13	D86550 /FEATURE= /DEFINITION=D86550 Human mRNA for	1512_at

phosphorylation regulated kinase 1A					serine/threonine protein kinase, complete cds	
ZFR(zinc finger RNA binding protein)	AI459274	Hs.173518	NM_016107	5	Cluster Incl. AI459274:tk11f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2150733 /clone_end=3 /gb=AI459274 /gi=4311853 /ug=Hs.87150 /len=687	33148_at
BAG5 (BCL2-associated athanogene 5)	AB020680	Hs.5443	NM_004873	14	Cluster Incl. AB020680:Homo sapiens mRNA for KIAA0873 protein, partial cds /cds=(0,1400) /gb=AB020680 /gi=4240234 /ug=Hs.5443 /len=4119	36463_at
GABPB1 (GA-binding protein transcription factor, beta subunit 1 (53kD))	D13317	Hs.78915	NM_005254	7q11.2	Cluster Incl. D13317:Human mRNA for transcription factor, E4TF1-53, complete cds /cds=(205,1356) /gb=D13317 /gi=286024 /ug=Hs.211616 /len=1552	35943_s_at
PTP4A2 (protein tyrosine phosphatase type IVA, member 2)	U14603	Hs.82911	NM_003479	1p35	Cluster Incl. U14603:Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence /cds=(423,926) /gb=U14603 /gi=894158 /ug=Hs.82911	38415_at

					/len=1526	
KIAA0414(KIAA0414 protein)	AB007874			9	Cluster Incl. AB007874:Homo sapiens KIAA0414 mRNA, partial cds /cds=(1132,2535) /gb=AB007874 /gi=2887448 /ug=Hs.127649 /len=5725	41695_at
DLST (dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex))	D26535	Hs.250801	NM_001933	14q24.3	Cluster Incl. D26535:Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) /cds=(43,1404) /gb=D26535 /gi=537349 /ug=Hs.179989 /len=2822	33258_g_at
KIAA0016(translocase of outer mitochondrial membrane 20 (yeast) homolog)	D13641	Hs.75187	Hs.75187	1	Cluster Incl. D13641:Human mRNA for KIAA0016 gene, complete cds /cds=(101,538) /gb=D13641 /gi=285986 /ug=Hs.75187 /len=3259	36198_at
HT010(uncharacterized hypothalamus protein HT010	AL049948	Hs.6375	NM_018471	2	Cluster Incl. AL049948:Homo sapiens mRNA; cDNA DKFZp564K0222 (from clone DKFZp564K0222) /cds=UNKNOWN	35750_at

					/gb=AL049948 /gi=4884195 /ug=Hs.6375 /len=1027	
CACNA1E (calcium channel, voltage-dependent, alpha 1E subunit)	L29385	Hs.166110	NM_000721	1q25-q31	Cluster Incl. L29385:Homo sapiens (clone pcDNA-alpha1E-3) voltage-dependent calcium channel alpha-1E-3 subunit mRNA, complete cds /cds=(165,6977) /gb=L29385 /gi=495869 /ug=Hs.166110 /len=7089	33624_at
ZFX (zinc finger protein, X-linked)	X59739	Hs.2074	NM_003410	xp21.3	Cluster Incl. X59739:Human ZFX mRNA for put. transcription activator, isoform 2 /cds=(78,2492) /gb=X59739 /gi=38021 /ug=Hs.2074 /len=5527	38931_at
TIAL1 (TIA1 cytotoxic granule-associated RNA-binding protein-like 1)	M96954	Hs.182741	NM_022333	10q	Cluster Incl. M96954:Homo sapiens nucleolysin TIAR mRNA, complete cds /cds=(45,1172) /gb=M96954 /gi=307313 /ug=Hs.182741 /len=1401	41761_at
	L03426				Cluster Incl. L03426:Human XE7 mRNA, complete alternate coding regions	34215_at

					/cds=(166,1323) /gb=L03426 /gi=340386 /ug=Hs.21595 /len=3233	
EP300 (E1A binding protein p300)	U01877	Hs.25272	NM_001429	22q13.2	Cluster Incl. U01877:Human p300 protein mRNA, complete cds /cds=(1199,8443) /gb=U01877 /gi=495300 /ug=Hs.25272 /len=9046	33896_at
RLBP1 (retinaldehyde-binding protein 1)	L34219	Hs.1933	NM_000326	15q26	Cluster Incl. L34219:Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds /cds=(100,1053) /gb=L34219 /gi=598228 /ug=Hs.1933 /len=1450	35887_at
ERAL1 (Era (E. coli G-protein homolog)-like 1)	AF082657	Hs.3426		17q11.2	Cluster Incl. AF082657:Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds /cds=(0,1332) /gb=AF082657 /gi=3415108 /ug=Hs.3426 /len=1839	34379_at
RAC1 (ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1))	D25274	Hs.173737	NM_018890	7p22	Cluster Incl. D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN /gb=D25274 /gi=464185 /ug=Hs.173737	40864_at

					/len=1232	
HPRP4P(PRP4/STK/WD splicing factor)	AI184802	Hs.8551	NM_004697	9	Cluster Incl. AI184802:qd24g04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1724694 /clone_end=3 /gb=AI184802 /gi=3735440 /ug=Hs.8551 /len=625	37936_at
KIN (antigenic determinant of recA protein (mouse) homolog)	AJ005273	Hs.123647	NM_012311	10p15-p14	Cluster Incl. AJ005273:Homo sapiens mRNA for Kin17 protein /cds=(65,1246) /gb=AJ005273 /gi=3850703 /ug=Hs.123647 /len=1518	37778_at
P2RX4 (purinergic receptor P2X, ligand-gated ion channel, 4)	U83993	Hs.321709	NM_002560	12q24.32	Cluster Incl. U83993:Human P2X4 purinoreceptor mRNA, complete cds /cds=(309,1475) /gb=U83993 /gi=4099120 /ug=Hs.9610 /len=2031	38332_at
VDAC2 (voltage-dependent anion channel 2)	L08666	Hs.78902	NM_003375	10q22	Cluster Incl. L08666:Homo sapiens porin (por) mRNA, complete cds and truncated cds /cds=UNKNOWN /gb=L08666 /gi=190199 /ug=Hs.78902 /len=1464	37697_s_at

DSIPI (delta sleep inducing peptide, immunoreactor)	AI635895	Hs.75450	NM_004089	xp21.1-q25	Cluster Incl. AI635895:tz82a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2295060 /clone_end=3 /gb=AI635895 /gi=4687225 /ug=Hs.75450 /len=1082	36629_at
ZNF134 (zinc finger protein 134 (clone pHZ-15))	U09412	Hs.357	NM_003435	19q13.4	Cluster Incl. U09412:Human zinc finger protein ZNF134 mRNA, complete cds /cds=(521,1567) /gb=U09412 /gi=488552 /ug=Hs.357 /len=2094	36295_at
SGT (small glutamine-rich tetratricopeptide repeat (TPR)-containing)	AL050156	Hs.203910	NM_003021	19p13	Cluster Incl. AL050156:Homo sapiens mRNA; cDNA DKFZp586N1020 (from clone DKFZp586N1020) /cds=(0,1050) /gb=AL050156 /gi=4884157 /ug=Hs.203910 /len=2277	32816_at
SRP19 (signal recognition particle 19kD)	X12791	Hs.2943	NM_003135	5q21-q22	Cluster Incl. X12791:Human mRNA for 19kD protein of signal recognition particle (SRP) /cds=(81,515) /gb=X12791 /gi=36112 /ug=Hs.2943 /len=894	35231_at

	W28360				Cluster Incl. W28360:46f9 Homo sapiens cDNA /gb=W28360 /gi=1308371 /ug=Hs.11498 /len=675	39040_at
MYCBP (c-myc binding protein)	D50692	Hs.78221	NM_012333	1p33-p32.2	D50692 /FEATURE= /DEFINITION=HUMAMY1 Homo sapiens mRNA for c-myc binding protein, complete cds	1904_at
KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2)	AF052728	Hs.188021	NM_000238	7q35-q36	Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively spliced, partial cds /cds=(0,284) /gb=AF052728 /gi=3549258 /ug=Hs.165664 /len=767	38225_at
HMG4 (high-mobility group (nonhistone chromosomal) protein 4)	AL034450	Hs.19114	NM_005342	xq28	Cluster Incl. AL034450:Human DNA sequence from clone 115K14 on chromosome Xq22.3-23 Contains high mobility group protein 2a, ESTs, STS /cds=(0,605) /gb=AL034450 /gi=4210359 /ug=Hs.194749 /len=730	31588_at

TLN1 (talin 1)	AB028950	Hs.18420	NM_006289	9p13	Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027 protein, partial cds /cds=(0,5088) /gb=AB028950 /gi=5689390 /ug=Hs.18420 /len=5542	32166_at
PPP1R11 (protein phosphatase 1, regulatory (inhibitor) subunit 11)	U53588	Hs.82887	NM_021959	6p21.3	Cluster Incl. U53588:Homo sapiens MHC class 1 region /cds=(199,579) /gb=U53588 /gi=1685104 /ug=Hs.82887 /len=1607	38412_at
ature database symbol	S82297	Hs.75415	NM_004048	15q21-q22.2	S82297 /FEATURE= /DEFINITION=S82297 beta 2-microglobulin {11bp deleted between nucleotides 98-99} [human, colon cancer cell line HCT, mRNA Mutant, 416 nt]	201_s_at
ASH2L (ash2 (absent, small, or homeotic, Drosophila, homolog)-like)	AB022785	Hs.6856	NM_004674	8p11.2	Cluster Incl. AB022785:Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene /cds=(12,1898) /gb=AB022785 /gi=4210446 /ug=Hs.6856 /len=2369	35804_at

RBMS1 (RNA binding motif, single stranded interacting protein 1)	Mssp-1	Hs.241567	NM_016839	2p14-q14.3	Single-Stranded Dna-Binding Protein Mssp-1	333_s_at
C3F(putative protein similar to nessy (Drosophila))	U72515	Hs.300423	NM_005768	12	Cluster Incl. U72515:Human C3f mRNA, complete cds /cds=(117,1262) /gb=U72515 /gi=1673519 /ug=Hs.189583 /len=1842	33710_at
TPM1 (tropomyosin 1 (alpha))	M19267	Hs.77899	NM_000366	15q22.1	Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	36791_g_at
LOC94392(hypothetical gene supported by AB007931; AF055010; AK001233; AK022322; AK022573; AK022924; AK023826; AK025149; AL049972; BC007962	AB007931			1	Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150	33860_at
HSD17B4 (hydroxysteroid (17-beta) dehydrogenase 4)	X87176	Hs.75441	NM_000414	5q21	Cluster Incl. X87176:H.sapiens mRNA for 17-beta-hydroxysteroid dehydrogenase /cds=(48,2258) /gb=X87176 /gi=1050516	36626_at

					/ug=Hs.75441 /len=2593	
KIAA0728(KIAA0728 protein)	AB018271	Hs.198689		6	Cluster Incl. AB018271:Homo sapiens mRNA for KIAA0728 protein, partial cds /cds=(0,3197) /gb=AB018271 /gi=3882176 /ug=Hs.198689 /len=3964	32780_at
SR-BP1(sigma receptor (SR31747 binding protein 1))]	U79528	Hs.24447	NM_005866	9	Cluster Incl. U79528:Human SR31747 binding protein 1 mRNA, complete cds /cds=(74,745) /gb=U79528 /gi=1916799 /ug=Hs.24447 /len=1650	33879_at
CSPG2 (chondroitin sulfate proteoglycan 2 (versican))	X15998	Hs.81800	NM_004385	5q14.3	Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224	38111_at
HCK (hemopoietic cell kinase)	M16591	Hs.89555	NM_002110	20q11-q12	Cluster Incl. M16591:Human hemopoietic cell protein-tyrosine kinase (HCK) gene, complete cds, clone lambda-a2/1a /cds=(168,1685) /gb=M16591 /gi=183911	40742_at

					/ug=Hs.89555 /len=2015	
	X92997				Cluster Incl. X92997:H.sapiens mRNA for IgG lambda light chain V-J-C region (clone Tgl4) /cds=(0,321) /gb=X92997 /gi=1070337 /ug=Hs.129722 /len=322	35530_f_at
TST (thiosulfate sulfurtransferase (rhodanese))	D87292	Hs.248267	NM_003312	22q13.1	Cluster Incl. D87292:Homo sapiens mRNA for rhodanese, complete cds /cds=(48,941) /gb=D87292 /gi=1877030 /ug=Hs.74097 /len=1137	36123_at
SSTR3 (somatostatin receptor 3)	M96738	Hs.225995	NM_001051	22q13.1	M96738 /FEATURE=cds /DEFINITION=HUMSSTR3X Human somatostatin receptor subtype 3 (SSTR3) gene, complete cds	557_s_at
KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2)	U04270	Hs.188021	NM_000238	7q35-q36	Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) mRNA, complete cds /cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.188021	38858_at

					/len=4070	
PTMS (parathymosin)	M24398	Hs.171814	NM_002824	17q12-q22	Cluster Incl. M24398:Human parathymosin mRNA, complete cds /cds=(300,608) /gb=M24398 /gi=339698 /ug=Hs.171814 /len=1109	40580_r_at
KIAA0859(KIAA0859 protein)]	AL049669	Hs.19469		1	Cluster Incl. AL049669:Human gene from PAC 612B18, chromosome 1 /cds=(272,1903) /gb=AL049669 /gi=4678746 /ug=Hs.19469 /len=2862	32262_at
SLC31A1 (solute carrier family 31 (copper transporters), member 1	U83460	Hs.73614	NM_001859	9q31-q32	Cluster Incl. U83460:Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds /cds=(152,724) /gb=U83460 /gi=2315986 /ug=Hs.73614 /len=1804	40364_at
HSPD1 (heat shock 60kD protein 1 (chaperonin))	W28589	Hs.79037	NM_002156	12	Cluster Incl. W28589:48h12 Homo sapiens cDNA /gb=W28589 /gi=1308537 /ug=Hs.184567 /len=965	40913_at

PIK3CA (phosphoinositide-3-kinase, catalytic, alpha polypeptide)	P110	Hs.85701	NM_006218	3q26.3	Phosphatidylinositol 3-Kinase P110, Beta Isoform	1163_at
[KIAA1055(KIAA1055 protein)	AB028978	Hs.126084		15	Cluster Incl. AB028978:Homo sapiens mRNA for KIAA1055 protein, partial cds /cds=(0,2607) /gb=AB028978 /gi=5689446 /ug=Hs.126084 /len=5876	39400_at
WDR7 (WD repeat domain 7)	AB011113	Hs.10881		18q21.1-q22	Cluster Incl. AB011113:Homo sapiens mRNA for KIAA0541 protein, partial cds /cds=(0,3484) /gb=AB011113 /gi=3043605 /ug=Hs.10881 /len=6072	41430_at
PRKWNK1 (protein kinase, lysine deficient 1)	U00946	Hs.184592	NM_018979	12p13.3	Cluster Incl. U00946:Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA /cds=UNKNOWN /gb=U00946 /gi=405048 /ug=Hs.184592 /len=1971	32185_at
TTC1 (tetratricopeptide repeat domain 1)	U46570	Hs.7733	NM_003314	5q32-q33.2	Cluster Incl. U46570:Human tetratricopeptide repeat protein (tpr1) mRNA, complete cds /cds=(50,928)	37321_at

					/gb=U46570 /gi=1688073 /ug=Hs.7733 /len=1407	
ST7 (suppression of tumorigenicity 7)	W02490	Hs.301974	NM_013437	8q22.2-q23.1	Cluster Incl. W02490:za48b02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-295755 /clone_end=5 /gb=W02490 /gi=1274488 /ug=Hs.5814 /len=623	40039_g_at
MINPP1 (multiple inositol polyphosphate histidine phosphatase, 1)	AL050356	Hs.95907	NM_004897	10q23	Cluster Incl. AL050356:Homo sapiens mRNA; cDNA DKFZp564L2016 (from clone DKFZp564L2016) /cds=UNKNOWN /gb=AL050356 /gi=4914568 /ug=Hs.95907 /len=2396	38325_at
NFYC (nuclear transcription factor Y, gamma)	Z74792	Hs.168157	NM_014223	1p32	Cluster Incl. Z74792:H.sapiens mRNA for CCAAT transcription binding factor subunit gamma /cds=(185,1192) /gb=Z74792 /gi=2564241 /ug=Hs.168157 /len=1965	40466_at
PK428(Ser-Thr protein kinase related to the myotonic dystrophy protein kinase)	U59305	Hs.44708	NM_003607	1	Cluster Incl. U59305:Human ser-thr protein kinase PK428 mRNA, complete cds /cds=(1288,2778) /gb=U59305	39962_at

						/gi=1695872 /ug=Hs.44708 /len=2785	
KIAA0674(KIAA0674 protein)]	AB014574	Hs.14799		9		Cluster Incl. AB014574:Homo sapiens mRNA for KIAA0674 protein, partial cds /cds=(0,3704) /gb=AB014574 /gi=3327161 /ug=Hs.14799 /len=4263	31826_at
IGKC (immunoglobulin kappa constant)	M63438	Hs.156110		2p12		Cluster Incl. M63438:Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds /cds=(0,1049) /gb=M63438 /gi=184847 /ug=Hs.156110 /len=1244	38194_s_at
SEC22L1 (SEC22, vesicle trafficking protein (S. cerevisiae)-like 1	AF047442	Hs.50785	NM_004892	1q21.2-q21.3		Cluster Incl. AF047442:Homo sapiens vesicle trafficking protein sec22b mRNA, complete cds /cds=(64,711) /gb=AF047442 /gi=3335139 /ug=Hs.50785 /len=1433	41597_s_at
HCK (hemopoietic cell kinase)	M16592	Hs.89555	NM_002110	20q11-q12		M16592 /FEATURE=mRNA /DEFINITION=HUMHCKB Human hemopoietic cell protein-tyrosine kinase	2045_s_at

					(HCK) gene, complete cds, clone HK24	
TFDP1 (transcription factor Dp-1)	L23959	Hs.79353	NM_007111	13q34	Cluster Incl. L23959:Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds /cds=(37,1269) /gb=L23959 /gi=414316 /ug=Hs.79353 /len=1440	37757_at
PCMT1 (protein-L-isoaspartate (D-aspartate) O-methyltransferase)	D13892	Hs.79137	NM_005389	6q24-q25	Cluster Incl. D13892:Human mRNA for carboxyl methyltransferase, complete cds /cds=(150,836) /gb=D13892 /gi=474983 /ug=Hs.79137 /len=1620	37736_at
MPHOSPH6 (M-phase phosphoprotein 6)	X98263	Hs.152720	NM_005792	16q24	Cluster Incl. X98263:H.sapiens mRNA for M-phase phosphoprotein, mpp6 /cds=(32,514) /gb=X98263 /gi=1770461 /ug=Hs.152720 /len=1079	31864_at
HCLS1 (hematopoietic cell-specific Lyn substrate 1)	X16663	Hs.14601	NM_005335	3q13	Cluster Incl. X16663:Human HS1 gene for heamatopoietic lineage cell specific protein /cds=(42,1502) /gb=X16663 /gi=32054 /ug=Hs.14601 /len=1950	31820_at

KIAA0451(KIAA0451 gene product)	AB007920			1	Cluster Incl. AB007920:Homo sapiens mRNA for KIAA0451 protein, complete cds /cds=(1482,2219) /gb=AB007920 /gi=3413863 /ug=Hs.18586 /len=6597	32206_at
CAT (catalase)	AL035079	Hs.76359	NM_001752	11p13	Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079 /gi=4775614 /ug=Hs.76359 /len=2287	37009_at
OAZ1 (ornithine decarboxylase antizyme 1)	D78361	Hs.125078		19p13.3	D78361 /FEATURE= /DEFINITION=HUMODAZ Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2	1315_at
VDAC3 (voltage-dependent anion channel 3)	AF038962	Hs.7381	NM_005662	8p11.2	Cluster Incl. AF038962:Homo sapiens voltage dependent anion channel protein mRNA, complete cds /cds=(99,950) /gb=AF038962 /gi=3329393 /ug=Hs.7381 /len=1384	36102_at
NCOA4 (nuclear receptor coactivator 4)	X77548	Hs.99908	NM_005437	10q11.2	Cluster Incl. X77548:H. sapiens cDNA for RFG /cds=(76,1920) /gb=X77548	39174_at

					/gi=469145 /ug=Hs.99908 /len=3418	
	D45288				Cluster Incl. D45288:HUMHG2121 Homo sapiens cDNA /gb=D45288 /gi=1136884 /ug=Hs.57079 /len=1479	35310_at
RFP (ret finger protein)	J03407	Hs.142653	NM_006510	6p22	Cluster Incl. J03407:Human rfp transforming protein mRNA, complete cds /cds=(234,1775) /gb=J03407 /gi=337371 /ug=Hs.142653 /len=1782	40176_at
BRCA1 (*breast cancer 1, early onset*)	L78833	Hs.194143	NM_007295	17q21	L78833 /FEATURE=exon#24 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds	604_at
BAZ1A (bromodomain adjacent to zinc finger domain, 1A)	AL050089	Hs.8858	NM_013448	14q12-q13	Cluster Incl. AL050089:Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518) /cds=(0,2435) /gb=AL050089 /gi=4884107 /ug=Hs.8858 /len=3215	37971_at

PPIE (peptidylprolyl isomerase E (cyclophilin E))	AF042386	Hs.33251	NM_006112	1p32	Cluster Incl. AF042386:Homo sapiens cyclophilin-33B (CYP-33) mRNA, complete cds /cds=(60,950) /gb=AF042386 /gi=2828150 /ug=Hs.33251 /len=1099	34366_g_at
CD163 (CD163 antigen)	Z22971	Hs.74076	NM_004244	12p13.3	Cluster Incl. Z22971:H.sapiens mRNA for M130 antigen extracellular variant /cds=(101,3550) /gb=Z22971 /gi=312147 /ug=Hs.166016 /len=3802	31438_s_at
RXRA (retinoid X receptor, alpha)	U66306	Hs.20084	NM_002957	9q34.3	Cluster Incl. U66306:Human retinoid X receptor alpha mRNA, 3 UTR, partial sequence /cds=UNKNOWN /gb=U66306 /gi=3411007 /ug=Hs.20084 /len=3772	32800_at
ADD2 (adducin 2 (beta))	U43959	Hs.247423	NM_017488	2p14-p13	Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145 /ug=Hs.4852 /len=1284	36052_at

GOLTC1 (golgi transport complex 1 (90 kDa subunit))	AF058718	Hs.239631	NM_006348	7q31	Cluster Incl. AF058718:Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds /cds=(51,2570) /gb=AF058718 /gi=3808234 /ug=Hs.239631 /len=3105	34737_at
KIAA0089(KIAA0089 protein)	D42047	Hs.82432		3	Cluster Incl. D42047:Human mRNA for KIAA0089 gene, partial cds /cds=(0,1236) /gb=D42047 /gi=577306 /ug=Hs.82432 /len=4043	38394_at
TGFA (transforming growth factor, alpha)	X70340	Hs.170009	NM_003236	2p13	X70340 /FEATURE=cds /DEFINITION=HSTGFAA H.sapiens mRNA for transforming growth factor alpha /NOTE=replacement of probe set 383_at	160025_at
OGDH (oxoglutarate dehydrogenase (lipoamide))	D10523	Hs.168669	NM_002541	7p14-p13	Cluster Incl. D10523:Human mRNA for 2-oxoglutarate dehydrogenase, complete cds /cds=(57,3065) /gb=D10523 /gi=531240 /ug=Hs.168669 /len=4122	40470_at

IQGAP2 (IQ motif containing GTPase activating protein 2)	U51903	Hs.78993	NM_006633	5q	Cluster Incl. U51903:Human RasGAP-related protein (IQGAP2) mRNA, complete cds /cds=(222,4949) /gb=U51903 /gi=1262925 /ug=Hs.78993 /len=5767	37276_at
ASML3B(acid sphingomyelinase-like phosphodiesterase)	Y08134	Hs.123659	NM_014474	1	Cluster Incl. Y08134:H.sapiens mRNA for ASM-like phosphodiesterase 3b /cds=(121,1518) /gb=Y08134 /gi=1552274 /ug=Hs.123659 /len=1610	37779_at
GIPR (gastric inhibitory polypeptide receptor)	X81832	Hs.251412	NM_000164	19q13.3	Cluster Incl. X81832:H.sapiens mRNA for glucose-dependant insulinotropic polypeptide receptor gene /cds=(466,1951) /gb=X81832 /gi=1030050 /ug=Hs.142900 /len=2181	35590_s_at
ITSN(human intersectin-SH3 domain-containing protein SH3P17)	U61166	Hs.307177		21q22.11	U61166 /FEATURE= /DEFINITION=HSU61166 Human SH3 domain-containing protein SH3P17 mRNA, complete cds	488_at

KIAA1155(KIAA1155 protein)	AF090102	Hs.102657		2	Cluster Incl. AF090102:Homo sapiens clone IMAGE 21785 /cds=UNKNOWN /gb=AF090102 /gi=4063637 /ug=Hs.102657 /len=1712	39527_at
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	41796_at
DOC-1R(tumor suppressor deleted *in oral* cancer-related 1)	AF089814	Hs.25664	NM_005851	11	Cluster Incl. AF089814:Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds /cds=(103,483) /gb=AF089814 /gi=3661528 /ug=Hs.25664 /len=931	35151_at
IGL@ (immunoglobulin lambda locus)	M18645	Hs.181125		22q11.1-q11.2	Cluster Incl. M18645:Human Ig rearranged lambda-chain mRNA VJC-region subgroup lambda-IV *from* heterohybridoma H6-3C4 /cds=(30,731) /gb=M18645 /gi=186103 /ug=Hs.181125 /len=872	33274_f_at

	S71043				Cluster Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype 2 {constant region, germ line} [human, peripheral blood neutrophils, Genomic, 1799 nt] /cds=(0,1022) /gb=S71043 /gi=546798 /ug=Hs.32225 /len=1047	33501_r_at
UBE2V1 (ubiquitin-conjugating enzyme E2 variant 1)	U49278	Hs.75875	NM_003349	20q13.2	Cluster Incl. U49278:Homo sapiens UEV-1 (UBE2V) mRNA, partial cds /cds=(0,231) /gb=U49278 /gi=1709703 /ug=Hs.75875 /len=3335	36959_at
CBX7 (chromobox homolog 7)	AL031846			22q13.1	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
	AL049675				Cluster Incl. AL049675:Human gene from PAC 886K2, chromosome 1 /cds=UNKNOWN /gb=AL049675 /gi=4678768 /ug=Hs.15535 /len=1074	32048_at

TPM1 (tropomyosin 1 (alpha))	M19267	Hs.77899	NM_000366	15q22.1	Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	36790_at
MYCBP (c-myc binding protein)	AB007191	Hs.78221	NM_012333	1p33-p32.2	Cluster Incl. AB007191:Homo sapiens mRNA for AMY-1, complete cds /cds=(38,349) /gb=AB007191 /gi=2443309 /ug=Hs.78221 /len=1492	37250_at
	AF052169				Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169 /gi=3360480 /ug=Hs.109438 /len=1385	38972_at
TOP3A (topoisomerase (DNA) III alpha)	U43431	Hs.91175	NM_004618	17p12-17p11.2	U43431 /FEATURE= /DEFINITION=HSU43431 Human DNA topoisomerase III mRNA, complete cds	1028_at
PCAF (p300/CBP-associated factor)	U57317	Hs.199061	NM_003884	3p24	U57317 /FEATURE= /DEFINITION=HSU57317 Homo sapiens p300/CBP-associated factor (P/CAF)	1012_at

					mRNA, complete cds	
RAD54L (RAD54 (S.cerevisiae)-like)	X97795	Hs.66718	NM_003579	1p32	X97795 /FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA homologous to S. cerevisiae RAD54	966_at
CTSE (cathepsin E)	J05036	Hs.1355	NM_001910	1q31	J05036 /FEATURE=mRNA /DEFINITION=HUMCTSE Human cathepsin E mRNA, complete cds	271_s_at
IGLL3 (immunoglobulin lambda-like polypeptide 3)	AI932613	Hs.296552		22q11.23	Cluster Incl. AI932613:wo05c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2454434 /clone_end=3 /gb=AI932613 /gi=5671350 /ug=Hs.62036 /len=570	41827_f_at
	S71043				Cluster Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype 2 {constant region, germ line} [human, peripheral blood neutrophils, Genomic, 1799 nt] /cds=(0,1022) /gb=S71043	33500_i_at

						/gi=546798 /ug=Hs.32225 /len=1047	
ZNF75 (zinc finger protein 75 (D8C6))	S67970	Hs.29159		xq26		Cluster Incl. S67970:ZNF75=KRAB zinc finger [human, lung fibroblast, mRNA, 1563 nt] /cds=UNKNOWN /gb=S67970 /gi=460902 /ug=Hs.29159 /len=1563	35222_at
PLSCR1 (phospholipid scramblase 1)	AB006746	Hs.198282	NM_021105	3q23		Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077	32775_r_at
LOC51112(CGI-87 protein)	AI652660	Hs.5008	NM_016030			Cluster Incl. AI652660:wb30c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2307186 /clone_end=3 /gb=AI652660 /gi=4736639 /ug=Hs.5008 /len=525	41590_at
	AF067420					Cluster Incl. AF067420:Homo sapiens SNC73 protein (SNC73) mRNA, complete cds /cds=(395,1549) /gb=AF067420	33499_s_at

					/gi=3201899 /ug=Hs.32225 /len=1594	
CSTF3 (cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD)	U15782	Hs.180034	NM_001326	11	Cluster Incl. U15782:Human cleavage stimulation factor 77kDa subunit mRNA, complete cds /cds=(131,2284) /gb=U15782 /gi=632497 /ug=Hs.180034 /len=2766	41183_at
CAPZA1 (capping protein (actin filament) muscle Z-line, alpha 1)	U56637	Hs.184270	NM_006135	1p36.13-q23.3	Cluster Incl. U56637:Human capping protein alpha subunit isoform 1 mRNA, complete cds /cds=(0,860) /gb=U56637 /gi=1336098 /ug=Hs.184270 /len=2366	40910_at
NEDD4L (reserved)	AB007899	Hs.12017	NM_015277	18q21	Cluster Incl. AB007899:Homo sapiens KIAA0439 mRNA, partial cds /cds=(0,2989) /gb=AB007899 /gi=2662158 /ug=Hs.12017 /len=4879	39356_at
CCNB1 (cyclin B1)	M25753:	Hs.23960	NM_031966	5q12	Cluster Incl. M25753:Human cyclin B mRNA, 3 end /cds=UNKNOWN /gb=M25753 /gi=181243 /ug=Hs.23960	34736_at

					/len=1452	
ITSN1 (intersectin 1 (SH3 domain protein))	AF064243	Hs.66392	NM_003024	21q22.1-q22.2	Cluster Incl. AF064243:Homo sapiens intersectin short form mRNA, complete cds /cds=(106,3768) /gb=AF064243 /gi=3859852 /ug=Hs.66392 /len=5272	35776_at
BCS1L (BCS1 (yeast homolog)-like)	AF038195	Hs.150922	NM_004328	2q33	Cluster Incl. AF038195:Homo sapiens clone 23661 unknown protein mRNA, complete cds /cds=(75,1334) /gb=AF038195 /gi=2795915 /ug=Hs.150922 /len=1391	31842_at
KIAA0229(KIAA0229 protein)	D86982	Hs.20060		6	Cluster Incl. D86982:Human mRNA for KIAA0229 gene, partial cds /cds=(0,3543) /gb=D86982 /gi=1504037 /ug=Hs.20060 /len=6335	40971_at
RNF24 (ring finger protein 24)	AL031670	Hs.30524	NM_007219	20p13-p12.1	Cluster Incl. AL031670:dJ681N20.2 (ferritin, light polypeptide-like 1) /cds=(200,727) /gb=AL031670	35083_at

					/gi=4469083 /ug=Hs.111334 /len=978	
SLC29A2 (solute carrier family 29 (nucleoside transporters), member 2)	AF034102	Hs.32951	NM_001532	11q13	Cluster Incl. AF034102:Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds /cds=(237,1607) /gb=AF034102 /gi=2811136 /ug=Hs.32951 /len=2522	39661_s_at
KIAA0436(putative L-type neutral amino acid transporter)]	AB007896			2	Cluster Incl. AB007896:Homo sapiens KIAA0436 mRNA, partial cds /cds=(0,2069) /gb=AB007896 /gi=2662152 /ug=Hs.110 /len=4661	38984_at
ACTB (actin, beta)	X00351	Hs.288061	NM_001101	7p15-p12	Homo sapiens /REF=X00351 /DEF=Human mRNA for beta-actin /LEN=1761 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HSAC07
CSPG2 (chondroitin sulfate proteoglycan 2 (versican))	D32039	Hs.81800	NM_004385	5q14.3	Cluster Incl. D32039:Human pgH3 mRNA for proteoglycan PG-M(V3), complete cds /cds=(105,2072) /gb=D32039 /gi=1008912	31682_s_at

					/ug=Hs.234753 /len=2087	
SLC29A1 (solute carrier family 29 (nucleoside transporters), member 1	U81375	Hs.25450	NM_004955	6p21.1-p21.2	Cluster Incl. U81375:Human placental equilibrative nucleoside transporter 1 (hENT1) mRNA, complete cds /cds=(178,1548) /gb=U81375 /gi=1845344 /ug=Hs.25450 /len=2162	33901_at
PVR (poliovirus receptor)	X64116	Hs.321018	NM_006505	19q13.2	Cluster Incl. X64116:H.sapiens PVR gene for poliovirus receptor (exon 1) /cds=(205,1299) /gb=X64116 /gi=35809 /ug=Hs.171844 /len=1300	32699_s_at
KNSL3 (kinesin-like 3)	AB012722	Hs.198256	NM_030615	6q27	Cluster Incl. AB012722:Homo sapiens gene for kinesin-like protein, complete cds /cds=(94,1248) /gb=AB012722 /gi=4115550 /ug=Hs.198256 /len=1342	31978_at
13CDNA73(putative gene product)	U50534	Hs.181304	NM_023037	13	U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence CG003	1529_at

ITGAV (integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51))	U07375	Hs.295726	NM_002210	2q31-q32	U07375 /FEATURE=cds /DEFINITION=HSU07375 Human integrin alpha v gene, promoter region and partial cds	2032_s_at
DPYD (dihydropyrimidine dehydrogenase)	U20938	Hs.1602	NM_000110	1p22	Cluster Incl. U20938:Human lymphocyte dihydropyrimidine dehydrogenase mRNA, complete cds /cds=(101,3178) /gb=U20938 /gi=1926407 /ug=Hs.1602 /len=4409	38220_at
KIAA0152(KIAA0152 gene product)	D63486	Hs.181418	NM_014730	12	Cluster Incl. D63486:Human mRNA for KIAA0152 gene, complete cds /cds=(128,1006) /gb=D63486 /gi=1469885 /ug=Hs.181418 /len=6322	41728_at

Table 5:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
GATA2 (GATA-binding protein 2)	M77810	Hs.334695	NM_002050	3q21	M77810 /FEATURE= /DEFINITION=HUMGATA2A Human transcription factor GATA-2 (GATA-2) mRNA, complete cds	1072_g_at
PRG2 (proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic	Z26248	Hs.99962	NM_002728	11q12	Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=940510 /ug=Hs.99962 /len=1637	39179_at
FAT2 (FAT tumor suppressor (Drosophila) homolog 2)	AB011535	Hs.158159	NM_001447	5q32-q33	Cluster Incl. AB011535:Homo sapiens mRNA for MEGF1, partial cds /cds=(0,1721) /gb=AB011535 /gi=3449295 /ug=Hs.158159 /len=3193	38202_at

PROC (protein C (inactivator of coagulation factors Va and VIIIa))	X02750	Hs.2351	NM_000312	2q13-q14	Cluster Incl. X02750:Human liver mRNA for protein C /cds=(97,1482) /gb=X02750 /gi=35689 /ug=Hs.2351 /len=1843	39255_at
	AC005764				Cluster Incl. AC005764:Homo sapiens chromosome 19, cosmid R31343 /cds=(0,1262) /gb=AC005764 /gi=3694626 /ug=Hs.126496 /len=1263	35512_at
CAMK2B (calcium/calmodulin-dependent protein kinase (CaM kinase) II beta)	AF112471	Hs.4884	NM_001220	7p14.3-p14.1	Cluster Incl. AF112471:Homo sapiens calcium/calmodulin-dependent protein kinase II beta subunit mRNA, alternatively spliced, complete cds /cds=(46,1599) /gb=AF112471 /gi=4139267 /ug=Hs.4884 /len=1750	34847_s_at
BRF2 (butyrate response factor 2 (EGF-response factor 2))	X78992	Hs.78909	NM_006887	2p22.3-2p21	Cluster Incl. X78992:H.sapiens ERF-2 mRNA /cds=(66,1544) /gb=X78992 /gi=509777 /ug=Hs.78909 /len=1629	32588_s_at
RPL7 (ribosomal protein L7)	X57958	Hs.153	NM_000971	8q	Cluster Incl. X57958:H.sapiens mRNA for ribosomal protein L7 /cds=(22,783)	36333_at

					/gb=X57958 /gi=35904 /ug=Hs.153 /len=847	
GADD45A (growth arrest and DNA-damage-inducible, alpha)	M60974	Hs.80409	NM_001924	1p31.2-p31.1	M60974 /FEATURE= /DEFINITION=HUMGADD45 Human growth arrest and DNA-damage-inducible protein (gadd45) mRNA, complete cds	1911_s_at
NUDEL(nuclear distribution gene E-like)]	AF038203	Hs.3850	NM_030808	17	Cluster Incl. AF038203:Homo sapiens clone 23596 mRNA sequence /cds=UNKNOWN /gb=AF038203 /gi=2795924 /ug=Hs.3850 /len=1473	34413_at
MAD (MAX dimerization protein)	L06895	Hs.109012	NM_002357	2p13-p12	L06895 /FEATURE= /DEFINITION=HUMMAD Homo sapiens antagonizer of myc transcriptional activity (Mad) mRNA, complete cds	1774_at
LRPAP1 (low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin	M63959	Hs.75140	NM_002337	4p16.3	Cluster Incl. M63959:Human alpha-2-macroglobulin receptor-associated protein mRNA, complete cds /cds=(13,1086) /gb=M63959 /gi=177873 /ug=Hs.75140	36194_at

					/len=1493	
RPL22 (ribosomal protein L22)	AI526079	Hs.326249	NM_000983	3q26	Cluster Incl. AI526079:DU3.2-7.G09 Homo sapiens cDNA, 3 end /clone_end=3 /gb=AI526079 /gi=4440197 /ug=Hs.234060 /len=801	33451_s_at
CLC (Charot-Leyden crystal protein)	L01664	Hs.132004	NM_013246	11q13.3	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	36809_at
GFI1 (growth factor independent 1)	U67369	Hs.73172	NM_005263	1p22	Cluster Incl. U67369:Human growth factor independence-1 (Gfi-1) mRNA, complete cds /cds=(267,1535) /gb=U67369 /gi=1698691 /ug=Hs.73172 /len=2799	33977_at
MYL6 (myosin, light polypeptide 6, alkali, smooth muscle and non-muscle)	M22919	Hs.77385	NM_021019	12	Cluster Incl. M22919:Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds	33994_g_at

					/cds=(42,353) /gb=M22919 /gi=189016 /ug=Hs.77385 /len=1259	
[EBBP(tripartite motif protein 16)]	AF096870	Hs.241305	NM_006470	17	Cluster Incl. AF096870:Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds /cds=(227,1921) /gb=AF096870 /gi=3916726 /ug=Hs.194540 /len=2568	38881_i_at
RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin))	X55988	Hs.728	NM_002934	14q24-q31	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	36766_at
RBMS3 (RNA binding motif, single stranded interacting protein)	AA523313	Hs.158446	NM_014483	3p24-p23	Cluster Incl. AA523313:ni41h09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-979457 /clone_end=3 /gb=AA523313 /gi=2264025 /ug=Hs.158446 /len=581	33583_r_at
ATBF1 (AT-binding transcription factor 1)	L32832	Hs.101842	NM_006885	16q22.3-q23.1	Cluster Incl. L32832:Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds /cds=(673,11784)	37114_at

					/gb=L32832 /gi=976346 /ug=Hs.101842 /len=11893	
ALDOA (aldolase A, fructose-bisphosphate)	X05236	Hs.273415	NM_000034	16q22-q24	Cluster Incl. X05236:Human fibroblast mRNA for aldolase A /cds=(146,1240) /gb=X05236 /gi=28596 /ug=Hs.183760 /len=1440	32336_at
DSIPI (delta sleep inducing peptide, immunoreactor)	AI635895	Hs.75450	NM_004089	xp21.1-q25	Cluster Incl. AI635895:tz82a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2295060 /clone_end=3 /gb=AI635895 /gi=4687225 /ug=Hs.75450 /len=1082	36629_at
BPI (bactericidal/permeability-increasing protein)	J04739	Hs.89535	NM_001725	20q11.23-q12	Cluster Incl. J04739:Human bactericidal permeability increasing protein (BPI) mRNA, complete cds /cds=(30,1493) /gb=J04739 /gi=179528 /ug=Hs.89535 /len=1813	37054_at
JUND (jun D proto-oncogene)	X56681	Hs.2780	NM_005354	19p13.2	Cluster Incl. X56681:Human junD mRNA /cds=(174,1217) /gb=X56681 /gi=34018	41483_s_at

					/ug=Hs.2780 /len=1891	
MYB (v-myb avian myeloblastosis viral oncogene homolog)	M13666	Hs.1334	NM_005375	6q22-q23	Cluster Incl. M13666:Human c-myb mRNA, 3 end /cds=(0,833) /gb=M13666 /gi=180657 /ug=Hs.1334 /len=1035	41854_at
EPX (eosinophil peroxidase)	X14346	Hs.46295	NM_000502	17q23.1	Cluster Incl. X14346:Human mRNA for eosinophil peroxidase /cds=(0,2108) /gb=X14346 /gi=31182 /ug=Hs.46295 /len=2558	34587_at
PGD (phosphogluconate dehydrogenase)	U30255	Hs.75888	NM_002631	1p36.3-p36.13	Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324 /ug=Hs.75888 /len=1536	36963_at
ATF2 (activating transcription factor 2)	U16028	Hs.198166	NM_001880	2q32	U16028 /FEATURE= /DEFINITION=HSU16028 Human CRE-BP1 transcription factor mRNA, complete cds	1994_at

TAGLN2 (transgelin 2)	D21261	Hs.75725	NM_003564	1q21-q25	Homo sapiens /REF=D21261 /DEF=Cluster Incl. :Human mRNA for KIAA0120 gene, complete cds /cds=(73,672) /gb= /gi=434762 /ug=Hs.75725 /len=1360 /LEN=1594	36678_at
GP9 (glycoprotein IX (platelet))	X52997	Hs.1144	NM_000174	3q21	Cluster Incl. X52997:Human mRNA for platelet glycoprotein IX /cds=(222,755) /gb=X52997 /gi=2160045 /ug=Hs.1144 /len=888	35101_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGA
LMOD1 (leiomodin 1 (smooth muscle))	X54162	Hs.79386	NM_012134	1q32	Cluster Incl. X54162:Human mRNA for a 64 Kd autoantigen expressed in thyroid and extra-ocular muscle /cds=(212,1930) /gb=X54162 /gi=28968 /ug=Hs.79386	37765_at

					/len=3849	
JUND (jun D proto-oncogene)	X56681	Hs.2780	NM_005354	19p13.2	X56681 /FEATURE=mRNA /DEFINITION=HSJUNDR Human junD mRNA	1612_s_at
CCNI (cyclin I)	D50310	Hs.79933	NM_006835	4	D50310 /FEATURE= /DEFINITION=HUMCYI Human mRNA for cyclin I, complete cds	1836_at
RPS4X (ribosomal protein S4, X-linked)	M58458	Hs.108124	NM_001007	xq13.1	Cluster Incl. M58458:Human ribosomal protein S4 (RPS4X) isoform mRNA, complete cds /cds=(35,826) /gb=M58458 /gi=337509 /ug=Hs.75344 /len=888	34643_at
RPS6 (ribosomal protein S6)	X67309	Hs.241507	NM_001010	9p21	Cluster Incl. X67309:H.sapiens gene for ribosomal protein S6 /cds=(42,791) /gb=X67309 /gi=36147 /ug=Hs.120856 /len=829	35125_at

MAD (MAX dimerization protein)	L06895	Hs.109012	NM_002357	2p13-p12	Cluster Incl. L06895:Homo sapiens antagonizer of myc transcriptional activity (Mad) mRNA, complete cds /cds=(147,812) /gb=L06895 /gi=187288 /ug=Hs.239794 /len=1002	34543_at
H2AFY (H2A histone family, member Y)	AF054174	Hs.75258	NM_004893	5q31.3-q32	Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete cds /cds=(173,1288) /gb=AF054174 /gi=3341991 /ug=Hs.75258 /len=1881	36576_at
SAT (spermidine/spermine N1-acetyltransferase)		Hs.28491	NM_002970	xp22.1	Spermidine/Spermine N1-Acetyltransferase, Alt. Splice 2	1173_g_at
IGHG3 (immunoglobulin heavy constant gamma 3 (G3m marker))	AI147237	Hs.300697		14q32.33	Cluster Incl. AI147237:qb36f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1698363 /clone_end=3 /gb=AI147237 /gi=3674919 /ug=Hs.210732 /len=474	34104_i_at
KIAA0225(KIAA0225 protein	D86978	Hs.84790		7	Cluster Incl. D86978:Human mRNA for KIAA0225 gene, partial cds /cds=(0,6043) /gb=D86978 /gi=1504029 /ug=Hs.84790	38728_at

HMG4 (high-mobility group (nonhistone chromosomal) protein 4)	AL034450	Hs.19114	NM_005342	Xq28	/len=6237 Cluster Incl. AL034450:Human DNA sequence from clone 115K14 on chromosome Xq22.3-23 Contains high mobility group protein 2a, ESTs, STS /cds=(0,605) /gb=AL034450 /gi=4210359 /ug=Hs.194749 /len=730	31588_at
MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))	AB023208	Hs.181002	NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
CRA(cisplatin resistance associated)	U78556	Hs.166066	NM_006697	1	/FEATURE= U78556 /DEFINITION=HSU78556 Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds	1229_at
	AF052169				Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169	38972_at

					/gi=3360480 /ug=Hs.109438 /len=1385	
CD164 (CD164 antigen, sialomucin)	D14043	Hs.43910	NM_006016	6q21	Cluster Incl. D14043:Human mRNA for MGC-24, complete cds /cds=(79,648) /gb=D14043 /gi=219924 /ug=Hs.43910 /len=2417	34819_at
PLXNB2 (plexin B2)	AB002313	Hs.3989		22q13.33	Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252	34780_at
KIAA1042(KIAA1042 protein)	AB028965	Hs.6705	NM_014965	3	Cluster Incl. AB028965:Homo sapiens mRNA for KIAA1042 protein, complete cds /cds=(216,3077) /gb=AB028965 /gi=5689420 /ug=Hs.6705 /len=5109	35789_at
CSPG2 (chondroitin sulfate proteoglycan 2 (versican))	X15998	Hs.81800	NM_004385	5q14.3	Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998	38111_at

					/gi=37662 /ug=Hs.81800 /len=8224	
DCK (deoxycytidine kinase)	M60527	Hs.709	NM_000788	4q13.3-q21.1	M60527 /FEATURE=mRNA /DEFINITION=HUMDCKATPB Human deoxycytidine kinase mRNA, complete cds	886_at
TGFBI (transforming growth factor, beta-induced, 68kD)	M77349	Hs.118787	NM_000358	5q31	M77349 /FEATURE= /DEFINITION=HUMTGFBIG Human transforming growth factor-beta induced gene product (BIGH3) mRNA, complete cds	1385_at
SIAT9 (sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3	AB018356	Hs.225939	NM_003896	2p24.3-p24.1	Cluster Incl. AB018356:Homo sapiens mRNA for GM3 synthase, complete cds /cds=(277,1365) /gb=AB018356 /gi=3779138 /ug=Hs.225939 /len=2359	34256_at
H2BFL (H2B histone family, member L)	AI688098	Hs.239884	NM_003526	6p21.3	Cluster Incl. AI688098:wc92f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2326119 /clone_end=3 /gb=AI688098	33458_r_at

					/gi=4899392 /ug=Hs.239884 /len=576	
SLU7(step II splicing factor SLU7)	AI660656	Hs.76325	NM_006425	5	Cluster Incl. AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2351436 /clone_end=3 /gb=AI660656 /gi=4764239 /ug=Hs.76325 /len=522	37006_at
KIAA0143(KIAA0143 protein)	D63477	Hs.84087		8	Cluster Incl. D63477:Human mRNA for KIAA0143 gene, partial cds /cds=(0,2658) /gb=D63477 /gi=1469867 /ug=Hs.84087 /len=5286	38472_at
CALM3 (calmodulin 3 (phosphorylase kinase, delta))	J04046	Hs.334330	NM_005184	19q13.2-q13.3	J04046 /FEATURE=mRNA /DEFINITION=HUMCAMA Human calmodulin mRNA, complete cds	1158_s_at
IGKC (immunoglobulin kappa constant)	M63438	Hs.156110		2p12	Cluster Incl. M63438:Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds /cds=(0,1049) /gb=M63438 /gi=184847 /ug=Hs.156110 /len=1244	38194_s_at

IRF4 (interferon regulatory factor 4)	U52682	Hs.82132	NM_002460	6p25-p23	Cluster Incl. U52682:Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds /cds=(125,1477) /gb=U52682 /gi=1378108 /ug=Hs.82132 /len=5320	37625_at
HLA-DMB (major histocompatibility complex, class II, DM beta)	U15085	Hs.1162	NM_002118	6p21.3	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	41609_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
MTMR1 (myotubularin related protein 1)	AJ224979	Hs.23200		Xq28	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4126155 /ug=Hs.23200 /len=2582	34654_at

LILRB4 (leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains),	AF072099	Hs.67846	NM_006847	19q13.4	Cluster Incl. AF072099:Homo sapiens immunoglobulin-like transcript 3 protein variant 1 gene, complete cds /cds=(0,1346) /gb=AF072099 /gi=3776463 /ug=Hs.67846 /len=1705	36753_at
SLC31A1 (solute carrier family 31 (copper transporters), member 1)	U83460	Hs.73614	NM_001859	9q31-q32	Cluster Incl. U83460:Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds /cds=(152,724) /gb=U83460 /gi=2315986 /ug=Hs.73614 /len=1804	40364_at
CST3 (cystatin C (amyloid angiopathy and cerebral hemorrhage))	AI362017	Hs.135084	NM_000099	20p11.2	Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2014362 /clone_end=3 /gb=AI362017 /gi=4113638 /ug=Hs.135084 /len=778	39689_at
KIAA0261(KIAA0261 protein)	D87450	Hs.154978		10	Cluster Incl. D87450:Human mRNA for KIAA0261 gene, partial cds /cds=(0,3865) /gb=D87450 /gi=1665788 /ug=Hs.154978 /len=6155	40086_at

ASB1 (ankyrin repeat and SOCS box-containing 1)	AF055024	Hs.153489	NM_016114	2q37	Cluster Incl. AF055024:Homo sapiens clone 24763 mRNA sequence /cds=UNKNOWN /gb=AF055024 /gi=3005752 /ug=Hs.153489 /len=1830	31875_at
HNRPA3 (heterogeneous nuclear ribonucleoprotein A3)	S63912	Hs.249247	NM_005758	10	Cluster Incl. S63912:D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt] /cds=(30,839) /gb=S63912 /gi=399757 /ug=Hs.234462 /len=3043	33817_at
HLA-DQB1 (major histocompatibility complex, class II, DQ beta 1)	M81141	Hs.73931	NM_002123	6p21.3	Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171	36773_f_at
MD-1(MD-1, RP105-associated)	AB020499	Hs.184018	NM_004271	6	Cluster Incl. AB020499:Homo sapiens BCG-regulated mRNA for MD-1 homologue, complete cds /cds=(131,358) /gb=AB020499 /gi=4586549 /ug=Hs.184018 /len=713	35869_at

POLR2B (polymerase (RNA) II (DNA directed) polypeptide B (140kD))	X63563	Hs.296014	NM_000938	4q12	Cluster Incl. X63563:H.sapiens mRNA for RNA polymerase II 140 kDa subunit /cds=(43,3567) /gb=X63563 /gi=36121 /ug=Hs.148027 /len=3748	39746_at
	M13560				Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080	35016_at
ITGB1 (integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12))	X07979	Hs.287797		10p11.2	Cluster Incl. X07979:Human mRNA for integrin beta 1 subunit /cds=(103,2499) /gb=X07979 /gi=31441 /ug=Hs.202661 /len=3614	32808_at
TRRAP (transformation/transcription domain-associated protein)	AF110377	Hs.203952	NM_003496	7q21.2-q22.1	Cluster Incl. AF110377:Homo sapiens PCAF-associated factor 400 (PAF400) mRNA, complete cds /cds=(129,11708) /gb=AF110377 /gi=4151928 /ug=Hs.203952 /len=12603	33810_at

SLC7A6 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	D87432	Hs.10315	NM_003983	16q22.1-q22.3	Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(261,1808) /gb=D87432 /gi=1665758 /ug=Hs.10315 /len=6296	39533_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41165_g_at
CPVL (carboxypeptidase, vitellogenic-like)	AC005162	Hs.95594	NM_031311	7p15-p14	Cluster Incl. AC005162:Homo sapiens BAC clone RG113D17 from 7p14-p15 /cds=(0,887) /gb=AC005162 /gi=3242752 /ug=Hs.95594 /len=888	38323_at
IGL@ (immunoglobulin lambda locus)	M18645	Hs.181125		22q11.1-q11.2	Cluster Incl. M18645:Human Ig rearranged lambda-chain mRNA VJC-region subgroup lambda-IV from heterohybridoma H6-3C4 /cds=(30,731) /gb=M18645 /gi=186103 /ug=Hs.181125 /len=872	33274_f_at

DKFZP564B0769(DKFZP564B0769 protein)	AL080186	Hs.18368		6	Cluster Incl. AL080186:Homo sapiens mRNA; cDNA DKFZp564B0769 (from clone DKFZp564B0769) /cds=(0,900) /gb=AL080186 /gi=5262664 /ug=Hs.18368 /len=2776	41784_at
PRKWNK1 (protein kinase, lysine deficient 1)	U00946	Hs.184592	NM_018979	12p13.3	Cluster Incl. U00946:Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA /cds=UNKNOWN /gb=U00946 /gi=405048 /ug=Hs.184592 /len=1971	32185_at
CD14 (CD14 antigen)	X06882	Hs.75627	NM_000591	5q31.1	Cluster Incl. X06882:Human gene for CD14 differentiation antigen /cds=(105,1232) /gb=X06882 /gi=29736 /ug=Hs.75627 /len=1356	36661_s_at
ALDH9A1 (aldehyde dehydrogenase 9 family, member A1)	U34252	Hs.2533	NM_000696	1q22-q23	Cluster Incl. U34252:Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds /cds=(377,1858) /gb=U34252 /gi=1049218 /ug=Hs.2533	33899_at

					/len=2688	
MRPS18-2(mitochondrial ribosomal protein S18-2)	AL050361	Hs.274417	NM_014046	6	Cluster Incl. AL050361:Homo sapiens mRNA; cDNA DKFZp564H0223 (from clone DKFZp564H0223) /cds=UNKNOWN /gb=AL050361 /gi=4914594 /ug=Hs.190161 /len=1608	32221_at
KSR (kinase suppressor of ras)	U43586	Hs.152094		17q11.2	U43586 /FEATURE= /DEFINITION=HSU43586 Human kinase suppressor of ras-1 (KSR1) mRNA, partial cds	1716_at
					Cluster Incl. AB002448:Homo sapiens mRNA from chromosome 5q21-22, clone-357Ex /cds=UNKNOWN /gb=AB002448 /gi=2943811 /ug=Hs.26968 /len=1270	36260_at
KIAA0471(KIAA0471 gene product)	AB007940			1	Cluster Incl. AB007940:Homo sapiens mRNA for KIAA0471 protein, complete cds /cds=(412,1524) /gb=AB007940	34445_at

					/gi=3413903 /ug=Hs.107325 /len=6834	
TRB@ (T cell receptor beta locus)	M12886	Hs.303157		7q35	M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	1105_s_at
					Cluster Incl. X92997:H.sapiens mRNA for IgG lambda light chain V-J-C region (clone Tgl4) /cds=(0,321) /gb=X92997 /gi=1070337 /ug=Hs.129722 /len=322	35530_f_at
IGLL3 (immunoglobulin lambda-like polypeptide 3)	AI932613	Hs.296552		22q11.23	Cluster Incl. AI932613:wo05c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2454434 /clone_end=3 /gb=AI932613 /gi=5671350 /ug=Hs.62036 /len=570	41827_f_at
SFTPC (surfactant, pulmonary-associated protein C)	J03553	Hs.1074	NM_003018	8p21	Cluster Incl. J03553:Human pulmonary surfactant protein (SP5) mRNA, complete cds /cds=(146,739) /gb=J03553 /gi=338306 /ug=Hs.1074 /len=963	38691_s_at

SMAP(thyroid hormone receptor coactivating protein)	AW020536	Hs.5464	NM_006696	5	Cluster Incl. AW020536:df11b12.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2482918 /clone_end=5 /gb=AW020536 /gi=5874066 /ug=Hs.169344 /len=514	32653_at
KIAA0982(KIAA0982 protein)	AB023199	Hs.27207	NM_014023	10	Cluster Incl. AB023199:Homo sapiens mRNA for KIAA0982 protein, complete cds /cds=(144,1628) /gb=AB023199 /gi=4589607 /ug=Hs.27207 /len=4586	35199_at
AQP3 (aquaporin 3)	N74607	Hs.234642	NM_004925	9p13	Cluster Incl. N74607:za55a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-296424 /clone_end=3 /gb=N74607 /gi=1231892 /ug=Hs.234642 /len=487	39248_at
					Cluster Incl. AL050166:Homo sapiens mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122) /cds=UNKNOWN /gb=AL050166 /gi=4884381 /ug=Hs.26295 /len=2654	39582_at

NAGA (N-acetylgalactosaminidase, alpha-)	Z99716	Hs.75372	NM_000262	22q11	Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606	36607_at
CLTC (clathrin, heavy polypeptide (Hc))	D21260	Hs.178710	NM_004859	17q11-qter	Cluster Incl. D21260:Human mRNA for KIAA0034 gene, complete cds /cds=(172,5199) /gb=D21260 /gi=434760 /ug=Hs.178710 /len=6111	41159_at
MGEA5 (meningioma expressed antigen 5 (hyaluronidase))	AB014579	Hs.5734	NM_012215	10q24.1-q24.3	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303	35317_at
ANXA5 (annexin A5)	U05770	Hs.300711	NM_001154	4q28-q32	Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U05770 /gi=2182176 /ug=Hs.79274 /len=1597	37747_at
HLA-DRA (major histocompatibility complex, class II, DR alpha)	J00194	Hs.76807	NM_019111	6p21.3	Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragments	37039_at

class II, DR alpha)					/cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199	
LRP1 (low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor))	X13916	Hs.89137	NM_002332	12q13-q14	Cluster Incl. X13916:Human mRNA for LDL-receptor related protein /cds=(466,14100) /gb=X13916 /gi=34338 /ug=Hs.89137 /len=14885	38775_at
					L47276 /FEATURE=UTR#1 /DEFINITION=HUMTOPATR Homo sapiens (cell line HL-60) alpha topoisomerase truncated-form mRNA, 3 UTR	904_s_at
CCNB1 (cyclin B1)	M25753	Hs.23960	NM_031966	5q12	Cluster Incl. M25753:Human cyclin B mRNA, 3 end /cds=UNKNOWN /gb=M25753 /gi=181243 /ug=Hs.23960 /len=1452	34736_at
FGFR1 (fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome))	X66945	Hs.748	NM_000604	8p11.2-p11.1	X66945 /FEATURE=cds /DEFINITION=HSNSAMTK H.sapiens N-sam mRNA for fibroblast growth factor	424_s_at

					receptor	
TAF2D (TATA box binding protein (TBP)-associated factor, RNA polymerase II, D, 100kD)	X95525	Hs.96103	NM_006951	10q24-q25.2	Cluster Incl. X95525:H.sapiens mRNA for TAFII100 protein /cds=(23,2422) /gb=X95525 /gi=1491717 /ug=Hs.96103 /len=3089	41050_at
UBE2M (ubiquitin-conjugating enzyme E2M (homologous to yeast UBC12))	AA587372	Hs.200478	NM_003969	19q13.2	Cluster Incl. AA587372:nn82f03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1090397 /clone_end=3 /gb=AA587372 /gi=2398186 /ug=Hs.200478 /len=636	33782_r_at
PRKCB1 (protein kinase C, beta 1)	X06318	Hs.77202	NM_002738	16p11.2	X06318 /FEATURE=cds /DEFINITION=HSPKCB1A Human mRNA for protein kinase C (PKC) type beta I	1336_s_at
AIM1 (absent in melanoma 1)	AI800499	Hs.161002		6q21	Cluster Incl. AI800499:tc11f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2063565 /clone_end=3 /gb=AI800499 /gi=5365971 /ug=Hs.161002 /len=403	32112_s_at

PLSCR1 (phospholipid scramblase 1)	AB006746	Hs.198282	NM_021105	3q23	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077	32775_r_at
					Cluster Incl. AL080216:Homo sapiens mRNA; cDNA DKFZp586K1123 (from clone DKFZp586K1123) /cds=UNKNOWN /gb=AL080216 /gi=5262707 /ug=Hs.26837 /len=2204	35187_at
ASH2L (ash2 (absent, small, or homeotic, Drosophila, homolog)-like)	AB022785	Hs.6856	NM_004674	8p11.2	Cluster Incl. AB022785:Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene /cds=(12,1898) /gb=AB022785 /gi=4210446 /ug=Hs.6856 /len=2369	35804_at
DXF68S1E(DNA segment, numerous copies, expressed probes (GS1 gene))	M86934			X	Cluster Incl. M86934:Human GS1 (protein of unknown function) mRNA, complete cds /cds=(35,679) /gb=M86934 /gi=183652 /ug=Hs.78991 /len=2058	37709_at

						Cluster Incl. AF067420:Homo sapiens SNC73 protein (SNC73) mRNA, complete cds /cds=(395,1549) /gb=AF067420 /gi=3201899 /ug=Hs.32225 /len=1594	33499_s_at
CD5 (CD5 antigen (p56-62))	X04391	Hs.58685	NM_014207	11q13		Cluster Incl. X04391:Human mRNA for lymphocyte glycoprotein T1/Leu-1 /cds=(72,1559) /gb=X04391 /gi=37186 /ug=Hs.234745 /len=2320	32953_at
						Cluster Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype 2 {constant region, germ line} [human, peripheral blood neutrophils, Genomic, 1799 nt] /cds=(0,1022) /gb=S71043 /gi=546798 /ug=Hs.32225 /len=1047	33500_i_at
PCF11(PCF11p homolog)	AB020631	Hs.123654	NM_015885	11		Cluster Incl. AB020631:Homo sapiens mRNA for KIAA0824 protein, partial cds /cds=(0,4936) /gb=AB020631 /gi=4240136 /ug=Hs.123654 /len=5834	41665_at

CRA(cisplatin resistance associated)	U78556	Hs.166066	NM_006697	1	U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds	1230_g_at
PCK2 (phosphoenolpyruvate carboxykinase 2 (mitochondrial))	X92720	Hs.75812	NM_004563	14q11.2-14q21.3	Cluster Incl. X92720:H.sapiens mRNA for phosphoenolpyruvate carboxykinase /cds=(66,1988) /gb=X92720 /gi=1403049 /ug=Hs.75812 /len=2147	37188_at
					Cluster Incl. S71043:Ig alpha 2=immunoglobulin A heavy chain allotype 2 {constant region, germ line} [human, peripheral blood neutrophils, Genomic, 1799 nt] /cds=(0,1022) /gb=S71043 /gi=546798 /ug=Hs.32225 /len=1047	33501_r_at
C18orf1 (chromosome 18 open reading frame 1)	AF009425	Hs.153498	NM_004338	18p11.2	Cluster Incl. AF009425:Homo sapiens clone 22 mRNA, alternative splicing variant alpha-2, complete cds /cds=(469,1335) /gb=AF009425	40045_g_at

					/gi=2271470 /ug=Hs.153498 /len=8440	
CAPN2 (calpain 2, (m/II) large subunit)	M23254	Hs.76288	NM_001748	1q41-q42	Homo sapiens /REF=M23254 /DEF=Cluster Incl. :Human Ca2-activated neutral protease large subunit (CANP) mRNA, complete cds /cds=(130,2232) /gb= /gi=511636 /ug=Hs.76288 /len=3213 /LEN=3435	37001_at
IGL@ (immunoglobulin lambda locus)	X57809	Hs.181125		22q11.1-q11.2	Cluster Incl. X57809:Human rearranged immunoglobulin lambda light chain mRNA /cds=(114,815) /gb=X57809 /gi=33714 /ug=Hs.181125 /len=915	33273_f_at
GALT (galactose-1-phosphate uridylyltransferase)	M60091	Hs.75641	NM_000155	9p13	Cluster Incl. M60091:Homo sapiens galactose-1-phosphate uridyl transferase (GALT) mRNA, complete cds /cds=(28,1167) /gb=M60091 /gi=182950 /ug=Hs.75641 /len=1295	36664_at

APLP2 (amyloid beta (A4) precursor-like protein 2)	S60099	Hs.279518	NM_001642	11q24	Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.64797 /len=3727	33944_at
CAST (calpastatin)	D16217	Hs.279607	NM_001750	5q14-q22	Cluster Incl. D16217:Human mRNA for calpastatin, complete cds /cds=(162,2288) /gb=D16217 /gi=303598 /ug=Hs.226067 /len=2493	41257_at
CSPG2 (chondroitin sulfate proteoglycan 2 (versican))	D32039	Hs.81800	NM_004385	5q14.3	Cluster Incl. D32039:Human pgH3 mRNA for proteoglycan PG-M(V3), complete cds /cds=(105,2072) /gb=D32039 /gi=1008912 /ug=Hs.234753 /len=2087	31682_s_at
USP9X (ubiquitin specific protease 9, X chromosome (Drosophila fat facets related))	X98296	Hs.77578	NM_004652	xp11.4	X98296 /FEATURE=cds /DEFINITION=HSUBIQHYD H.sapiens mRNA for ubiquitin hydrolase	969_s_at

SAMHD1 (SAM domain and HD domain, 1)	AL050267			20pter-q12	Cluster Incl. AL050267:Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032) /cds=(75,1955) /gb=AL050267 /gi=4886492 /ug=Hs.23889 /len=2195	34714_at
SHARP(Msx2 interacting nuclear target protein)	AL096858	Hs.184245	NM_015001	1	Cluster Incl. AL096858:Novel human gene mapping to chomosome 1 /cds=(331,10116) /gb=AL096858 /gi=5541864 /ug=Hs.184245 /len=11145	32172_at
KIAA0528(KIAA0528 gene product)	AB011100	Hs.30656		12	Cluster Incl. AB011100:Homo sapiens mRNA for KIAA0528 protein, complete cds /cds=(799,3507) /gb=AB011100 /gi=3043579 /ug=Hs.30656 /len=4682	35252_at
					Cluster Incl. N95443:zb81c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-310006 /clone_end=3 /gb=N95443 /gi=1267753 /ug=Hs.19180 /len=611	33716_at

LOC56007(hypothetical protein 23851)	AF035313	Hs.10065		5	Cluster Incl. AF035313:Homo sapiens clone 23851 mRNA sequence /cds=UNKNOWN /gb=AF035313 /gi=2661075 /ug=Hs.10065 /len=1369	39517_at
KIAA0332(KIAA0332 protein)	AB002330			3	Cluster Incl. AB002330:Human mRNA for KIAA0332 gene, partial cds /cds=(0,3087) /gb=AB002330 /gi=2224604 /ug=Hs.7976 /len=6823	38030_at
CSPG2 (chondroitin sulfate proteoglycan 2 (versican))	X15998	Hs.81800	NM_004385	5q14.3	Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224	38112_g_at
GAS7 (growth arrest-specific 7)	AB007854	Hs.226133	NM_003644	17p	Cluster Incl. AB007854:Homo sapiens KIAA0394 mRNA, complete cds /cds=(121,1359) /gb=AB007854 /gi=2662068 /ug=Hs.226133 /len=7979	33387_at

ICSBP1 (interferon consensus sequence binding protein 1)	M91196	Hs.14453	NM_002163	16q24	Cluster Incl. M91196:Homo sapiens DNA-binding protein mRNA, complete cds /cds=(47,1327) /gb=M91196 /gi=2275152 /ug=Hs.2286 /len=1538	32941_at
IFI30 (interferon, gamma-inducible protein 30)	J03909	Hs.14623	NM_006332	19p13.1	J03909 /FEATURE= /DEFINITION=HUMIIP Human gamma-interferon-inducible protein (IP-30) mRNA, complete cds	925_at
MGC4175(hypothetical protein MGC4175)	AI656421	Hs.322404	NM_024315	7	Cluster Incl. AI656421:tt50h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2244259 /clone_end=3 /gb=AI656421 /gi=4740400 /ug=Hs.5671 /len=566	41809_at
KIAA0810(KIAA0810 protein)	AB018353	Hs.7531	NM_025154		Cluster Incl. AB018353:Homo sapiens mRNA for KIAA0810 protein, partial cds /cds=(0,2475) /gb=AB018353 /gi=3882340 /ug=Hs.7531 /len=4047	36588_at
					Cluster Incl. AI700633:we38g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-	34840_at

						2343412 /clone_end=3 /gb=AI700633 /gi=4988533 /ug=Hs.4815 /len=565	
AHNAK (AHNAK nucleoprotein (desmoyokin))	M80899	Hs.301417		11q12-q13		Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /cds=(0,3835) /gb=M80899 /gi=178282 /ug=Hs.76549 /len=4051	37027_at
WEE1 (wee1+ (S. pombe) homolog)	W28575	Hs.75188	NM_003390	11p15.3-p15.1		Cluster Incl. W28575:51f12 Homo sapiens cDNA /gb=W28575 /gi=1308730 /ug=Hs.8151 /len=906	38102_at
MAD1L1 (MAD1 (mitotic arrest deficient, yeast, homolog)-like 1)	U33822	Hs.7345	NM_003550	7p22		U33822 /FEATURE= /DEFINITION=HSU33822 Human tax1-binding protein TXBP181 mRNA, complete cds	499_at
ECGF1 (endothelial cell growth factor 1 (platelet-derived))	M63193	Hs.73946	NM_001953	22q13.33		Cluster Incl. M63193:Human platelet-derived endothelial cell growth factor mRNA, complete cds /cds=(123,1571) /gb=M63193 /gi=189700 /ug=Hs.73946	36879_at

					/len=1587	
GBF1 (golgi-specific brefeldin A resistance factor 1)	D87435	Hs.155499	NM_004193	10q24	Cluster Incl. D87435:Human mRNA for KIAA0248 gene, partial cds /cds=(0,5077) /gb=D87435 /gi=1665764 /ug=Hs.155499 /len=5634	40123_at
RSN (restin (Reed-Steinberg cell-expressed intermediate filament-associated protein))	X64838	Hs.31638	NM_002956	12q24.3	Cluster Incl. X64838:H.sapiens mRNA for restin /cds=(132,4415) /gb=X64838 /gi=35998 /ug=Hs.31638 /len=5857	34350_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38095_i_at
CAPZA2 (capping protein (actin filament) *muscle Z-line, alpha 2*)	U03851	Hs.75546	NM_006136	7q31.2-q31.3	Cluster Incl. U03851:Human capping protein alpha mRNA, partial cds /cds=(16,870) /gb=U03851 /gi=433307	36641_at

					/ug=Hs.75546 /len=2263	
ATP6A1 (ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD,	AA056747	Hs.281866	NM_001690	3p13-q13.2	Cluster Incl. AA056747:zk81f02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-489243 /clone_end=3 /gb=AA056747 /gi=1549122 /ug=Hs.5119 /len=559	34889_at
RBBP4 (retinoblastoma-binding protein 4)	X74262	Hs.16003	NM_005610	5p15.2	Cluster Incl. X74262:H.sapiens RbAp48 mRNA encoding retinoblastoma binding protein /cds=(84,1361) /gb=X74262 /gi=397375 /ug=Hs.16003 /len=2314	40418_at
KIAA0852(KIAA0852 protein)	AB020659	Hs.35276	NM_014941	22	Cluster Incl. AB020659:Homo sapiens mRNA for KIAA0852 protein, complete cds /cds=(1364,4276) /gb=AB020659 /gi=4240192 /ug=Hs.35276 /len=4467	35683_at
HLA-DQB1 (major histocompatibility complex, class II, DQ beta 1)	M60028	Hs.73931	NM_002123	6p21.3	Cluster Incl. M60028:Human MHC class II HLA-DQ-beta (DQB1,DQw9), complete cds /cds=(57,842) /gb=M60028 /gi=188114 /ug=Hs.73931 /len=1192	36878_f_at

KIAA0826(KIAA0826 protein)	AB020633	Hs.169600		4	Cluster Incl. AB020633:Homo sapiens mRNA for KIAA0826 protein, partial cds /cds=(0,3710) /gb=AB020633 /gi=4240140 /ug=Hs.169600 /len=5770	40492_at
AP3B1 (adaptor-related protein complex 3, beta 1 subunit)	U81504	Hs.155172	NM_003664	5p14.3-q14.3	Cluster Incl. U81504:Homo sapiens beta-3A-adaptin subunit of the AP-3 complex mRNA, complete cds /cds=(92,3376) /gb=U81504 /gi=2199511 /ug=Hs.155172 /len=3950	32039_at
					Cluster Incl. AL109698:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 26539 /cds=UNKNOWN /gb=AL109698 /gi=5689808 /ug=Hs.8065 /len=2035	37590_g_at
GJA8 (gap junction protein, alpha 8, 50kD (connexin 50))	U34802	Hs.157433	NM_005267	1q21.1	Cluster Incl. U34802:Human intrinsic membrane protein MP70 (Cx50) gene, complete cds /cds=(0,1298) /gb=U34802 /gi=1002998 /ug=Hs.157433 /len=1299	31778_at

JAK1 (Janus kinase 1 (a protein tyrosine kinase))	M64174	Hs.50651	NM_002227	1p32.3-p31.3	Cluster Incl. M64174:Human protein-tyrosine kinase (JAK1) mRNA, complete cds /cds=(75,3503) /gb=M64174 /gi=190734 /ug=Hs.50651 /len=3541	41594_at
CDC2 (cell division cycle 2, G1 to S and G2 to M)	D88357	Hs.184572	NM_001786	10q21.1	Cluster Incl. D88357:Homo sapiens mRNA for CDC2 delta T, complete cds /cds=(27,749) /gb=D88357 /gi=3126638 /ug=Hs.184572 /len=780	33324_s_at
NNT (nicotinamide nucleotide transhydrogenase)	U40490	Hs.18136	NM_012343	5p13.1-5cen	Cluster Incl. U40490:Human nicotinamide nucleotide transhydrogenase mRNA, nuclear gene encoding mitochondrial protein, complete cds /cds=(143,3403) /gb=U40490 /gi=1110519 /ug=Hs.18136 /len=4232	41722_at
ITPR3 (inositol 1,4,5-triphosphate receptor, type 3)	U01062	Hs.77515	NM_002224	6p21	Cluster Incl. U01062:Human type 3 inositol 1,4,5-trisphosphate receptor (ITPR3) mRNA, complete cds /cds=(36,8051) /gb=U01062 /gi=453367 /ug=Hs.77515	37343_at

					/len=8833	
KIAA0662(KIAA0662 gene product)	AB014562	Hs.93868		9	Cluster Incl. AB014562:Homo sapiens mRNA for KIAA0662 protein, partial cds /cds=(0,2034) /gb=AB014562 /gi=3327137 /ug=Hs.93868 /len=3944	39117_at
PAFAH1B1 (platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD))	L13385	Hs.77318	NM_000430	17p13.3	Cluster Incl. L13385:Homo sapiens(clone 71) Miller-Dieker lissencephaly protein (LIS1) mRNA, complete cds /cds=(217,1449) /gb=L13385 /gi=349823 /ug=Hs.77318 /len=5243	32569_at
PSMD12 (proteasome (prosome, macropain) 26S subunit, non-ATPase, 12)	AB003103	Hs.4295	NM_002816	17	AB003103 /FEATURE= /DEFINITION=AB003103 Homo sapiens mRNA for 26S proteasome subunit p55, complete cds	1192_at
LY64 (lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kD)	D83597	Hs.87205	NM_005582	5q12	Cluster Incl. D83597:Homo sapiens mRNA for RP105, complete cds /cds=(142,2127) /gb=D83597 /gi=1843410 /ug=Hs.87205	40715_at

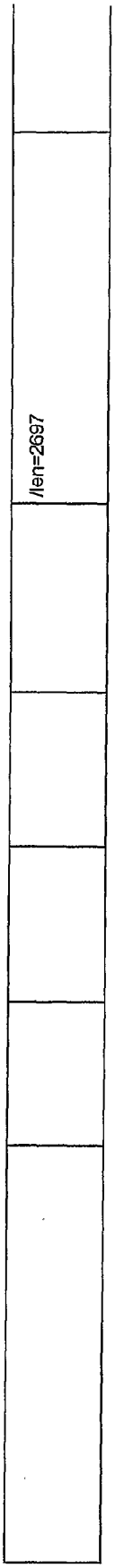

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Table 6:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	
CCR2 (chemokine (C-C motif) receptor 2)	U95626	Hs.395	NM_000647	3p21	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at
CCR2 (chemokine (C-C motif) receptor 2)	NM_000647	Hs.395	NM_000647	3p21	Cluster Incl. NM_000647 NM_000648:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at
AZU1 (azurocidin 1 (cationic antimicrobial protein 37))	M96326	Hs.72885	NM_001700	19p13.3	Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771)	33963_at

protein 37))					/gb=M96326 /gi=179301 /ug=Hs.72885 /len=913	
CAMP (cathelicidin antimicrobial peptide)	Z38026	Hs.51120	NM_004345	3p21.3	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	36710_at
	D872				Cluster Incl. D872+B792:Homo sapiens mRNA for rhodanese, complete cds /cds=(48,941) /gb=D87292 /gi=1877030 /ug=Hs.74097 /len=1137	36123_at
ZWINT (ZW10 interactor)	AF067656	Hs.42650	NM_007057	10q21-q22	Cluster Incl. AF067656:Homo sapiens ZW10 interactor Zwint mRNA, complete cds /cds=(24,857) /gb=AF067656 /gi=3901271 /ug=Hs.42650 /len=1639	35995_at
CAT (catalase)	AL035079	Hs.76359	NM_001752	11p13	Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079 /gi=4775614 /ug=Hs.76359 /len=2287	37009_at

NUCB2 (nucleobindin 2)	X76732	Hs.3164	NM_005013	11p15.1-p14	Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /gb=X76732 /gi=2706486 /ug=Hs.3164 /len=1586	35643_at
RAD54L (RAD54 (S.cerevisiae)-like)	X97795	Hs.66718	NM_003579	1p32	X97795 /FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA homologous to S. cerevisiae RAD54	966_at
SLC29A1 (solute carrier family 29 (nucleoside transporters), member 1)	U81375	Hs.25450	NM_004955	6p21.1-p21.2	Cluster Incl. U81375:Human placental equilibrative nucleoside transporter 1 (hENT1) mRNA, complete cds /cds=(178,1548) /gb=U81375 /gi=1845344 /ug=Hs.25450 /len=2162	33901_at
[KIAA0101(KIAA0101 gene product)	D14657	Hs.81892	NM_014736	15	Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836	38116_at

MPO (myeloperoxidase)	M19507	Hs.1817	NM_000250	17q23.1	Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	33284_at
PCNA (proliferating cell nuclear antigen)	M15796	Hs.78996	NM_002592	20pter-p12	M15796 /FEATURE= /DEFINITION=HUMCYL Human cyclin protein gene, complete cds	1884_s_at
PRDX3 (peroxiredoxin 3)	D49396	Hs.75454	NM_006793	10q25-q26	Cluster Incl. D49396:Human mRNA for Apo1_Human (MER5(Aop1-Mouse)-like protein), complete cds /cds=(6,776) /gb=D49396 /gi=682747 /ug=Hs.75454 /len=1531	36631_at
IGLL1 (immunoglobulin lambda-like polypeptide 1)	M27749	Hs.288168	NM_020070	22q11.23	Cluster Incl. M27749:Human immunoglobulin-related 14.1 protein mRNA, complete cds /cds=(118,759) /gb=M27749 /gi=186145 /ug=Hs.170116 /len=847	38514_at

SNL (singed (Drosophila)-like (sea urchin fascin homolog like))	U03057	Hs.118400	NM_003088	7p22	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	39070_at
TUBB2(tubulin, beta, 2)	X02344	Hs.251653	NM_006088		Cluster Incl. X02344:Homo sapiens beta 2 gene /cds=(0,1337) /gb=X02344 /gi=37493 /ug=Hs.184582 /len=1338	33679_f_at
SPINK2 (serine protease inhibitor, Kazal type, 2 (acrosin-trypsin inhibitor)	X57655	Hs.98243	NM_021114	4	Cluster Incl. X57655:H.sapiens RNA for acrosin-trypsin inhibitor (HUSI-II) /cds=(68,322) /gb=X57655 /gi=32549 /ug=Hs.98243 /len=594	41071_at
TARS (threonyl-tRNA synthetase	M63180	Hs.84131	NM_003191	5p13-cen	Cluster Incl. M63180:Human threonyl-tRNA synthetase mRNA, complete cds /cds=(138,2276) /gb=M63180 /gi=339679 /ug=Hs.84131 /len=2644	38473_at
					Rad2	1515_at

ELA2 (elastase 2, neutrophil)	M34379	Hs.99863	NM_001972	19p13.3	Cluster Incl. M34379:Human elastase/medullasin mRNA, complete cds /cds=(38,841) /gb=M34379 /gi=187116 /ug=Hs.99863 /len=920	37096_at
SCGF (stem cell growth factor; lymphocyte secreted C-type lectin)	AF020044	Hs.105927	NM_002975	19q13.3	Cluster Incl. AF020044:Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds /cds=(179,1150) /gb=AF020044 /gi=2828595 /ug=Hs.105927 /len=1391	37147_at
HNRPAB (heterogeneous nuclear ribonucleoprotein A/B)	M65028	Hs.81361	NM_004499 NM_031266	5q35	Cluster Incl. M65028:Human hnRNP type A/B protein mRNA, complete cds /cds=(142,996) /gb=M65028 /gi=337450 /ug=Hs.81361 /len=1537	38094_at
RAB32 (RAB32, member RAS oncogene family)	U59878	Hs.32217	NM_006834	6	Cluster Incl. U59878:Human low-Mr GTP-binding protein (RAB32) mRNA, partial cds /cds=(0,632) /gb=U59878 /gi=1388196 /ug=Hs.32217 /len=980	41523_at

CTSG (cathepsin G)	M16117	Hs.100764	NM_001911	14q11.2	Cluster Incl. M16117:Human cathepsin G mRNA, complete cds /cds=(8,775) /gb=M16117 /gi=181181 /ug=Hs.100764 /len=857	37105_at
H2AFY (H2A histone family, member Y)	AF054174	Hs.75258	NM_004893	5q31.3-q32	Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete cds /cds=(173,1288) /gb=AF054174 /gi=3341991 /ug=Hs.75258 /len=1881	36576_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMG
	L47276				L47276 /FEATURE=UTR#1 /DEFINITION=HUMTOPATR Homo sapiens (cell line HL-60) alpha topoisomerase truncated-form mRNA, 3	904_s_at

					UTR	
KIAA0222(KIAA0222 gene product)	AL044599	Hs.48450	NM_014643	18	Cluster Incl. AL044599:DKFZp434N192_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N192 /clone_end=3 /gb=AL044599 /gi=5432814 /ug=Hs.48450 /len=1067	34843_at
H2AFX (H2A histone family, member X)	X14850	Hs.147097	NM_002105	11q23.2-q23.3	Cluster Incl. X14850:Human H2A.X mRNA encoding histone H2A.X /cds=(73,504) /gb=X14850 /gi=31972 /ug=Hs.147097 /len=1585	40195_at
LOC94392(hypothetical gene supported by AB007931; AF055010; AK001233; AK022322;	AB007931			1	Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150	33860_at
CCNB1 (cyclin B1)	M25753	Hs.23960	NM_031966	5q12	Cluster Incl. M25753:Human cyclin B mRNA, 3 end /cds=UNKNOWN	34736_at

						/gb=M25753 /gi=181243 /ug=Hs.23960 /len=1452	
LOC85295(hypothetical gene supported by V00599; BC001938; BC007605; BC008791	V00599			6		V00599 /FEATURE=mRNA /DEFINITION=HSTUB2 Human mRNA fragment encoding beta-tubulin. (from clone D-beta-1)	151_s_at
MLC1(KIAA0027 protein	D25217	Hs.74518	NM_015166	22		Cluster Incl. D25217:Human mRNA for KIAA0027 gene, partial cds /cds=(0,1317) /gb=D25217 /gi=434776 /ug=Hs.74518 /len=3435	36897_at
PRTN3 (proteinase 3 (serine proteinase, neutrophil, Wegener granulomatosis autoantigen	X55668	Hs.928	NM_002777	19p13.3		Cluster Incl. X55668:Human mRNA for proteinase 3 /cds=(0,764) /gb=X55668 /gi=35687 /ug=Hs.928 /len=965	37066_at
ALDH2 (aldehyde dehydrogenase 2 family (mitochondrial)	X05409	Hs.195432	NM_000690	12q24.2		Cluster Incl. X05409:Human RNA for mitochondrial aldehyde dehydrogenase I ALDH I (EC 1.2.1.3) /cds=(36,1586) /gb=X05409 /gi=28605 /ug=Hs.195432	32747_at

					/len=1989	
KNSL6 (kinesin-like 6 (mitotic centromere-associated kinesin)	U63743	Hs.69360	NM_006845	1	Cluster Incl. U63743:Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds /cds=(54,2231) /gb=U63743 /gi=1695881 /ug=Hs.69360 /len=2740	36837_at
TST (thiosulfate sulfurtransferase (rhodanese))	X59434	Hs.248267	NM_003312	22q13.1	Cluster Incl. X59434:Human rohu mRNA for rhodanese /cds=(34,924) /gb=X59434 /gi=432375 /ug=Hs.74097 /len=1232	36124_at
PAI-RBP1(PAI-1 mRNA-binding protein	AL080119	Hs.165998	NM_015640	1	Cluster Incl. AL080119:Homo sapiens mRNA; cDNA DKFZp564M2423 (from clone DKFZp564M2423) /cds=(85,1248) /gb=AL080119 /gi=5262550 /ug=Hs.165998 /len=2183	40440_at
RAB13 (RAB13, member RAS oncogene family	X75593	Hs.151536	NM_002870	12q13	Cluster Incl. X75593:H.sapiens mRNA for rab 13 /cds=(139,750) /gb=X75593 /gi=452319 /ug=Hs.151536 /len=1238	40210_at

NCOA4 (nuclear receptor coactivator 4)	X77548	Hs.99908	NM_005437	10q11.2	Cluster Incl. X77548:H. sapiens cDNA for RFG /cds=(76,1920) /gb=X77548 /gi=469145 /ug=Hs.99908 /len=3418	39174_at
ANXA1 (annexin A1)	X05908	Hs.78225	NM_000700	9q12-q21.2	Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X05908 /gi=34387 /ug=Hs.78225 /len=1399	37403_at
FEN1 (flap structure-specific endonuclease 1)	AC004770	Hs.4756	NM_004111	11q12	Cluster Incl. AC004770:Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene /cds=(2644,3786) /gb=AC004770 /gi=3212836 /ug=Hs.4756 /len=4522	41583_at
MYCBP (c-myc binding protein)	D50692	Hs.78221	NM_012333	1p33-p32.2	D50692 /FEATURE= /DEFINITION=HUMAMY1 Homo sapiens mRNA for c-myc binding protein, complete cds	1904_at
					Rad2	1516_g_at

IGFBP7 (insulin-like growth factor binding protein 7)	L19182	Hs.119206	NM_001553	4q12	L19182 /FEATURE= /DEFINITION=HUMMAC25X Human MAC25 mRNA, complete cds	2062_at
ICA1 (islet cell autoantigen 1 (69kD))	U38260	Hs.167927	NM_004968	7p22	Cluster Incl. U38260:Human islet cell autoantigen ICAp69 mRNA, complete cds /cds=(169,942) /gb=U38260 /gi=1675205 /ug=Hs.167927 /len=1415	32634_s_at
KIAA1055(KIAA1055 protein	AB028978	Hs.126084		15	Cluster Incl. AB028978:Homo sapiens mRNA for KIAA1055 protein, partial cds /cds=(0,2607) /gb=AB028978 /gi=5689446 /ug=Hs.126084 /len=5876	39400_at
CSF1 (colony stimulating factor 1 (macrophage))	M37435	Hs.173894	NM_000757	1p21-p13	M37435 /FEATURE= /DEFINITION=HUMCSDF1 Human macrophage-specific colony-stimulating factor (CSF-1) mRNA, complete cds	882_at
	W28186				Cluster Incl. W28186:43c2 Homo sapiens cDNA /gb=W28186 /gi=1308134	41188_at

					/ug=Hs.180320 /len=941	
SYNGR1 (synaptogyrin 1)	AL022326	Hs.6139	NM_004711	22q13.1	Cluster Incl. AL022326:dJ333H23.2.2 (Synaptogyrin 1A (SYNGR1A)) /cds=(43,744) /gb=AL022326 /gi=3550039 /ug=Hs.6139 /len=4406	35354_at
RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	X55988	Hs.728	NM_002934	14q24-q31	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	36766_at
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	AI126134	Hs.100000	NM_002964	1q21	Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at
IQGAP2 (IQ motif containing GTPase activating protein 2)	U51903	Hs.78993	NM_006633	5q	Cluster Incl. U51903:Human RasGAP-related protein (IQGAP2) mRNA, complete cds /cds=(222,4949) /gb=U51903 /gi=1262925 /ug=Hs.78993 /len=5767	37276_at

H1F0 (H1 histone family, member 0)	Z97630	Hs.226117	NM_005318	22q13.1	Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome 22q12-13 Contains H1F0(H1 histone family, member 0) gene, 2-amino-3-ketobutyrate -CoA ligase(nuclear gene encoding mitochondrial protein), GALR3 (galanin receptor) gene, ESTs, GSSs and CpG islands /cds=(381,965) /gb=Z97630 /gi=4582128 /ug=Hs.226117 /len=2527	33386_at
ADAM15 (a disintegrin and metalloproteinase domain 15 (metargidin))	U41767	Hs.92208	NM_003815	1q21.3	Cluster Incl. U41767:Human metargidin precursor mRNA, complete cds /cds=(7,2451) /gb=U41767 /gi=1235673 /ug=Hs.92208 /len=2725	38282_at
AKR1C3 (aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type	D17793	Hs.78183	NM_003739	10p15-p14	Cluster Incl. D17793:Human mRNA for KIAA0119 gene, complete cds /cds=(51,1022) /gb=D17793 /gi=457407 /ug=Hs.78183 /len=1204	37399_at
DF (D component of complement (adipsin))	M84526	Hs.155597	NM_001928	19	Cluster Incl. M84526:Human adipsin/complement factor D mRNA,	40282_s_at

					complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	
OAZ1 (ornithine decarboxylase antizyme 1)	D78361	Hs.125078		19p13.3	D78361 /FEATURE= /DEFINITION=HUMODAZ Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2	1315_at
ERG (v-ets avian erythroblastosis virus E26 oncogene related)	M21535	Hs.45514	NM_004449	21	M21535 /FEATURE= /DEFINITION=HUMERG11 Human erg protein (ets-related gene) mRNA, complete cds	914_g_at
GPSN2 (glycoprotein, synaptic 2)	AF038958	Hs.306122	NM_004868	19p13.	Cluster Incl. AF038958:Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds /cds=(76,1002) /gb=AF038958 /gi=3329385 /ug=Hs.109051 /len=1116	38966_at
DEFA1 (defensin, alpha 1, myeloid-related sequence)	AL036554	Hs.274463	NM_004084	8p23.2-p23.1	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5	31793_at

						/clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	
MGST2 (microsomal glutathione S-transferase 2)	U77604	Hs.81874	NM_002413	4q28-q31		U77604 /FEATURE= /DEFINITION=HSU77604 Homo sapiens microsomal glutathione S-transferase 2 (MGST2) mRNA, complete cds	820_at
TOP2A (topoisomerase (DNA) II alpha (170kD))	AI375913	Hs.156346	NM_001067	17q21-q22		Cluster Incl. AI375913:tc14c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2063822 /clone_end=3 /gb=AI375913 /gi=4175903 /ug=Hs.156346 /len=916	40145_at
DEFA3 (defensin, alpha 3, neutrophil-specific)	L12691	Hs.294176	NM_005217	8pter-p23.3		Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364 /ug=Hs.178741 /len=452	31506_s_at
CKS2 (CDC28 protein kinase 2)	X54942	Hs.83758	NM_001827	9q22		Cluster Incl. X54942:H.sapiens ckshs2 mRNA for Cks1 protein homologue /cds=(95,334) /gb=X54942 /gi=29978	40690_at

					/ug=Hs.83758 /len=612	
CSTA (cystatin A (stefin A))	AA570193	Hs.2621	NM_005213	3q21	Cluster Incl. AA570193:nf38c11.s1 Homo sapiens cDNA /clone=IMAGE-916052 /gb=AA570193 /gi=2344173 /ug=Hs.2621 /len=450	39581_at
HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)	L24521	Hs.89525	NM_004494	xq25	Cluster Incl. L24521:Human transformation-related protein mRNA, 3 end /cds=(0,1108) /gb=L24521 /gi=403459 /ug=Hs.169225 /len=1240	36446_s_at
TFDP2 (transcription factor Dp-2 (E2F dimerization partner 2)	L40386	Hs.19131	NM_006286	3q23	L40386 /FEATURE=mRNA /DEFINITION=HUMDP2M Human DP-2 mRNA, complete cds	633_s_at
TYMS (thymidylate synthetase)	X02308	Hs.82962	NM_001071	18p11.32	Cluster Incl. X02308:Human mRNA for thymidylate synthase (EC 2.1.1.45) /cds=(105,1046) /gb=X02308 /gi=37478 /ug=Hs.82962 /len=1536	37899_at

H2AV(histone H2A.F/Z variant	AW007731	Hs.301005	NM_012412	7	Cluster Incl. AW007731:wt68d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512629 /clone_end=3 /gb=AW007731 /gi=5856509 /ug=Hs.9242 /len=659	39092_at
EPB72 (erythrocyte membrane protein band 7.2 (stomatin)	X85116	Hs.160483	NM_004099	9q34.1	Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035	40419_at
GNAQ (guanine nucleotide binding protein (G protein), q polypeptide	U40038	Hs.296261	NM_002072	9q21	Cluster Incl. U40038:Human GTP-binding protein alpha q subunit (GNAQ) mRNA, complete cds /cds=(42,1121) /gb=U40038 /gi=1181670 /ug=Hs.180950 /len=1450	38581_at
HBD (hemoglobin, delta)	V00505	Hs.36977	NM_000519	11p15.5	Cluster Incl. V00505:Human gene for delta-globin /cds=(50,493) /gb=V00505 /gi=30510 /ug=Hs.36977 /len=624	33516_at
TTK (TTK protein kinase)	M86699	Hs.169840	NM_003318	6q13-q21	M86699 /FEATURE= /DEFINITION=HUMTTK Human kinase (TTK) mRNA, complete cds	572_at

KIAA0661(95 kDa retinoblastoma protein binding protein	AB014561	Hs.65238	NM_014771	16	Cluster Incl. AB014561:Homo sapiens mRNA for KIAA0661 protein, complete cds /cds=(92,3097) /gb=AB014561 /gi=3327135 /ug=Hs.65238 /len=4199	35768_at
MCM3 (minichromosome maintenance deficient (S. cerevisiae) 3	D38073	Hs.179565	NM_002388	6p12	Cluster Incl. D38073:Human mRNA for hRlf beta subunit (p102 protein), complete cds /cds=(77,2503) /gb=D38073 /gi=862331 /ug=Hs.179565 /len=3071	33252_at
KIAA0161(ubiquitin conjugating enzyme 7 interacting protein 4	D79983	Hs.78894	NM_014746	2	Cluster Incl. D79983:Human mRNA for KIAA0161 gene, complete cds /cds=(348,1226) /gb=D79983 /gi=1136383 /ug=Hs.78894 /len=5559	37695_at
CCNB1 (cyclin B1	M25753	Hs.23960	NM_031966	5q12	M25753 /FEATURE=mRNA /DEFINITION=HUMCYCB Human cyclin B mRNA, 3 end	1945_at
PK428(Ser-Thr protein kinase related to the myotonic dystrophy protein kinase	U59305	Hs.44708	NM_003607	1	Cluster Incl. U59305:Human ser-thr protein kinase PK428 mRNA, complete cds /cds=(1288,2778) /gb=U59305	39962_at

					/gi=1695872 /ug=Hs.44708 /len=2785	
MYB (v-myb avian myeloblastosis viral oncogene homolog	M15024	Hs.1334	NM_005375	6q22-q23	M15024 /FEATURE= /DEFINITION=HUMCMYBLA Human c-myb mRNA, complete cds	2042_s_at
OAT (ornithine aminotransferase (gyrate atrophy)	M12267	Hs.75485	NM_000274	10q26	Cluster Incl. M12267:Human ornithine aminotransferase mRNA, complete cds /cds=(54,1373) /gb=M12267 /gi=189328 /ug=Hs.75485 /len=2013	36636_at
LDHA (lactate dehydrogenase A)	X02152	Hs.2795	NM_005566	11p15.4	Cluster Incl. X02152:Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) /cds=(97,1095) /gb=X02152 /gi=34312 /ug=Hs.2795 /len=1661	41485_at
P311(P311 protein)	U30521	Hs.142827	NM_004772	8	Cluster Incl. U30521:Human P311 HUM (3.1) mRNA, complete cds /cds=(202,408) /gb=U30521 /gi=963091 /ug=Hs.142827 /len=2036	39710_at

AGPS (alkylglycerone phosphate synthase	Y09443	Hs.22580	NM_003659	2q31	Cluster Incl. Y09443:H.sapiens mRNA for alkyl-dihydroxyacetonephosphate synthase precursor /cds=(15,1991) /gb=Y09443 /gi=1922284 /ug=Hs.22580 /len=2074	39225_at
GSN (gelsolin (amyloidosis, Finnish type)	X04412	Hs.290070	NM_000177	9q33	Cluster Incl. X04412:Human mRNA for plasma gelsolin - /cds=(14,2362) /gb=X04412 /gi=35447 /ug=Hs.80562 /len=2602	32612_at
ALDH3B1 (aldehyde dehydrogenase 3 family, member B1	U10868	Hs.83155	NM_000694	11q13	Cluster Incl. U10868:Human aldehyde dehydrogenase ALDH7 mRNA, complete cds /cds=(47,1453) /gb=U10868 /gi=601779 /ug=Hs.83155 /len=2790	40685_at
TFDP1 (transcription factor Dp-1	L23959	Hs.79353	NM_007111	13q34	L23959 /FEATURE= /DEFINITION=HUMDP1A Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds	1670_at

TUBG1 (tubulin, gamma 1)	M61764	Hs.21635	NM_001070	17q21-q22	Cluster Incl. M61764:Human gamma-tubulin mRNA, complete cds /cds=(24,1379) /gb=M61764 /gi=183702 /ug=Hs.21635 /len=1568	33346_r_at
LMO2 (LIM domain only 2 (rhombotin-like 1)	X61118	Hs.184585	NM_005574	11p13	Cluster Incl. X61118:Human TTG-2 mRNA for a cysteine rich protein with LIM motif /cds=UNKNOWN /gb=X61118 /gi=663012 /ug=Hs.184585 /len=2292	32184_at
TPM1 (tropomyosin 1 (alpha)	M19267	Hs.77899	NM_000366	15q22.1	Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	36791_g_at
VBP1 (von Hippel-Lindau binding protein 1)	U56833	Hs.198307	NM_003372	xq28	U56833 /FEATURE= /DEFINITION=HSU56833 Human VHL binding protein-1 (VBP-1) mRNA, partial cds	171_at
TK1 (thymidine kinase 1, soluble	K02581	Hs.105097	NM_003258	17q23.2-q25.3	Cluster Incl. K02581:Human thymidine kinase mRNA, complete cds /cds=(57,761)	41400_at

					/gb=K02581 /gi=339708 /ug=Hs.105097 /len=1421	
HPRT1 (hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	M31642	Hs.82314	NM_000194	xq26.1	Cluster Incl. M31642:Human hypoxanthine phosphoribosyltransferase (HPRT) mRNA, complete cds /cds=(85,741) /gb=M31642 /gi=184349 /ug=Hs.82314 /len=1331	37640_at
TUBB (tubulin, beta polypeptide	J00314	Hs.336780	NM_001069	6p21.3	J00314 /FEATURE=mRNA#1 /DEFINITION=HUMTBBM40 Human beta-tubulin gene, clone m40	709_at
SERPINB1 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1)	M93056	Hs.183583	NM_030666	6p25	Cluster Incl. M93056:Human monocyte/neutrophil elastase inhibitor mRNA sequence /cds=UNKNOWN /gb=M93056 /gi=188621 /ug=Hs.183583 /len=1298	33305_at
MAPKAPK3 (mitogen-activated protein kinase-activated protein kinase 3)	U09578	Hs.227789	NM_004635	3p21.3	U09578 /FEATURE= /DEFINITION=HSU09578 Homo sapiens MAPKAP kinase (3pK) mRNA, complete	1637_at

					cds	
KNSL2 (kinesin-like 2)	D14678	Hs.20830		6p21.3	D14678 /FEATURE= /DEFINITION=HUMMHCB Human mRNA for kinesin-related protein, partial cds	348_at
KNSL1 (kinesin-like 1)	U37426	Hs.8878	NM_004523	10q24.1	Cluster Incl. U37426:Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds /cds=(90,3260) /gb=U37426 /gi=1171152 /ug=Hs.8878 /len=4858	40726_at
MCM6 (minichromosome maintenance deficient (mis5, S. pombe) 6	D84557	Hs.155462	NM_005915	2q21	Cluster Incl. D84557:Homo sapiens mRNA for HsMcm6, complete cds /cds=(61,2526) /gb=D84557 /gi=1944481 /ug=Hs.155462 /len=2917	40117_at
KCNAB2 (potassium voltage-gated channel, shaker-related subfamily, beta member 2	AF044253	Hs.298184	NM_003636	1p36.3	Cluster Incl. AF044253:Homo sapiens potassium channel beta 2 subunit (HKvbeta2.2) mRNA, alternatively spliced, complete cds /cds=(0,1061) /gb=AF044253 /gi=2827465	31901_at

					/ug=Hs.154417 /len=1062	
KRT10 (keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris))	X14487	Hs.99936	NM_000421	17q21-q23	Cluster Incl. X14487:Human gene for acidic (type I) cytokeratin 10 /cds=(25,1806) /gb=X14487 /gi=28316 /ug=Hs.99936 /len=2166	38610_s_at
TNFRSF7 (tumor necrosis factor receptor superfamily, member 7)	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	38578_at
NCOA1 (nuclear receptor coactivator 1)	AJ000882	Hs.74002	NM_003743	2p23	Cluster Incl. AJ000882:Homo sapiens mRNA for steroid receptor coactivator 1e /cds=(201,4400) /gb=AJ000882 /gi=2924310 /ug=Hs.74002 /len=4709	36118_at
SNRPN (small nuclear ribonucleoprotein polypeptide N)	U41303	Hs.48375	NM_022807	15q12	Cluster Incl. U41303:Human small nuclear ribonuleoprotein particle N (SNRPN) mRNA, complete cds /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375	34842_at

					/len=1326	
NCOA1 (nuclear receptor coactivator 1)	U59302	Hs.74002	NM_003743	2p23	U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	484_at
CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at
SSH3BP1 (spectrin SH3 domain binding protein 1)	AF001628	Hs.24752	NM_005470	10p11.2	Cluster Incl. AF001628:Homo sapiens interactor protein AblBP4 (AblBP4) mRNA, complete cds /cds=(48,1403) /gb=AF001628 /gi=4100618 /ug=Hs.204036 /len=2175	38924_s_at
PKD2 (polycystic kidney disease 2 (autosomal dominant))	AL050147	Hs.91146	NM_016457	19q13.2	Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630)	38269_at

					/gb=AL050147 /gi=4884153 /ug=Hs.91146 /len=1837	
MAPK3 (mitogen-activated protein kinase 3)	X60188	Hs.861		16p12-p11.2	X60188 /FEATURE=mRNA /DEFINITION=HSERK1 Human ERK1 mRNA for protein serine/threonine kinase	1000_at
HLA-DMA (major histocompatibility complex, class II, DM alpha)	X62744	Hs.77522	NM_006120	6p21.3	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079	37344_at
	AF038199				Cluster Incl. AF038199:Homo sapiens clone 23728 mRNA sequence /cds=UNKNOWN /gb=AF038199 /gi=2795920 /ug=Hs.153106 /len=1112	38154_at
FCGR2B (Fc fragment of IgG, low affinity IIb, receptor for (CD32))	M28696	Hs.278443	NM_004001	1q23	Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-RII) mRNA, complete cds /cds=(41,916) /gb=M28696 /gi=184843 /ug=Hs.233450	34663_at

					/len=1416	
LYN (v-yes-1 Yamaguchi sarcoma viral related oncogene homolog)	M16038	Hs.80887	NM_002350	8q13	Cluster Incl. M16038:Human lyn mRNA encoding a tyrosine kinase /cds=(297,1835) /gb=M16038 /gi=187268 /ug=Hs.80887 /len=2298	32616_at
CELSR1 (cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog)	AL031588	Hs.252387	NM_014246	22q13.3	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	41660_at
LRMP (lymphoid-restricted membrane protein)	U10485	Hs.40202	NM_006152	12p12	Cluster Incl. U10485:Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds /cds=(574,2241) /gb=U10485 /gi=505685 /ug=Hs.40202 /len=2417	35974_at

NAF1(Nef-associated factor 1)	AJ011896	Hs.109281	NM_006058	5	Cluster Incl. AJ011896:Homo sapiens mRNA for HIV-1, Nef-associated factor 1 beta (Naf1 beta) /cds=(110,2017) /gb=AJ011896 /gi=3758820 /ug=Hs.109281 /len=2710	38970_s_at
KIAA1002(KIAA1002 protein)	AB023219	Hs.20340			Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete cds /cds=(800,3322) /gb=AB023219 /gi=4589647 /ug=Hs.102483 /len=4331	41366_at
DKFZP434C171(DKFZP434C171 protein)	AL080169	Hs.209100	NM_015621	5	Cluster Incl. AL080169:Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171) /cds=(0,544) /gb=AL080169 /gi=5262637 /ug=Hs.209100 /len=2595	34183_at
SEP2(septin 6)	D50918	Hs.90998	NM_015129	X	Cluster Incl. D50918:Human mRNA for KIAA0128 gene, partial cds /cds=(0,1276) /gb=D50918 /gi=1469178 /ug=Hs.90998 /len=4612	38826_at

PFTK1 (PFTAIRE protein kinase 1)	AB020641	Hs.57856	NM_012395	7q21-q22	Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641 /gi=4240156 /ug=Hs.57856 /len=4957	36502_at
DCTD (dCMP deaminase)	L39874	Hs.76894	NM_001921	4	L39874 /FEATURE=expanded_cds /DEFINITION=HUMDODDA Homo sapiens deoxycytidylate deaminase gene, complete cds	631_g_at
SQV7L(nucleotide-sugar transporter similar to C. elegans sqv-7)	AJ005866	Hs.90078		9	Cluster Incl. AJ005866:Homo sapiens mRNA for putative Sqv-7-like protein, partial /cds=(0,785) /gb=AJ005866 /gi=4008516 /ug=Hs.90078 /len=1321	38005_at
SH3GLB1 (SH3-domain, GRB2-like, endophilin B1)	AB007960	Hs.136309	NM_016009	1p22	Cluster Incl. AB007960:chromosome 1 specific transcript KIAA0491 /cds=UNKNOWN /gb=AB007960 /gi=3413934 /ug=Hs.136309 /len=5717	39691_at

PPP1CC (protein phosphatase 1, catalytic subunit, gamma isoform)	X74008	Hs.79081	NM_002710	12q24.1-q24.2	Homo sapiens /REF=X74008 /DEF=Cluster Incl. :H.sapiens mRNA for protein phosphatase 1 gamma /cds=(154,1125) /gb= /gi=402777 /ug=Hs.79081 /len=2263 /LEN=2431	37725_at
CD37 (CD37 antigen)	X14046	Hs.153053	NM_001774	19p13-q13.4	Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908) /gb=X14046 /gi=29793 /ug=Hs.153053 /len=1125	31870_at
HLA-DMB (major histocompatibility complex, class II, DM beta)	U15085	Hs.1162	NM_002118	6p21.3	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	41609_at
LAMA5 (laminin, alpha 5)	AB011105	Hs.11669	NM_005560	20q13.2-q13.3	Cluster Incl. AB011105:Homo sapiens mRNA for KIAA0533 protein, partial cds /cds=(0,4939) /gb=AB011105 /gi=3043589 /ug=Hs.11669 /len=5117	41610_at

EIF4B (eukaryotic translation initiation factor 4B)	X55733	Hs.93379	NM_001417	12q13.11-12q14.3	Cluster Incl. X55733:H.sapiens initiation factor 4B cDNA /cds=(0,1835) /gb=X55733 /gi=288099 /ug=Hs.93379 /len=1836	39110_at
PRKCB1 (protein kinase C, beta 1)	X07109	Hs.77202	NM_002738	16p11.2	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II /NOTE=replacement of probe set 1216_at	160029_at
HBOA(histone acetyltransferase)	AI951946	Hs.21907	NM_007067	X	Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523	41338_at
CDC10 (CDC10 (cell division cycle 10, S. cerevisiae, homolog))	S72008	Hs.184326	NM_001788	7p14.3-p14.1	Cluster Incl. S72008:hCDC10=CDC10 homolog [human, fetal lung, mRNA, 2314 nt] /cds=(48,1304) /gb=S72008 /gi=560622 /ug=Hs.184326 /len=2314	32175_at
KIAA0226(KIAA0226 gene product)	D86979	Hs.141296		3	Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(622,2877) /gb=D86979 /gi=1504031	31802_at

					/ug=Hs.141296 /len=5891	
BLK (B lymphoid tyrosine kinase)	S76617	Hs.2243	NM_001715	8p23-p22	S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]	854_at
HLA-DQB1 (major histocompatibility complex, class II, DQ beta 1)	M81141	Hs.73931	NM_002123	6p21.3	Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171	36773_f_at
DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796	7	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
PIM2 (pim-2 oncogene)	U77735	Hs.80205	NM_006875	X	U77735 /FEATURE= /DEFINITION=HSU77735 Human pim-2 protooncogene homolog pim-2h mRNA, complete cds	1633_g_at

FCER2 (Fc fragment of IgE, low affinity II, receptor for (CD23A))	M15059	Hs.1416	NM_002002	19p13.3	Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds (H107 epitope) /cds=(213,1178) /gb=M15059 /gi=182447 /ug=Hs.1416 /len=1530	34960_g_at
UBE2G2 (ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7))	AF032456	Hs.192853	NM_003343	21q22.3	Cluster Incl. AF032456:Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds /cds=(55,552) /gb=AF032456 /gi=3004908 /ug=Hs.192853 /len=2890	32236_at
SH3BP5 (SH3-domain binding protein 5 (BTK-associated))	AB005047	Hs.109150	NM_004844	1q43	Cluster Incl. AB005047:Homo sapiens mRNA for SH3 binding protein, complete cds /cds=(63,1340) /gb=AB005047 /gi=3116213 /ug=Hs.109150 /len=2570	38968_at
TRIP3 (thyroid hormone receptor interactor 3)	L40410	Hs.2210		17	Cluster Incl. L40410:Homo sapiens thyroid receptor interactor (TRIP3) mRNA, 3 end of cds /cds=(0,458) /gb=L40410 /gi=703109 /ug=Hs.2210 /len=867	41251_at

DKFZP586F2423(hypothetical protein DKFZp586F2423)	AL080209	Hs.13659		7	Cluster Incl. AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4241	39692_at
KIAA0911(calsyntenin 1)	AB020718	Hs.29665	NM_014944	1	Cluster Incl. AB020718:Homo sapiens mRNA for KIAA0911 protein, complete cds /cds=(793,3738) /gb=AB020718 /gi=4240310 /ug=Hs.29665 /len=5219	41498_at
UBE2N (ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13))	D83004	Hs.75355	NM_003348	12	Cluster Incl. D83004:Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds /cds=(63,521) /gb=D83004 /gi=1181557 /ug=Hs.75355 /len=1203	36604_at
KIAA0542(KIAA0542 gene product)	AB011114	Hs.62209		22	Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, complete cds /cds=(393,3299) /gb=AB011114	36545_s_at

					/gi=3043607 /ug=Hs.62209 /len=5280	
					Transcription Factor Oct-1a/1b, Alt. Splice 2, Oct-1b	1171_s_at
SWAP2(suppressor of white apricot homolog 2)	AF042800	Hs.43543	NM_007056	19	Cluster Incl. AF042800:Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds /cds=(143,2122) /gb=AF042800 /gi=3941325 /ug=Hs.43543 /len=2233	36005_at
MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))	AB023208	Hs.181002	NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41165_g_at

					Cluster Incl. AI700633:we38g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2343412 /clone_end=3 /gb=AI700633 /gi=4988533 /ug=Hs.4815 /len=565	34840_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
ITGB7 (integrin, beta 7)	M68892	Hs.1741	NM_000889	12q13.13	M68892 /FEATURE= /DEFINITION=HUMINTB7 Human integrin beta-7 subunit mRNA, complete cds	2019_s_at
CD19 (CD19 antigen)	M28170	Hs.96023	NM_001770	16p11.2	M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	1096_g_at
PRKRIR (protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor))	AL049970	Hs.177574	NM_004705	11q13.5	Cluster Incl. AL049970:Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102) /cds=(0,965)	41141_at

repressor of (P58 repressor))					/gb=AL049970 /gi=4884219 /ug=Hs.177574 /len=2724	
NIFU(nitrogen fixation cluster-like)	U47101	Hs.9908		12	Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819	39165_at
UBE2D2 (ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5))	AI310002	Hs.108332	NM_003339	5p14.2-q23.3	Cluster Incl. AI310002:qo77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1914548 /clone_end=3 /gb=AI310002 /gi=4004873 /ug=Hs.108332 /len=656	38705_at
	AB018272				Cluster Incl. AB018272:Homo sapiens mRNA for KIAA0729 protein, partial cds /cds=(0,3591) /gb=AB018272 /gi=3882178 /ug=Hs.180948 /len=4143	41218_at
PSCD1 (pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1))	M85169	Hs.1050	NM_004762	17q25	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001	38666_at

					/ug=Hs.1050 /len=3301	
LYN (v-yes-1 Yamaguchi sarcoma viral related oncogene homolog)	M16038	Hs.80887	NM_002350	8q13	M16038 /FEATURE= /DEFINITION=HUMLYN Human lyn mRNA encoding a tyrosine kinase	1402_at
HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)	X00457	Hs.914		6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	38833_at
IGHM (immunoglobulin heavy constant mu)	X58529	Hs.302063		14q32.33	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325	41166_at
BCL11A (B-cell CLL/lymphoma 11A (zinc finger protein))	W27619	Hs.130881	NM_022893	2p24.3-p24.1	Cluster Incl. W27619:35c7 Homo sapiens cDNA /gb=W27619 /gi=1307567 /ug=Hs.25816 /len=674	41356_at

KIAA0663(KIAA0663 gene product)	AB014563	Hs.17969	NM_014827	1	Cluster Incl. AB014563:Homo sapiens mRNA for KIAA0663 protein, complete cds /cds=(213,2645) /gb=AB014563 /gi=3327139 /ug=Hs.17969 /len=4365	41170_at
TAB2(TAK1-binding protein 2)	AB018276	Hs.109727	NM_015093	6	Cluster Incl. AB018276:Homo sapiens mRNA for KIAA0733 protein, partial cds /cds=(0,1586) /gb=AB018276 /gi=3882186 /ug=Hs.109727 /len=3479	38980_at
SETBP1 (SET binding protein 1)	AB022660	Hs.151717	NM_015559	18q21.1	Cluster Incl. AB022660:Homo sapiens mRNA for SET-binding protein (SEB), complete cds /cds=(5,4633) /gb=AB022660 /gi=5478317 /ug=Hs.151717 /len=5744	34990_at
JAK1 (Janus kinase 1 (a protein tyrosine kinase))	AL039831	Hs.50651	NM_002227	1p32.3-p31.3	Cluster Incl. AL039831:DKFZp434D1112_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5866713 /ug=Hs.50651	34877_at

					/len=579	
ADPRTL3 (ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 3)	AL050034	Hs.271742	NM_005485	3p22.2-p21.1	Cluster Incl. AL050034:Homo sapiens mRNA; cDNA DKFZp566G0224 (from clone DKFZp566G0224) /cds=(0,1380) /gb=AL050034 /gi=4884274 /ug=Hs.33573 /len=1762	39670_at
IGBP1 (immunoglobulin (CD79A) binding protein 1)	Y08915	Hs.3631	NM_001551	xq13.1-q13.3	Cluster Incl. Y08915:H.sapiens mRNA for alpha 4 protein /cds=(8,1027) /gb=Y08915 /gi=1877201 /ug=Hs.3631 /len=1321	34391_at
S100A1 (S100 calcium-binding protein A1)	X58079	Hs.292707	NM_006271	1q21	Cluster Incl. X58079:Human mRNA for S100 alpha protein /cds=(113,397) /gb=X58079 /gi=36175 /ug=Hs.234348 /len=594	34674_at
HLA-DRB1 (major histocompatibility complex, class II, DR beta 1)	M32578	Hs.180255	NM_002124	6p21.3	Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305	41723_s_at

					/ug=Hs.181366 /len=1216	
SP140(nuclear body protein Sp140)	U36500	Hs.309943	NM_007237	2	Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173653 /ug=Hs.85283 /len=3252	40700_at
NCOA3 (nuclear receptor coactivator 3)	AF012108	Hs.225977	NM_006534	20q12	Cluster Incl. AF012108:Homo sapiens Amplified in Breast Cancer (AIB1) mRNA, complete cds /cds=(200,4462) /gb=AF012108 /gi=2331249 /ug=Hs.225977 /len=6818	33381_at
TRIAD3(TRIAD3 protein)	AA650210	Hs.86228	NM_019011	7	Cluster Incl. AA650210:ns88b12.s1 Homo sapiens cDNA /clone=IMAGE-1190687 /gb=AA650210 /gi=2577538 /ug=Hs.116406 /len=528	37476_at
ZNF9 (zinc finger protein 9 (a cellular retroviral nucleic acid binding protein))	U19765	Hs.2110	NM_003418	3q13.3-q24	Cluster Incl. U19765:Human nucleic acid binding protein gene, complete cds /cds=(14,547) /gb=U19765 /gi=790570	32841_at

					/ug=Hs.2110 /len=1665	
APOC4 (apolipoprotein C-IV)	U32576	Hs.110675	NM_001646	19q13.2	Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, complete cds /cds=(40,423) /gb=U32576 /gi=975892 /ug=Hs.110675 /len=613	34454_r_at
CBX7 (chromobox homolog 7)	AL031846			22q13.1	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
	W30677				Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614	34871_at
IL2RB (interleukin 2 receptor, beta)	AL022314	Hs.75596	NM_000878	22q13.1	Cluster Incl. AL022314:dJ1170K4.1 (novel protein similar to KIAA0176 and mouse, worm and fly proteins) /cds=(185,1057) /gb=AL022314 /gi=4090209 /ug=Hs.94810	41036_at

					/len=1854	
RERE (arginine-glutamic acid dipeptide (RE) repeats)	AB007927	Hs.194369	NM_012102	1p36.1-p36.2	Cluster Incl. AB007927:Homo sapiens mRNA for KIAA0458 protein, complete cds /cds=(155,3961) /gb=AB007927 /gi=3413877 /ug=Hs.194369 /len=6642	32253_at
CD79A (CD79A antigen (immunoglobulin-associated alpha))	U05259	Hs.79630	NM_001783	19q13.2	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107	38017_at
PLCG1 (phospholipase C, gamma 1 (formerly subtype 148))	AL022394	Hs.268177	NM_002660	20q12-q13.1	Cluster Incl. AL022394:dJ511B24.2 (1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 /cds=(68,3940) /gb=AL022394 /gi=3288442 /ug=Hs.317 /len=5151	34351_at
TRIP7 (thyroid hormone receptor interactor 7)	AA845349	Hs.77558		6	Cluster Incl. AA845349:ak01g01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-	37348_s_at

					1404720 /clone_end=3 /gb=AA845349 /gi=2933108 /ug=Hs.77558 /len=965	
YWHAQ (tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide)	X56468	Hs.74405	NM_006826	22q12-qter	Cluster Incl. X56468:Human mRNA for 14.3.3 protein, a protein kinase regulator /cds=(125,862) /gb=X56468 /gi=23221 /ug=Hs.74405 /len=1862	32530_at
CGR19(cell growth regulatory with ring finger domain)	U66469	Hs.59106	NM_006568	14	U66469 /FEATURE= /DEFINITION=HSU66469 Human cell growth regulator CGR19 mRNA, complete cds	450_g_at
EZH1 (enhancer of zeste (Drosophila) homolog 1)	AB002386	Hs.194669	NM_001991	17q21.1-q21.3	Cluster Incl. AB002386:Human mRNA for KIAA0388 gene, complete cds /cds=(100,2343) /gb=AB002386 /gi=2224716 /ug=Hs.194669 /len=4606	32259_at
KIAA0746(KIAA0746 protein)	AB018289	Hs.49500		4	Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein, partial cds /cds=(0,3091) /gb=AB018289 /gi=3882212	41585_at

					/ug=Hs.49500 /len=4086	
PRKCB1 (protein kinase C, beta 1)	X07109	Hs.77202	NM_002738	16p11.2	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II	1217_g_at
TC21(oncogene TC21)	AI365215	Hs.206097	NM_012250	11	Cluster Incl. AI365215:qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2029426 /clone_end=3 /gb=AI365215 /gi=4124904 /ug=Hs.206097 /len=918	32827_at
RRN3(RNA polymerase I transcription factor RRN3)	AF001549	Hs.110103	NM_018427	16	Cluster Incl. AF001549:Human Chromosome 16 BAC clone CIT987SK-A-270G1 /cds=(167,487) /gb=AF001549 /gi=3355302 /ug=Hs.110103 /len=848	39620_at
XAP4(HBV associated factor)	AA160708	Hs.247280	NM_031229	20	Cluster Incl. AA160708:zo72c02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-592418 /clone_end=5 /gb=AA160708 /gi=1736075 /ug=Hs.18563 /len=643	32203_at

EEF2 (eukaryotic translation elongation factor 2)	Z11692	Hs.75309	NM_001961	19pter-q12	Cluster Incl. Z11692:H.sapiens mRNA for elongation factor 2 /cds=(0,2576) /gb=Z11692 /gi=31107 /ug=Hs.75309 /len=3080	36587_at
	U79277				Cluster Incl. U79277:Human clone 23548 mRNA sequence /cds=UNKNOWN /gb=U79277 /gi=1710245 /ug=Hs.71848 /len=1545	36760_at
KIAA0640(SWAP-70 protein)	AB014540	Hs.153026		11	Cluster Incl. AB014540:Homo sapiens mRNA for KIAA0640 protein, partial cds /cds=(0,1812) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824	31869_at
BLNK (B-cell linker)	AF068180	Hs.167746	NM_013314	10q23.2-q23.33	Cluster Incl. AF068180:Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds /cds=(153,1523) /gb=AF068180 /gi=3406748 /ug=Hs.167746 /len=1790	38242_at

HNRPC (heterogeneous nuclear ribonucleoprotein C (C1/C2))	M16342	Hs.182447	NM_031314	2q32	Cluster Incl. M16342:Human nuclear ribonucleoprotein particle (hnRNP) C protein mRNA, complete cds /cds=UNKNOWN /gb=M16342 /gi=184266 /ug=Hs.182447 /len=1666	33666_at
KIAA0747(KIAA0747 protein)	AB018290	Hs.8309	NM_015292	12	Cluster Incl. AB018290:Homo sapiens mRNA for KIAA0747 protein, partial cds /cds=(0,3219) /gb=AB018290 /gi=3882214 /ug=Hs.8309 /len=4026	38424_at
M17S2 (membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125))	D30756	Hs.277721	NM_031858	17q21.1	Cluster Incl. D30756:Human mRNA for KIAA0049 gene, complete cds /cds=(140,3040) /gb=D30756 /gi=488500 /ug=Hs.233745 /len=4654	33444_at
CSK (c-src tyrosine kinase)	X59932	Hs.77793	NM_004383	15q23-q25	X59932 /FEATURE=mRNA /DEFINITION=HSCSRCKIN Human mRNA for C-SRC-kinase	1768_s_at
KIAA0239(KIAA0239 protein)	D87076	Hs.9729	NM_015288	5	Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,1716)	38342_at

					/gb=D87076 /gi=1510152 /ug=Hs.9729 /len=5630	
NFATC1 (nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1)	U08015	Hs.96149	NM_006162	18q23	Cluster Incl. U08015:Human NF-ATc mRNA, complete cds /cds=(239,2389) /gb=U08015 /gi=500631 /ug=Hs.96149 /len=2743	39143_at
TLK1 (tousled-like kinase 1)	D50927	Hs.18895	NM_012290	8p22-p12	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927 /gi=1469196 /ug=Hs.18895 /len=4454	32219_at

Table 7:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
MGC4175(hypothetical protein MGC4175)	AI656421	Hs.322404	NM_024315	7	Cluster Incl. AI656421:tt50h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2244259 /clone_end=3 /gb=AI656421 /gi=4740400 /ug=Hs.5671 /len=566	41809_at
SH3BP5 (SH3-domain binding protein 5 (BTK-associated))	AB005047	Hs.109150	NM_004844	1q43	Cluster Incl. AB005047:Homo sapiens mRNA for SH3 binding protein, complete cds /cds=(63,1340) /gb=AB005047 /gi=3116213 /ug=Hs.109150 /len=2570	38968_at
MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))	AB023208	Hs.181002	NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at

LEF1 (lymphoid enhancer-binding factor 1)	AL049409	Hs.44865	NM_016269	4q23-q25	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	36021_at
PRDM2 (PR domain containing 2, with ZNF domain)	D45132	Hs.26719	NM_012231	1p36	D45132 /FEATURE= /DEFINITION=HUMHOXY1 Homo sapiens mRNA for zinc-finger DNA-binding protein, complete cds	316_g_at
ARHH (ras homolog gene family, member H)	Z35227	Hs.109918	NM_004310	4p13	Cluster Incl. Z35227:H.sapiens TTF mRNA for small G protein /cds=(579,1154) /gb=Z35227 /gi=609016 /ug=Hs.109918 /len=1427	37416_at
SSH3BP1 (spectrin SH3 domain binding protein 1)	AF006516	Hs.24752	NM_005470	10p11.2	Cluster Incl. AF006516:Homo sapiens eps8 binding protein e3B1 mRNA, complete cds /cds=(66,1508) /gb=AF006516 /gi=2245670 /ug=Hs.24752 /len=3189	33886_at

ABLIM (actin binding LIM protein)	D31883	Hs.158203	NM_002313	10q25	Cluster Incl. D31883:Human mRNA for KIAA0059 gene, complete cds /cds=(221,1609) /gb=D31883 /gi=505093 /ug=Hs.158203 /len=6754	40155_at
SNRPA1 (small nuclear ribonucleoprotein polypeptide A')	X13482	Hs.80506	NM_003090	22q	Cluster Incl. X13482:Human mRNA for U2 snRNP-specific A protein /cds=(56,823) /gb=X13482 /gi=37546 /ug=Hs.80506 /len=1033	37585_at
UBE2D2 (ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5))	AI310002	Hs.108332	NM_003339	5p14.2-q23.3	Cluster Incl. AI310002:qo77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1914548 /clone_end=3 /gb=AI310002 /gi=4004873 /ug=Hs.108332 /len=656	38705_at
TERF1 (telomeric repeat binding factor (NIMA-interacting) 1)	U40705	Hs.194562	NM_017489	8q13	Cluster Incl. U40705:Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds /cds=UNKNOWN /gb=U40705 /gi=2078442 /ug=Hs.194562 /len=2686	32255_i_at

PPP3CC (protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma))	S46622	Hs.75206	NM_005605	8	Cluster Incl. S46622:calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] /cds=(286,1794) /gb=S46622 /gi=258000 /ug=Hs.75206 /len=2134	32541_at
FIP2(tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein)	AF061034	Hs.278898	NM_021980	10	Cluster Incl. AF061034:Homo sapiens FIP2 alternatively translated mRNA, complete cds /cds=UNKNOWN /gb=AF061034 /gi=3127082 /ug=Hs.182236 /len=2116	41743_i_at
EP300 (E1A binding protein p300)	U01877	Hs.25272	NM_001429	22q13.2	Cluster Incl. U01877:Human p300 protein mRNA, complete cds /cds=(1199,8443) /gb=U01877 /gi=495300 /ug=Hs.25272 /len=9046	33896_at
PSCD1 (pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1))	M85169	Hs.1050	NM_004762	17q25	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	38666_at

SYNE-2(synaptic nuclei expressed gene 2)	AL080133	Hs.57749	NM_015180	14	Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	41815_at
BCL7A (B-cell CLL/lymphoma 7A)	X89984	Hs.211563	NM_020993	12q24.13	Cluster Incl. X89984:H.sapiens mRNA for BCL7A protein /cds=(953,1648) /gb=X89984 /gi=929614 /ug=Hs.211563 /len=4522	32842_at
RCN2 (reticulocalbin 2, EF-hand calcium binding domain)	X78669	Hs.79088	NM_002902	15q23	Cluster Incl. X78669:H.sapiens ERC-55 mRNA /cds=(66,1019) /gb=X78669 /gi=469884 /ug=Hs.79088 /len=1700	37727_i_at
CD79A (CD79A antigen (immunoglobulin-associated alpha))	U05259	Hs.79630	NM_001783	19q13.2	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107	38017_at
UBE2N (ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13))	D83004	Hs.75355	NM_003348	12	Cluster Incl. D83004:Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds /cds=(63,521)	36604_at

					gene product, complete cds /cds=(63,521) /gb=D83004 /gi=1181557 /ug=Hs.75355 /len=1203	
DNTT (deoxynucleotidyltransferase, terminal)	M11722	Hs.272537	NM_004088	10q23-q24	Cluster Incl. M11722:Human terminal transferase mRNA, complete cds /cds=(328,1854) /gb=M11722 /gi=339436 /ug=Hs.234772 /len=2068	34168_at
WEE1 (wee1+ (S. pombe) homolog)	W28575	Hs.75188	NM_003390	11p15.3-p15.1	Cluster Incl. W28575:51f12 Homo sapiens cDNA /gb=W28575 /gi=1308730 /ug=Hs.8151 /len=906	38102_at
HSF2 (heat shock transcription factor 2)	Z99129	Hs.158195	NM_004506	6pter-p25.1	Cluster Incl. Z99129:Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs a	33443_at

ARFD1 (ADP-ribosylation factor domain protein 1, 64kD)	L04510	Hs.792	NM_001656	5	Cluster Incl. L04510:Human nucleotide binding protein mRNA, complete cds /cds=(22,1746) /gb=L04510 /gi=292069 /ug=Hs.792 /len=3334	37537_at
CTGF (connective tissue growth factor)	X78947	Hs.75511	NM_001901	6q23.1	Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312	36638_at
MALT1 (mucosa associated lymphoid tissue lymphoma translocation gene 1)	AB026118	Hs.180566	NM_006785	18q21	Cluster Incl. AB026118:Homo sapiens mRNA for MALT1, complete cds /cds=(65,2506) /gb=AB026118 /gi=5706377 /ug=Hs.188735 /len=2819	32350_at
SSH3BP1 (spectrin SH3 domain binding protein 1)	AF001628	Hs.24752	NM_005470	10p11.2	Cluster Incl. AF001628:Homo sapiens interactor protein AblBP4 (AblBP4) mRNA, complete cds /cds=(48,1403) /gb=AF001628 /gi=4100618 /ug=Hs.204036 /len=2175	38924_s_at

NR3C1 (nuclear receptor subfamily 3, group C, member 1)	M10901	Hs.75772	NM_000176	5q31	Cluster Incl. M10901:Human glucocorticoid receptor alpha mRNA, complete cds /cds=(132,2465) /gb=M10901 /gi=183032 /ug=Hs.75772 /len=4788	36690_at
TUBA1 (tubulin, alpha 1 (testis specific))	X06956	Hs.75318		2q	Cluster Incl. X06956:Human HALPHA44 gene for alpha-tubulin, exons 1-3 /cds=(0,1343) /gb=X06956 /gi=32014 /ug=Hs.75318 /len=1344	36591_at
KIAA0082(KIAA0082 protein)	D43949	Hs.154045		6	Cluster Incl. D43949:Human mRNA for KIAA0082 gene, partial cds /cds=(0,1824) /gb=D43949 /gi=603952 /ug=Hs.154045 /len=3186	40054_at
PRDM2 (PR domain containing 2, with ZNF domain)	D45132	Hs.26719	NM_012231	1p36	D45132 /FEATURE= /DEFINITION=HUMHOXY1 Homo sapiens mRNA for zinc-finger DNA-binding protein, complete cds	315_at

BARD1 (BRCA1 associated RING domain 1)	U76638	Hs.54089	NM_000465	2q34-q35	U76638 /FEATURE= /DEFINITION=HSU76638 Human BRCA1-associated RING domain protein (BARD1) mRNA, complete cds	1801_at
LYSAL1 (lysosomal apyrase-like 1)	AB002390	Hs.201377	NM_004901	8	Cluster Incl. AB002390:Human mRNA for KIAA0392 gene, partial cds /cds=(0,1652) /gb=AB002390 /gi=2280487 /ug=Hs.201377 /len=5422	33788_at
ARPP-19(cyclic AMP phosphoprotein, 19kD)	AL120559	Hs.7351	NM_006628	15	Cluster Incl. AL120559:DKFZp761B219_r1 Homo sapiens cDNA, 5 end /clone=DKFZp761B219 /clone_end=5 /gb=AL120559 /gi=5926458 /ug=Hs.7351 /len=588	36872_at
MADH7 (MAD (mothers against decapentaplegic, Drosophila) homolog 7)	AF010193	Hs.100602	NM_005904	18	AF010193 /FEATURE= /DEFINITION=AF010193 Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds	1857_at

FLJ20500(hypothetical protein)	AA522530	Hs.111244	NM_019058	10	Cluster Incl. AA522530:ni38d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-979127 /clone_end=3 /gb=AA522530 /gi=2263242 /ug=Hs.111244 /len=891	39827_at
					Glucocorticoid Receptor, Beta	706_at
	AF035315				Cluster Incl. AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence /cds=UNKNOWN /gb=AF035315 /gi=2661077 /ug=Hs.180737 /len=1331	33267_at
SYNE-1B(synaptic nuclear envelope 1)	AB018339	Hs.8182		6	Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
CTNNAL1 (catenin (cadherin-associated protein), alpha-like 1)	U97067	Hs.58488	NM_003798	9q31.2	Cluster Incl. U97067:Homo sapiens alpha-catenin-like protein mRNA, complete cds /cds=(43,2247) /gb=U97067 /gi=3342777 /ug=Hs.58488 /len=2446	35331_at

UBL3 (ubiquitin-like 3)	AL080177	Hs.173091	NM_007106	13q12-q13	Cluster Incl. AL080177:Homo sapiens mRNA; cDNA DKFZp434K151 (from clone DKFZp434K151) /cds=(109,462) /gb=AL080177 /gi=5262650 /ug=Hs.173091 /len=3313	40839_at
MICB (MHC class I polypeptide-related sequence B)	U65416	Hs.211580	NM_005931	6p21.3	Cluster Incl. U65416:Human MHC class I molecule (MICB) gene, complete cds /cds=(5,1156) /gb=U65416 /gi=1815636 /ug=Hs.211580 /len=2367	35937_at
DYRK3 (dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3)	Y12735	Hs.38018	NM_003582	1q32.	Cluster Incl. Y12735:Homo sapiens mRNA for protein kinase, Dyrk3 /cds=(252,1913) /gb=Y12735 /gi=2765228 /ug=Hs.38018 /len=2141	39931_at
KIAA0256(KIAA0256 gene product)	D87445	Hs.118978		15	Cluster Incl. D87445:Human mRNA for KIAA0256 gene, complete cds /cds=(1424,3331) /gb=D87445 /gi=1665778 /ug=Hs.118978 /len=6935	41634_at

PPM1B (protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform)	AJ005801	Hs.5687	NM_002706	2p21	Cluster Incl. AJ005801:Homo sapiens mRNA for protein phosphatase 2C (beta) /cds=(0,1439) /gb=AJ005801 /gi=3378167 /ug=Hs.169652 /len=1440	32665_at
FOXO1A (forkhead box O1A (rhabdomyosarcoma))	AF032885	Hs.170133	NM_002015	13q14.1	Cluster Incl. AF032885:Homo sapiens forkhead protein (FKHR) mRNA, complete cds /cds=(385,2352) /gb=AF032885 /gi=2895491 /ug=Hs.170133 /len=5723	40570_at
DUSP11 (dual specificity phosphatase 11 (RNA/RNP complex 1-interacting))	AF023917	Hs.14611	NM_003584	2	Cluster Incl. AF023917:Homo sapiens protein tyrosine phosphatase PIR1 mRNA, complete cds /cds=(124,1116) /gb=AF023917 /gi=3387789 /ug=Hs.14611 /len=1574	39727_at
FBXO21 (F-box only protein 21)	AB020682	Hs.184227		12	Cluster Incl. AB020682:Homo sapiens mRNA for KIAA0875 protein, partial cds /cds=(0,1866) /gb=AB020682 /gi=4240238 /ug=Hs.184227 /len=4168	32169_at

KIAA0105(Wilms' tumour 1-associating protein)	D14661	Hs.119	NM_004906	6	Cluster Incl. D14661:Human mRNA for KIAA0105 gene, complete cds /cds=(124,579) /gb=D14661 /gi=285946 /ug=Hs.119 /len=1622	41635_at
KIAA0922(KIAA0922 protein)	AB023139	Hs.37892	NM_015196	4	Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505	39929_at
KIAA0118(KIAA0118 protein)	D42087	Hs.184627	NM_014999	12	Cluster Incl. D42087:Human mRNA for KIAA0118 gene, *partial cds* /cds=(0,485) /gb=D42087 /gi=576555 /ug=Hs.184627 /len=1413	33326_at
HNRPH2 (heterogeneous nuclear ribonucleoprotein H2 (H'))	U01923	Hs.278857	NM_019597	xq22	Cluster Incl. U01923:Human BTK region clone ftp-3 mRNA /cds=UNKNOWN /gb=U01923 /gi=460085 /ug=Hs.177025 /len=2220	41131_f_at
SCML2 (sex comb on midleg (Drosophila)-like 2)	Y18004	Hs.171558	NM_006089	xp22	Cluster Incl. Y18004:Homo sapiens mRNA for SCML2 protein /cds=(91,2193)	38518_at

2)						/gb=Y18004 /gi=4490941 /ug=Hs.171558 /len=4130	
MTMR6 (myotubularin related protein 6)	AF072928	Hs.79877		13q12		Cluster Incl. AF072928:Homo sapiens myotubularin related protein 6 mRNA, partial cds /cds=(0,1398) /gb=AF072928 /gi=3916215 /ug=Hs.79877 /len=3358	38035_at
RASGRP1 (RAS guanyl releasing protein 1 (calcium and DAG-regulated))	AF081195	Hs.182591	NM_005739	15q15		Cluster Incl. AF081195:Homo sapiens calcium and DAG-regulated guanine nucleotide exchange factor II mRNA, complete cds /cds=(103,2496) /gb=AF081195 /gi=3928854 /ug=Hs.182591 /len=5075	33291_at
IFITM1 (interferon induced transmembrane protein 1 (9-27))	J04164	Hs.146360	NM_003641	11		J04164 /FEATURE= /DEFINITION=HUM927A Human interferon-inducible protein 9-27 mRNA, complete cds	675_at
MAP-1(modulator of apoptosis 1)	AI670788	Hs.24719	NM_022151	14		Cluster Incl. AI670788:tz10c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-	34767_at

					2288162 /clone_end=3 /gb=AI670788 /gi=4850519 /ug=Hs.24719 /len=762	
SP3 (Sp3 transcription factor)	X68560	Hs.44450		2q31	Cluster Incl. X68560:H.sapiens SPR-2 mRNA for GT box binding protein /cds=(0,2094) /gb=X68560 /gi=38417 /ug=Hs.44450 /len=3504	41573_at
KLF7 (Kruppel-like factor 7 (ubiquitous))	AA478904	Hs.21599	NM_003709	2q32	Cluster Incl. AA478904:zv20c05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-754184 /clone_end=5 /gb=AA478904 /gi=2207538 /ug=Hs.21599 /len=577	34216_at
PIK3CA (phosphoinositide-3-kinase, catalytic, alpha polypeptide)	Z29090	Hs.85701	NM_006218	3q26.3	Cluster Incl. Z29090:H.sapiens mRNA for phosphatidylinositol 3-kinase /cds=(12,3218) /gb=Z29090 /gi=472990 /ug=Hs.85701 /len=3424	40704_at
ZNF161 (zinc finger protein 161)	D28118	Hs.6557	NM_007146	3q26.2	Cluster Incl. D28118:Human mRNA for DB1, complete cds /cds=(41,1591) /gb=D28118 /gi=529640 /ug=Hs.167558	32628_at

					/len=2306	
FIP2(tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein)	AF061034	Hs.278898	NM_021980	10	Cluster Incl. AF061034:Homo sapiens FIP2 alternatively translated mRNA, complete cds /cds=UNKNOWN /gb=AF061034 /gi=3127082 /ug=Hs.182236 /len=2116	41742_s_at
CDKN1B (cyclin-dependent kinase inhibitor 1B (p27, Kip1))	AI304854	Hs.238990	NM_004064	12p13.1-p12	Cluster Incl. AI304854:qo19f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1908989 /clone_end=3 /gb=AI304854 /gi=3988543 /ug=Hs.238990 /len=625	33847_s_at
SMC4L1 (SMC4 (structural maintenance of chromosomes 4, yeast)-like 1)	AB019987	Hs.50758	NM_005496	3q26.1	Cluster Incl. AB019987:Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds /cds=(112,3978) /gb=AB019987 /gi=4092845 /ug=Hs.50758 /len=4086	34878_at
	AL050161				Cluster Incl. AL050161:Homo sapiens mRNA; cDNA DKFZp586B0222 (from clone DKFZp586B0222) /cds=UNKNOWN	40803_at

					/gb=AL050161 /gi=4884375 /ug=Hs.172089 /len=1573	
GMFB (glia maturation factor, beta)	AB001106	Hs.151413	NM_004124	14q22.1	AB001106 /FEATURE= /DEFINITION=AB001106 Homo sapiens mRNA for glia maturation factor, complete cds	763_at
CDKN1B (cyclin-dependent kinase inhibitor 1B (p27, Kip1))	AI304854	Hs.238990	NM_004064	12p13.1-p12	Cluster Incl. AI304854:qo19f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1908989 /clone_end=3 /gb=AI304854 /gi=3988543 /ug=Hs.238990 /len=625	33848_r_at
TC21(oncogene TC21)	AI365215	Hs.206097	NM_012250	11	Cluster Incl. AI365215:qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2029426 /clone_end=3 /gb=AI365215 /gi=4124904 /ug=Hs.206097 /len=918	32827_at
KIAA1014(KIAA1014 protein)	AB023231	Hs.6834		13	Cluster Incl. AB023231:Homo sapiens mRNA for KIAA1014 protein, partial cds /cds=(0,2213) /gb=AB023231 /gi=4589677	35802_at

					/ug=Hs.6834 /len=3116	
RBM5 (RNA binding motif protein 5)	AF091263	Hs.201675	NM_005778	3p21.3	Cluster Incl. AF091263:Homo sapiens RNA binding motif protein 5 (RBM5) mRNA, complete cds /cds=(148,2595) /gb=AF091263 /gi=4140646 /ug=Hs.201675 /len=3097	32804_at
FLJ11220(hypothetical protein FLJ11220)	AL050064	Hs.3623	NM_018364	1	Cluster Incl. AL050064:Homo sapiens mRNA; cDNA DKFZp566L033 (from clone DKFZp566L033) /cds=UNKNOWN /gb=AL050064 /gi=4884294 /ug=Hs.129812 /len=2989	37828_at
SIAT9 (sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase))	AB018356	Hs.225939	NM_003896	2p24.3-p24.1	Cluster Incl. AB018356:Homo sapiens mRNA for GM3 synthase, complete cds /cds=(277,1365) /gb=AB018356 /gi=3779138 /ug=Hs.225939 /len=2359	34256_at
MTMR1 (myotubularin related protein 1)	AJ224979	Hs.23200		xq28	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200	34654_at

					/len=2582	
SPF30(splicing factor 30, survival of motor neuron-related)	AF107463	Hs.79968	NM_005871	10	Cluster Incl. AF107463:Homo sapiens splicing factor mRNA, complete cds /cds=(182,898) /gb=AF107463 /gi=3986747 /ug=Hs.79968 /len=1147	38040_at
ADNP (activity-dependent neuroprotector)	AB018327	Hs.3657	NM_015339	20q13.13-q13.2	Cluster Incl. AB018327:Homo sapiens mRNA for KIAA0784 protein, partial cds /cds=(0,3222) /gb=AB018327 /gi=3882288 /ug=Hs.3657 /len=4282	34394_at
KIAA0136(DNA segment, Chr 16, Johns Hopkins University 32, expressed)	D50926	Hs.70359		21q22.13	Cluster Incl. D50926:Human mRNA for KIAA0136 gene, partial cds /cds=(0,2854) /gb=D50926 /gi=1469194 /ug=Hs.70359 /len=4197	36845_at
SMG1(PI-3-kinase-related kinase SMG-1)	AC003007	Hs.110613	NM_014006	16	Cluster Incl. AC003007:Human Chromosome 16 BAC clone CIT987SK-A-61E3 /cds=(0,1742) /gb=AC003007 /gi=2911728 /ug=Hs.181634 /len=2410	41733_at

CCNE2 (cyclin E2)	AF091433	Hs.30464	NM_004702	8p22-q21.3	Cluster Incl. AF091433:Homo sapiens cyclin E2 mRNA, complete cds /cds=(37,1251) /gb=AF091433 /gi=3769613 /ug=Hs.30464 /len=2648	35249_at
TACC1 (transforming, acidic coiled-coil containing protein 1)	AF049910	Hs.173159	NM_006283	8p11	Cluster Incl. AF049910:Homo sapiens TACC1 (TACC1) mRNA, complete cds /cds=(320,2737) /gb=AF049910 /gi=3435156 /ug=Hs.173159 /len=7735	40841_at
RYBP (RING1 and YY1 binding protein)	AL049940	Hs.7910	NM_012234	3p21.1-cen	Cluster Incl. AL049940:Homo sapiens mRNA; cDNA DKFZp564E1922 (from clone DKFZp564E1922) /cds=UNKNOWN /gb=AL049940 /gi=4884183 /ug=Hs.7910 /len=3555	37732_at
TCF3 (transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47))	M31523	Hs.101047		19p13.3	M31523 /FEATURE= /DEFINITION=HUMTFAA Human transcription factor (E2A) mRNA, complete cds	1373_at

KLRB1 (killer cell lectin-like receptor subfamily B, member 1)	U11276	Hs.169824	NM_002258	12p13	Cluster Incl. U11276:Human hNKR-P1a protein (NKR-P1A) mRNA, complete cds /cds=(60,737) /gb=U11276 /gi=538270 /ug=Hs.169824 /len=738	35449_at
TERF1 (telomeric repeat binding factor (NIMA-interacting) 1)	U74382	Hs.194562	NM_017489	8q13	U74382 /FEATURE= /DEFINITION=HSU74382 Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete cds	1329_s_at
BRD1 (bromodomain-containing 1)	Z98885	Hs.127950	NM_014577	22q13.33	Cluster Incl. Z98885:Human DNA sequence from clone 522J7 on chromosome 22q13.3. Contains part of a 60S Ribosomal protein L5 pseudogene and a Peregrin (BR140) LIKE gene downstream of a putative CpG island. Contains ESTs, STSs and GSSs /cds=(185,3361) /gb=Z	39894_f_at
TGFBR2 (transforming growth factor, beta receptor II (70-80kD))	D50683	Hs.82028	NM_003242	3p22	D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-betaIIR alpha, complete	1815_g_at

					cds	
LPIN1 (lipin 1)	D80010	Hs.81412		2p21	Cluster Incl. D80010:Human mRNA for KIAA0188 gene, partial cds /cds=(0,2700) /gb=D80010 /gi=1136435 /ug=Hs.81412 /len=5307	38098_at
DKFZP586J0619(DKFZP586J0619 protein)	AL050110	Hs.112184			Cluster Incl. AL050110:Homo sapiens mRNA; cDNA DKFZp586J0619 (from clone DKFZp586J0619) /cds=(0,1923) /gb=AL050110 /gi=4884139 /ug=Hs.112184 /len=2224	39022_at
CASP7 (caspase 7, apoptosis-related cysteine protease)	U67319	Hs.9216	NM_001227	10q25	Cluster Incl. U67319:Human Lice2 beta cysteine protease mRNA, complete cds /cds=(228,1238) /gb=U67319 /gi=1894912 /ug=Hs.9216 /len=2602	38281_at
DCK (deoxycytidine kinase)	M60527	Hs.709	NM_000788	4q13.3-q21.1	M60527 /FEATURE=mRNA /DEFINITION=HUMDCKATPB Human deoxycytidine kinase mRNA, complete cds	886_at

KIAA0080(KIAA0080 protein)	D38522	Hs.74554		1	Cluster Incl. D38522:Human mRNA for KIAA0080 gene, partial cds /cds=(0,318) /gb=D38522 /gi=559331 /ug=Hs.74554 /len=4001	36144_at
POU2AF1 (POU domain, class 2, associating factor 1)	Z49194	Hs.2407	NM_006235	11q23.1	Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407 /len=3301	36239_at
LOC57158(hypothetical protein LOC57158)	AL035447	Hs.134594	NM_020433	20	Cluster Incl. AL035447:Human DNA sequence from clone 1183I21 on chromosome 20q12. Contains a novel gene and the first exon of a putative novel gene for a protein similar to predicted fly and worm proteins. Contains ESTs, STSs, GSSs and a putative CpG isla	36934_at
KIAA0794(KIAA0794 protein)	AB018337	Hs.127287		3	Cluster Incl. AB018337:Homo sapiens mRNA for KIAA0794 protein, partial cds /cds=(0,1472) /gb=AB018337 /gi=3882308	41691_at

						/ug=Hs.127287 /len=4656	
CD8A (CD8 antigen, alpha polypeptide (p32))	M12824	Hs.85258	NM_001768	2p12		Cluster Incl. M12824:Human T-cell differentiation antigen Leu-2/T8 mRNA, partial cds /cds=(87,794) /gb=M12824 /gi=339426 /ug=Hs.85258 /len=1975	40699_at
KIAA0275(KIAA0275 gene product)	D87465	Hs.74583	NM_014767	10		Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(316,1590) /gb=D87465 /gi=1665814 /ug=Hs.74583 /len=5316	36155_at
FLJ20259(hypothetical protein FLJ20259)	W27545	Hs.9956	NM_017730			Cluster Incl. W27545:32c4 Homo sapiens cDNA /gb=W27545 /gi=1307349 /ug=Hs.9956 /len=950	38362_at
EP300 (E1A binding protein p300)	U01877	Hs.25272	NM_001429	22q13.2		U01877 /FEATURE= /DEFINITION=HSU01877 Human p300 protein mRNA, complete cds	551_at

SEC24B (SEC24 (S. cerevisiae) related gene family, member B)	AJ131245	Hs.7239	NM_006323	4	Cluster Incl. AJ131245:Homo sapiens mRNA for Sec24 protein (Sec24B isoform) /cds=(155,3961) /gb=AJ131245 /gi=3947689 /ug=Hs.7239 /len=4742	35845_at
SCYE1 (small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating))	U10117	Hs.333513	NM_004757	4q24-q26	Cluster Incl. U10117:Human endothelial-monocyte activating polypeptide II mRNA, complete cds /cds=(49,987) /gb=U10117 /gi=498909 /ug=Hs.146401 /len=1057	39734_at
MADH3 (MAD (mothers against decapentaplegic, Drosophila) homolog 3)	U68019	Hs.211578	NM_005902	15q21-q22	U68019 /FEATURE= /DEFINITION=HSU68019 Homo sapiens mad protein homolog (hMAD-3) mRNA, complete cds	1433_g_at
OS-9(amplified in osteosarcoma)	U41635	Hs.76228	NM_006812	12	Cluster Incl. U41635:Human OS-9 precurosor mRNA, complete cds /cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736	36996_at

PLOD3 (procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3)	AF046889	Hs.153357	NM_001084	7q22	Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735	39801_at
APLP2 (amyloid beta (A4) precursor-like protein 2)	S60099	Hs.279518	NM_001642	11q24	Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.64797 /len=3727	33944_at
NME2 (non-metastatic cells 2, protein (NM23B) expressed in)	X58965	Hs.275163	NM_002512	17q21.3	X58965 /FEATURE= /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2 gene	1980_s_at
MPB1 (MYC promoter-binding protein 1)	M55914	Hs.284127	NM_005945	1pter-p35	M55914 /FEATURE= /DEFINITION=HUMCMYCQ Human c-myc binding protein (MBP-1) mRNA, complete cds	2035_s_at

CST3 (cystatin C (amyloid angiopathy and cerebral hemorrhage))	AI362017	Hs.135084	NM_000099	20p11.2	Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2014362 /clone_end=3 /gb=AI362017 /gi=4113638 /ug=Hs.135084 /len=778	39689_at
RPN2 (*ribophorin II*)	AL031659	Hs.75722	NM_002951	20q12-q13.1	Cluster Incl. AL031659:dJ343K2.2.1 (ribophorin II (isoform 1)) /cds=(284,2179) /gb=AL031659 /gi=4468296 /ug=Hs.75722 /len=2488	36676_at

Table 8:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
SGP28(specific granule protein (28 kDa); cysteine-rich secretory protein-3	X94323	Hs.54431	NM_006061	6	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	36464_at
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at
FLJ10140(hypothetical protein FLJ10140)	AL031588	Hs.250671	NM_018006	22	Cluster Incl. AL031588:dJ1163J1.3 (novel protein similar to mouse B99) /cds=(0,2140) /gb=AL031588 /gi=4007108 /ug=Hs.122552 /len=2821	39872_at

CAMP (cathelicidin antimicrobial peptide)	Z38026	Hs.51120	NM_004345	3p21.3	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	36710_at
LCN2 (lipocalin 2 (oncogene 24p3)	AI762213	Hs.204238	NM_005564	9q34	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at
UGCG (UDP-glucose ceramide glucosyltransferase	D50840	Hs.152601	NM_003358	9q31	Cluster Incl. D50840:Homo sapiens mRNA for ceramide glucosyltransferase, complete cds /cds=(290,1474) /gb=D50840 /gi=1350551 /ug=Hs.152601 /len=1637	40215_at
KLF5 (Kruppel-like factor 5 (intestinal)	D14520	Hs.84728	NM_001730	13q21.2-13q22.2	Cluster Incl. D14520:Human mRNA for GC-Box binding protein BTEB2, complete cds /cds=(558,1217) /gb=D14520 /gi=303596 /ug=Hs.84728 /len=1301	37926_at

SCYC2 (small inducible cytokine subfamily C, member 2)	D63789	Hs.174228	NM_003175	1q23-q25	Cluster Incl. D63789:Homo sapiens DNA for SCM-1beta precursor, complete cds /cds=(21,365) /gb=D63789 /gi=1754608 /ug=Hs.174228 /len=485	31495_at
DEFA4 (defensin, alpha 4, corticostatin)	AI250799	Hs.2582	NM_001925	8p23	Cluster Incl. AI250799:qi36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1858620 /clone_end=3 /gb=AI250799 /gi=3847328 /ug=Hs.2582 /len=542	34546_at
SYNE-1B(synaptic nuclear envelope 1)	AB018339	Hs.8182		6	Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
CCR2 (chemokine (C-C motif) receptor 2)	U95626	Hs.395	NM_000647	3p21	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at

CLC (Charot-Leyden crystal protein)	L01664	Hs.132004	NM_013246	11q13.3	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	36809_at
CEACAM8 (carcinoembryonic antigen-related cell adhesion molecule 8)	M33326	Hs.41	NM_001816	19q13.2	Cluster Incl. M33326:Human nonspecific cross-reacting antigen - (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	33530_at
CYP4F3 (cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase))	D12620	Hs.106242	NM_000896	19p13.2	D12620 /FEATURE= /DEFINITION=HUMCYT1 Homo sapiens mRNA for cytochrome P-450LTBV, complete cds	1305_s_at
KIAA0601(KIAA0601 protein)	W28504	Hs.174174		1	Cluster Incl. W28504:48e7 Homo sapiens cDNA /gb=W28504 /gi=1308515 /ug=Hs.154085 /len=1007	36338_at
LOC96807(hypothetical gene supported by X89214; NM_020995	X89214			16	Cluster Incl. X89214:H.sapiens mRNA for haptoglobin related protein	36984_f_at

X89214; NM_020995					/cds=(138,1295) /gb=X89214 /gi=1495457 /ug=Hs.75990 /len=1460	
CEACAM6 (carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross	M18728	Hs.73848	NM_002483	19q13.2	Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	36105_at
CDA (cytidine deaminase)	L27943	Hs.72924	NM_001785	1p36.2-p35	L27943 /FEATURE=mRNA /DEFINITION=HUMCYDE Homo sapiens cytidine deaminase (CDA) mRNA, complete cds	1117_at
ARG1 (arginase, liver)	M14502	Hs.289057	NM_000045	6q23	M14502 /FEATURE=mRNA /DEFINITION=HUMARGL Human liver arginase mRNA, complete cds	1962_at
BPI (bactericidal/permeability-increasing protein)	J04739	Hs.89535	NM_001725	20q11.23-q12	Cluster Incl. J04739:Human bactericidal permeability increasing protein (BPI) mRNA, complete cds /cds=(30,1493) /gb=J04739 /gi=179528 /ug=Hs.89535	37054_at

					/len=1813	
MMP8 (matrix metalloproteinase 8 (neutrophil collagenase)	J05556	Hs.73862	NM_002424	11q22.3	J05556 /FEATURE=mRNA /DEFINITION=HUMCLGNA Homo sapiens collagenase mRNA, complete cds	681_at
BN51T (BN51 (BHK21) temperature sensitivity complementing	M17754	Hs.1276	NM_001722	8q21	Cluster Incl. M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M17754 /gi=179512 /ug=Hs.1276 /len=1881	41694_at
MME (membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	J03779	Hs.1298	NM_000902	3q25.1-q25.2	J03779 /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblastic leukemia antigen (CALLA) mRNA, complete cds	1389_at
RBM9 (RNA binding motif protein 9	AL009266	Hs.5011	NM_014309	22q13.1	Cluster Incl. AL009266:H. sapiens cDNA similar to C. elegans RNA binding protein U14946, Q10572, complete cds /cds=(170,1273) /gb=AL009266 /gi=2664428 /ug=Hs.155156 /len=1876	40260_g_at

LBP (lipopolysaccharide-binding protein	AF013512	Hs.154078	NM_004139	20q11.23-q12	Cluster Incl. AF013512:untitled /cds=(106,1551) /gb=AF013512 /gi=2653816 /ug=Hs.154078 /len=1887	35013_at
ORM1 (orosomucoid 1)	X02544	Hs.572	NM_000607	9q31-q32	Cluster Incl. X02544:Human mRNA for alpha1-acid glycoprotein (orosomucoid) /cds=(78,683) /gb=X02544 /gi=24444 /ug=Hs.572 /len=803	35315_at
CD24 (CD24 antigen (small cell lung carcinoma cluster 4 antigen)	L33930	Hs.286124	NM_013230	6q21	L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3 region	266_s_at
NCF4 (neutrophil cytosolic factor 4 (40kD)	AL008637	Hs.196352	NM_000631	22q13.1	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648)	38894_g_at

						/gb=AL008637 /gi=3136	
	AF035315					Cluster Incl. AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence /cds=UNKNOWN /gb=AF035315 /gi=2661077 /ug=Hs.180737 /len=1331	33267_at
CEACAM1 (carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein	X16354	Hs.50964	NM_001712	19q13.2	/FEATURE= /DEFINITION=HSTM1CEA Human mRNA for transmembrane carcinoembryonic antigen BGPa (formerly TM1-CEA)	X16354	988_at
QPCT (glutaminyl-peptide cyclotransferase (glutaminyl cyclase	X71125	Hs.79033	NM_012413	2p22.3-2p22.1	cyclotransferase	Cluster Incl. X71125:H.sapiens mRNA for glutamine /cds=UNKNOWN /gb=X71125 /gi=398375 /ug=Hs.234747 /len=1556	35966_at

DEFA1 (defensin, alpha 1, myeloid-related sequence	AL036554	Hs.274463	NM_004084	8p23.2-p23.1	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	31793_at
NR2F6 (nuclear receptor subfamily 2, group F, member 6)	AI189624	Hs.239752	NM_005234	19p13.1	Cluster Incl. AI189624:qd32h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1725471 /clone_end=3 /gb=AI189624 /gi=3740833 /ug=Hs.239752 /len=833	41312_r_at
TCN1 (transcobalamin I (vitamin B12 binding protein, R binder family)	J05068	Hs.2012	NM_001062	11q11-q12	Cluster Incl. J05068:human transcobalamin I mRNA, complete cds /cds=(75,1376) /gb=J05068 /gi=307478 /ug=Hs.2012 /len=1537	35919_at
IL8RA (interleukin 8 receptor, alpha)	U11870	Hs.194778	NM_000634	2q35	U11870 /FEATURE=mRNA /DEFINITION=HSU11870 Human interleukin-8 receptor type A (IL8RBA) gene, promoter and complete cds	1352_at

KIAA0604(KIAA0604 gene product	AB011176	Hs.129801	NM_014693	3	Cluster Incl. AB011176:Homo sapiens mRNA for KIAA0604 protein, complete cds /cds=(138,2435) /gb=AB011176 /gi=3043731 /ug=Hs.129801 /len=3228	35536_at
FRAT2 (frequently rearranged in advanced T-cell lymphomas 2	AF062739	Hs.140720		10q23-q24.1	Cluster Incl. AF062739:Homo sapiens GSK-3 binding protein FRAT2 (FRAT2) mRNA, partial cds- /cds=(0,341) /gb=AF062739 /gi=3243176 /ug=Hs.140720 /len=481	40171_at
LOC90355(hypothetical gene supported by AF038182; BC009203	AF038182	Hs.25925		5	Cluster Incl. AF038182:Homo sapiens clone 23860 mRNA sequence /cds=UNKNOWN /gb=AF038182 /gi=2795902 /ug=Hs.25925 /len=1508	33466_at
CPNE3 (copine III)	AB014536	Hs.14158	NM_003909	8p22-q21.3	Cluster Incl. AB014536:Homo sapiens mRNA for KIAA0636 protein, complete cds /cds=(120,1733) /gb=AB014536 /gi=3327085 /ug=Hs.14158 /len=4737	39706_at

GAS11 (growth arrest-specific 11	AF050078	Hs.54877	NM_001481	16q24.3	Cluster Incl. AF050078:untitled /cds=(122,1558) /gb=AF050078 /gi=3818466 /ug=Hs.54877 /len=3186	36479_at
CHIT1 (chitinase 1 (chitotriosidase)	U29615	Hs.91093	NM_003465	1q31-q32	Cluster Incl. :Human chitotriosidase precursor mRNA, complete cds /cds=(12,1412) /gb=U29615 /gi=1050957 /ug=Hs.91093 /len=1633	37061_at
RAB31 (RAB31, member RAS oncogene family	U59877	Hs.223025	NM_006868	18p11.3	Cluster Incl. U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds /cds=(60,644) /gb=U59877 /gi=1388194 /ug=Hs.223025 /len=907	33371_s_at
TUBA1 (tubulin, alpha 1 (testis specific)	X06956	Hs.75318		2q3	Cluster Incl. X06956:Human HALPHA44 gene for alpha-tubulin, exons 1-3 /cds=(0,1343) /gb=X06956 /gi=32014 /ug=Hs.75318 /len=1344	36591_at
STX3A (syntaxin 3A	U32315	Hs.82240	NM_004177	11cen-11q12.3	Cluster Incl. U32315:Human syntaxin 3 mRNA, complete cds /cds=(38,907) /gb=U32315 /gi=929990 /ug=Hs.82240	38381_at

					/len=1903	
	AA524802				Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-954213 /gb=AA524802 /gi=2265730 /ug=Hs.203907 /len=500	32877_i_at
PDI2(peptidyl arginine deiminase, type II)	AB023211	Hs.33455		1	Cluster Incl. AB023211:Homo sapiens mRNA for KIAA0994 protein, partial cds /cds=(0,2061) /gb=AB023211 /gi=4589631 /ug=Hs.33455 /len=4343	35674_at
ITGAM (integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170),	J03925	Hs.172631	NM_000632	16p11.2	Cluster Incl. J03925:Human Mac-1 gene encoding complement receptor type 3, CD11b, complete cds /cds=(72,3533) /gb=J03925 /gi=187284 /ug=Hs.172631 /len=4699	38533_s_at
ALOX5AP (arachidonate 5-lipoxygenase-activating protein	AI806222	Hs.100194	NM_001629	13q12	Cluster Incl. AI806222:wf26e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2356746 /clone_end=3 /gb=AI806222	37099_at

					/gi=5392788 /ug=Hs.100194 /len=563	
DEFA3 (defensin, alpha 3, neutrophil-specific	L12691	Hs.294176	NM_005217	8pter-p23.3	Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364 /ug=Hs.178741 /len=452	31506_s_at
P63(transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment	X69910	Hs.74368	NM_006825	12	Cluster Incl. X69910:H.sapiens p63 mRNA for transmembrane protein /cds=(84,1889) /gb=X69910 /gi=297407 /ug=Hs.74368 /len=2898	32529_at
ANXA3 (annexin A3	M20560	Hs.1378	NM_005139	4q13-q22	Cluster Incl. M20560:Human lipocortin-III mRNA, complete cds /cds=(46,1017) /gb=M20560 /gi=186967 /ug=Hs.1378 /len=1339	31792_at
					Tubulin, Alpha 1, Isoform 44	330_s_at
SLC2A5 (solute carrier family 2 (facilitated glucose/fructose transporter), member 5	M55531	Hs.33084	NM_003039	1p36.2	Cluster Incl. M55531:Human glucose transport-like 5 (GLUT5) mRNA, complete cds /cds=(75,1580) /gb=M55531	34362_at

						/gi=183297 /ug=Hs.33084 /len=2218	
SIM2 (single-minded (Drosophila) homolog 2	U80457	Hs.27311	NM_005069		21q22.13	Cluster Incl. U80457:Human transcription factor SIM2 short form mRNA, complete cds /cds=(92,1804) /gb=U80457 /gi=2062418 /ug=Hs.27311 /len=2844	39609_at
	U72507					Cluster Incl. U72507:Human 40871 mRNA, partial sequence /cds=UNKNOWN /gb=U72507 /gi=1673508 /ug=Hs.234216 /len=1414	39245_at
LCP2 (lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD	U20158	Hs.2488	NM_005565		5q33.1-qter	Cluster Incl. U20158:Human 76 kDa tyrosine phosphoprotein SLP-76 mRNA, complete cds /cds=(255,1856) /gb=U20158 /gi=806765 /ug=Hs.2488 /len=2032	39319_at

NCF4 (neutrophil cytosolic factor 4 (40kD)	AL008637	Hs.196352	NM_000631	22q13.1	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136	38893_at
MYL2 (myosin, light polypeptide 2, regulatory, cardiac, slow	X66141	Hs.75535	NM_000432	12q23-q24.3	Cluster Incl. X66141:H.sapiens mRNA for cardiac ventricular myosin light chain-2 /cds=(30,530) /gb=X66141 /gi=34845 /ug=Hs.75535 /len=784	36640_at
PPP2R5A (protein phosphatase 2, regulatory subunit B (B56), alpha isoform	L42373	Hs.155079	NM_006243	1q41	L42373 /FEATURE=mRNA /DEFINITION=HUMPP2A Homo sapiens phosphatase 2A B56-alpha (PP2A) mRNA, complete cds	903_at
FCN1 (ficolin (collagen/fibrinogen domain-containing) 1	S80990	Hs.252136	NM_002003	9q34	Cluster Incl. S80990:ficolin [human, uterus, mRNA, 1736 nt] /cds=(532,1512) /gb=S80990 /gi=1911529 /ug=Hs.169237	36447_at

					/len=1723	
IL8RA (interleukin 8 receptor, alpha	U11870	Hs.194778	NM_000634	2q35	U11870 /FEATURE=mRNA /DEFINITION=HSU11870 Human interleukin-8 receptor type A (IL8RBA) gene, promoter and complete cds	1353_g_at
NFIB (nuclear factor I/B	U85193	Hs.33287	NM_005596	9p24.1	Cluster Incl. :Human nuclear factor I-B2 (NFIB2) mRNA, complete cds /cds=(209,1471) /gb=U85193 /gi=1814408 /ug=Hs.239235 /len=2424	34720_at
NS1-BP(NS1-binding protein)	AB020657	Hs.197298	NM_006469	1	Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete cds /cds=(630,2558) /gb=AB020657 /gi=4240188 /ug=Hs.197298 /len=3682	33752_at
PLXNC1 (plexin C1	AF030339	Hs.286229	NM_005761	12	Cluster Incl. AF030339:Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds /cds=(249,4955) /gb=AF030339	32193_at

					/gi=3176761 /ug=Hs.184697 /len=5121	
AIF1 (allograft inflammatory factor 1	Y14768	Hs.76364	NM_001623	6p21.3	Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /cds=(10,744) /gb=Y14768 /gi=3805800 /ug=Hs.890 /len=896	40729_s_at
CD59 (CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32	M84349	Hs.119663	NM_000611	11p13	Cluster Incl. M84349:Human transmembrane protein (CD59) gene /cds=(18,404) /gb=M84349 /gi=180150 /ug=Hs.119663 /len=1840	39351_at
SLPI (secretory leukocyte protease inhibitor (antileukoproteinase)	X04470	Hs.251754	NM_003064	20pter-p12.3	Cluster Incl. X04470:Human mRNA for antileukoprotease (ALP) from cervix uterus /cds=(18,416) /gb=X04470 /gi=28638 /ug=Hs.169793 /len=594	32275_at
OGG1 (8-oxoguanine DNA glycosylase	AB019529	Hs.96398	NM_002542	3p26.2	Cluster Incl. AB019529:Homo sapiens mRNA for OGG1 protein type 2c, partial cds /cds=(0,303) /gb=AB019529	34146_at

					/gi=4587151 /ug=Hs.227236 /len=585	
CEACAM1 (carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	S71326	Hs.50964	NM_001712	19q13.2	Cluster Incl. S71326:BGPc=biliary glycoprotein adhesion molecule {alternatively spliced} [human, HT29 colon carcinoma cell line, mRNA Partial, 1473 nt] /cds=(0,1394) /gb=S71326 /gi=550030 /ug=Hs.50964 /len=1473	36082_at
KIAA0374(syntaphilin)	AB002372			20	Cluster Incl. AB002372:Human mRNA for KIAA0374 gene, complete cds /cds=(642,2258) /gb=AB002372 /gi=2224688 /ug=Hs.100837 /len=5530	41107_at
KIAA1564(KIAA1564 protein	U00930	Hs.173421		14	Cluster Incl. U00930:Human clone C4E 1.63 (CAC)n/(GTG)n repeat-containing mRNA /cds=UNKNOWN /gb=U00930 /gi=405043 /ug=Hs.204196 /len=3276	40981_at
LTA4H (leukotriene A4 hydrolase)	J03459	Hs.81118	NM_000895	12q22	Cluster Incl. J03459:Human leukotriene A-4 hydrolase mRNA, complete cds /cds=(68,1903) /gb=J03459 /gi=187172	38081_at

					/ug=Hs.81118 /len=2060	
COL17A1 (collagen, type XVII, alpha 1)	M91669	Hs.117938	NM_000494	10q24.3	Cluster Incl. M91669:Human Bullous pemphigoid autoantigen BP180 gene, 3 end /cds=(0,4598) /gb=M91669 /gi=179516 /ug=Hs.117938 /len=4669	41618_at
EPB72 (erythrocyte membrane protein band 7.2 (stomatin)	X85116	Hs.160483	NM_004099	9q34.1	Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035	40419_at
PRG2 (proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic	Z26248	Hs.99962	NM_002728	11q12	Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=940510 /ug=Hs.99962 /len=1637	39179_at
IL18RAP (interleukin 18 receptor accessory protein)	AF077346	Hs.158315	NM_003853	2p24.3-p24.1	Cluster Incl. AF077346:Homo sapiens interleukin-18 receptor accessory protein-like mRNA, complete cds /cds=(483,2282) /gb=AF077346 /gi=3851059 /ug=Hs.158315 /len=2681	33093_at

FBN1 (fibrillin 1 (Marfan syndrome))	X63556	Hs.750	NM_000138	15q21.1	Cluster Incl. X63556:H.sapiens mRNA for fibrillin /cds=(0,9010) /gb=X63556 /gi=397553 /ug=Hs.750 /len=9927	32535_at
LSP1 (lymphocyte-specific protein 1)	M33552	Hs.56729	NM_002339	11p15.5	Cluster Incl. M33552:Human lymphocyte-specific protein 1 (LSP1) mRNA, complete cds /cds=(108,1127) /gb=M33552 /gi=187237 /ug=Hs.56729 /len=1631	36493_at
VNN2 (vanin 2)	D89974	Hs.121102	NM_004665	6q23-q24	Cluster Incl. D89974:Homo sapiens mRNA for glycosylphosphatidyl inositol-anchored protein GPI-80, complete cds /cds=(11,1573) /gb=D89974 /gi=5541649 /ug=Hs.121102 /len=2004	34498_at
PIR121(p53 inducible protein)	L47738	Hs.258503		5	Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881	37579_at

BASP1 (brain abundant, membrane attached signal protein 1)	AF039656	Hs.79516	NM_006317	5p15.1-p14	Cluster Incl. AF039656:Homo sapiens neuronal tissue-enriched acidic protein (NAP-22) mRNA, complete cds /cds=(52,735) /gb=AF039656 /gi=2773159 /ug=Hs.79516 /len=1467	32607_at
CSF1 (colony stimulating factor 1 (macrophage))	M37435	Hs.173894	NM_000757	1p21-p13	M37435 /FEATURE= /DEFINITION=HUMCSDF1 Human macrophage-specific colony-stimulating factor (CSF-1) mRNA, complete cds	882_at
KIAA0370(KIAA0370 protein)	AB002368			16	Cluster Incl. AB002368:Human mRNA for KIAA0370 gene, partial cds /cds=(0,2406) /gb=AB002368 /gi=2224680 /ug=Hs.70500 /len=5724	35830_at
LILRA3 (leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3)	AF025527	Hs.113277	NM_006865	19q13.4	Cluster Incl. AF025527:Homo sapiens leucocyte immunoglobulin-like receptor-4 (LIR-4) mRNA, complete cds /cds=(93,1412) /gb=AF025527 /gi=2653860 /ug=Hs.113277 /len=1606	35094_f_at

CHRNE (cholinergic receptor, nicotinic, epsilon polypeptide)	X66403	Hs.278295	NM_000080	17p13-p12	Cluster Incl. X66403:H.sapiens mRNA for acetylcholine receptor (epsilon subunit) /cds=(11,1492) /gb=X66403 /gi=560152 /ug=Hs.112028 /len=2457	39834_at
[HSPC022(HSPC022 protein)	W68830	Hs.301175	NM_014029	22	Cluster Incl. W68830:zd37g06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-342874 /clone_end=5 - /gb=W68830 /gi=1377739 /ug=Hs.173466 /len=614	32736_at
AHCP(Autosomal Highly Conserved Protein)	AL050128	Hs.95260	NM_016255	6	Cluster Incl. AL050128:Homo sapiens mRNA; cDNA DKFZp586G051 (from clone DKFZp586G051) /cds=UNKNOWN /gb=AL050128 /gi=4884335 /ug=Hs.95260 /len=1950	38318_at
MACS (myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L))	D10522	Hs.75607	NM_002356	6q22.2	Cluster Incl. D10522:Homo sapiens mRNA for 80K-L protein, complete cds /cds=(369,1367) /gb=D10522 /gi=219893 /ug=Hs.75607 /len=2589	32434_at

CBX7 (chromobox homolog 7)	AL031846			22q13.1	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
MGAM (maltase-glucoamylase (alpha-glucosidase))	AF016833	Hs.122785	NM_004668	7	Cluster Incl. AF016833:Homo sapiens maltase-glucoamylase mRNA, complete cds /cds=(54,5627) /gb=AF016833 /gi=2826520 /ug=Hs.122785 /len=6483	34509_at
GCA (grancalcin, EF-hand calcium-binding protein)	M81637	Hs.79381	NM_012198	2p14-q14.3	Cluster Incl. M81637:Human grancalcin mRNA, complete cds /cds=(119,772) /gb=M81637 /gi=183030 /ug=Hs.79381 /len=1652	37556_at
TALDO1 (transaldolase 1)	AF010400	Hs.77290	NM_006755	11p15.5-p15.4	Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242	37311_at
CPT1B (carnitine palmitoyltransferase I, muscle)	Y08683	Hs.29331	NM_004377	22q13.33	Cluster Incl. Y08683:H.sapiens mRNA for carnitine palmitoyltransferase I type II /cds=(51,2369) /gb=Y08683 /gi=1871536	35935_at

					/ug=Hs.211565 /len=2624	
KIAA1109(KIAA1109 protein)	AB029032	Hs.6606		4	Cluster Incl. AB029032:Homo sapiens mRNA for KIAA1109 protein, partial cds /cds=(0,5873) /gb=AB029032 /gi=5689554 /ug=Hs.6606 /len=6377	36814_at
PSTPIP1 (proline-serine-threonine phosphatase interacting protein 1)	U94778	Hs.129758	NM_003978	15q24-q25.1	Cluster Incl. U94778:Human PEST phosphatase interacting protein homolog (H-PIP) mRNA, complete cds /cds=(216,1466) /gb=U94778 /gi=4100161 /ug=Hs.129758 /len=1656	34914_at
PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39208_i_at
ANXA11 (annexin A11)	L19605	Hs.75510	NM_001157	10q22-q23	Cluster Incl. L19605:Homo sapiens 56K autoantigen annexin XI gene mRNA, complete cds /cds=(178,1695) /gb=L19605	36637_at

					/gi=457128 /ug=Hs.75510 /len=1958	
PGLYRP (peptidoglycan recognition protein)	AF076483	Hs.137583	NM_005091	19q13.2-q13.3	Cluster Incl. AF076483:Homo sapiens peptidoglycan recognition protein precursor (PGRP) mRNA, complete cds /cds=(44,634) /gb=AF076483 /gi=3342532 /ug=Hs.137583 /len=690	31381_at
SDF2 (stromal cell-derived factor 2)	D50645	Hs.118684	NM_006923	17q11.2	Cluster Incl. D50645:Homo sapiens mRNA for SDF2, complete cds /cds=(39,674) /gb=D50645 /gi=1741867 /ug=Hs.118684 /len=1085	41627_at
PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39209_r_at
tissue-activating peptide III, neutrophil-activating peptide-2))					Cluster Incl. AB002369:Human mRNA for KIAA0371 gene, complete cds /cds=(247,3843) /gb=AB002369	35739_at

					/gi=2224682 /ug=Hs.63302 /len=5886	
TNFRSF12 (tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein))	U83600	Hs.180338	NM_003790	1p36.2	U83600 /FEATURE=mRNA /DEFINITION=HSU83600 Human death domain receptor 3 (DDR3) mRNA, alternatively spliced form 2, partial cds	1210_s_at
KCNQ2 (potassium voltage-gated channel, KQT-like subfamily, member 2)	Y15065	Hs.4975	NM_004518	20q13.3	Cluster Incl. Y15065:Homo sapiens mRNA for voltage gated potassium channel /cds=(42,2576) /gb=Y15065 /gi=2826772 /ug=Hs.4975 /len=7407	41589_at
INHA (inhibin, alpha)	M13981	Hs.1734	NM_002191	2q33-q36	M13981 /FEATURE= /DEFINITION=HUMINHA Human inhibin A-subunit mRNA, complete cds	255_s_at
RAC1 (ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1))	D25274	Hs.173737	NM_006908	7p22	Cluster Incl. D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN /gb=D25274 /gi=464185 /ug=Hs.173737 /len=1232	40864_at

KIAA0014(KIAA0014 gene product)	D25216	Hs.155650	NM_014665	8	Cluster Incl. D25216:Human mRNA for KIAA0014 gene, complete cds /cds=(146,1627) /gb=D25216 /gi=434774 /ug=Hs.155650 /len=5323	32062_at
MLH1 (mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2))	AF001359	Hs.57301	NM_000249	3p21.3	AF001359 /FEATURE= /DEFINITION=AF001359 Homo sapiens DNA mismatch repair protein (hMLH1) mRNA, alternatively spliced, partial cds	1944_f_at
NMP200(nuclear matrix protein NMP200 related to splicing factor PRP19)	AI761148	Hs.173980	NM_014502	11	Cluster Incl. AI761148:wh97h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2388733 /clone_end=3 /gb=AI761148 /gi=5176815 /ug=Hs.173980 /len=443	33231_at
CST3 (cystatin C (amyloid angiopathy and cerebral hemorrhage))	AI362017	Hs.135084	NM_000099	20p11.2	Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2014362 /clone_end=3 /gb=AI362017 /gi=4113638 /ug=Hs.135084 /len=778	39689_at

EIF3S2 (eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD))	U39067	Hs.192023	NM_003757	1p34.1	Cluster Incl. U39067:Homo sapiens translation initiation factor eIF3 p36 subunit mRNA, complete cds /cds=(17,994) /gb=U39067 /gi=1718194 /ug=Hs.192023 /len=1402	32230_at
CNIL(cornichon homolog (Drosophila))	AF104398	Hs.201673	NM_005776	14	Cluster Incl. AF104398:Homo sapiens cornichon mRNA, complete cds /cds=(56,490) /gb=AF104398 /gi=4063708 /ug=Hs.201673 /len=1379	32803_at
SERPINA6 (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase,antitrypsin), member 6)	J02943	Hs.1305	NM_001756	14q32.1	Cluster Incl. J02943:Human corticosteroid binding globulin mRNA, complete cds /cds=(35,1252) /gb=J02943 /gi=179970 /ug=Hs.1305 /len=1422	37833_at
RAC1 (ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1))	M29870	Hs.173737	NM_006908	7p22	M29870 /FEATURE= /DEFINITION=HUMRACA Human ras-related C3 botulinum toxin substrate (rac) mRNA, complete cds	2050_s_at

PLOD3 (procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3)	AF046889	Hs.153357	NM_001084	7q22	Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735	39801_at
SET (SET translocation (myeloid leukemia-associated))	M93651	Hs.145279	NM_003011	9q34	Cluster Incl. M93651:Human set gene, complete cds /cds=(3,836) /gb=M93651 /gi=338038 /ug=Hs.145279 /len=2562	40189_at
GPX1 (glutathione peroxidase 1)	X13710	Hs.76686	NM_000581	3p21.3	Cluster Incl. X13710:H.sapiens unspliced mRNA for glutathione peroxidase /cds=UNKNOWN /gb=X13710 /gi=35387 /ug=Hs.76686 /len=1100	37033_s_at
SAM68(src associated in mitosis, 68 kDa)	M88108	Hs.119537	NM_006559	1	Cluster Incl. M88108:Human p62 mRNA, complete cds /cds=(106,1437) /gb=M88108 /gi=189499 /ug=Hs.119537 /len=2685	39346_at
CD5 (CD5 antigen (p56-62))	X04391	Hs.58685	NM_014207	11q13	Cluster Incl. X04391:Human mRNA for lymphocyte glycoprotein T1/Leu-1	32953_at

					/cds=(72,1559) /gb=X04391 /gi=37186 /ug=Hs.234745 /len=2320	
APLP2 (amyloid beta (A4) precursor-like protein 2)	S60099	Hs.279518	NM_001642	11q24	Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.64797 /len=3727	33944_at
ZNF212 (zinc finger protein 212)	U38864	Hs.108139	NM_012256	7q36.1	Cluster Incl. U38864:Human zinc-finger protein C2H2-150 mRNA, complete cds /cds=(220,1065) /gb=U38864 /gi=1055340 /ug=Hs.108139 /len=2235	41426_at
MTVR(Mouse Mammary Turmor Virus Receptor homolog)	AF052151	Hs.18686			Cluster Incl. AF052151:Homo sapiens clone 24574 mRNA sequence /cds=UNKNOWN /gb=AF052151 /gi=3360461 /ug=Hs.18686 /len=1337	32209_at
LOC56928(hypothetical protein from EUROIMAGE 42353)	AC004410	Hs.284161		19	Cluster Incl. AC004410:Homo sapiens chromosome 19, fosmid 39554 /cds=(0,1196) /gb=AC004410 /gi=2959558	35426_at

					/ug=Hs.167352 /len=1197	
					Cluster Incl. W28227:43h1 Homo sapiens cDNA /gb=W28227 /gi=1308175 /ug=Hs.167985 /len=843	40558_at
DNPEP (aspartyl aminopeptidase)	AF005050	Hs.258551	NM_012100	2q35	Cluster Incl. AF005050:Homo sapiens aspartyl aminopeptidase mRNA, complete cds /cds=(170,1588) /gb=AF005050 /gi=4101588 /ug=Hs.108117 /len=1694	38703_at
KIAA0911(calsyntenin 1)	AB020718	Hs.29665	NM_014944	1	Cluster Incl. AB020718:Homo sapiens mRNA for KIAA0911 protein, complete cds /cds=(793,3738) /gb=AB020718 /gi=4240310 /ug=Hs.29665 /len=5219	41498_at
UQCRC2 (ubiquinol-cytochrome c reductase core protein II)	J04973	Hs.173554	NM_003366	16p12	Cluster Incl. J04973:Human cytochrome bc-1 complex core protein II mRNA, complete cds /cds=(53,1414) /gb=J04973 /gi=180927 /ug=Hs.173554 /len=1588	40854_at

P2RX4 (purinergic receptor P2X, ligand-gated ion channel, 4)	U83993	Hs.321709	NM_002560	12q24.32	Cluster Incl. U83993:Human P2X4 purinoreceptor mRNA, complete cds /cds=(309,1475) /gb=U83993 /gi=4099120 /ug=Hs.9610 /len=2031	38332_at
CLCN7 (chloride channel 7)	Z67743	Hs.80768	NM_001287	16p13	Cluster Incl. Z67743:H.sapiens mRNA for CLC-7 chloride channel protein /cds=(0,2369) /gb=Z67743 /gi=1177439 /ug=Hs.80768 /len=2393	38069_at
NME2 (non-metastatic cells 2, protein (NM23B) expressed in)	X58965	Hs.275163	NM_002512	17q21.3	X58965 /FEATURE= /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2 gene	1980_s_at

Table 9:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
					c /FEATURE= /DEFINITION=HUM4AI Human mRNA for eukaryotic initiation factor 4AI	1199_at
MPB1 (MYC promoter-binding protein 1)	M55914	Hs.284127	NM_005945	1pter-p35	M55914 /FEATURE= /DEFINITION=HUMCMYCQ Human c-myc binding protein (MBP-1) mRNA, complete cds	2035_s_at
TXN (thioredoxin)	AI653621	Hs.76136	NM_003329	9q31	Cluster Incl. AI653621:tz21b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2289213 /clone_end=3 /gb=AI653621 /gi=4737600 /ug=Hs.76136 /len=598	36992_at

RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin))	X55988	Hs.728	NM_002934	14q24-q31	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	36766_at
RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin))	X95735	Hs.728	NM_002934	14q24-q31	Cluster Incl. X95735:Homo sapiens mRNA for zyxin /cds=(71,1789) /gb=X95735 /gi=1545953 /ug=Hs.75873 /len=2217	36958_at
NME2 (non-metastatic cells 2, protein (NM23B) expressed in)	X58965	Hs.275163	Hs.275163	17q21.3	X58965 /FEATURE= /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2 gene	1980_s_at
H2AFY (H2A histone family, member Y)	AF054174	Hs.75258	NM_004893	5q31.3-q32	Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete cds /cds=(173,1288) /gb=AF054174 /gi=3341991 /ug=Hs.75258 /len=1881	36576_at
IDH2 (isocitrate dehydrogenase 2 (NADP+), mitochondrial)	X69433	Hs.5337	Hs.5337	15q26.1	Cluster Incl. X69433:H.sapiens mRNA for mitochondrial isocitrate dehydrogenase (NADP+) /cds=(86,1444) /gb=X69433	32332_at

					/gi=872120 /ug=Hs.182740 /len=1751	
TST (thiosulfate sulfurtransferase (rhodanese))	X59434	Hs.248267	NM_003312	22q13.1	Cluster Incl. X59434:Human rohu mRNA for rhodanese /cds=(34,924) /gb=X59434 /gi=432375 /ug=Hs.74097 /len=1232	36124_at
PGD (phosphogluconate dehydrogenase)	U30255	Hs.75888	NM_002631	1p36.3-p36.13	Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324 /ug=Hs.75888 /len=1536	36963_at
PSMA6 (proteasome (prosome, macropain) subunit, alpha type, 6)	X59417	Hs.336907		14q13	Cluster Incl. X59417:H.sapiens PROS-27 mRNA /cds=(62,802) /gb=X59417 /gi=35681 /ug=Hs.74077 /len=964	36122_at
CD63 (CD63 antigen (melanoma 1 antigen)	X62654	Hs.76294	NM_001780	12q12-q13	Cluster Incl. X62654:H.sapiens gene for Me491/CD63 antigen /cds=(69,785) /gb=X62654 /gi=430755 /ug=Hs.76294 /len=873	37003_at

ALDOA (aldolase A, fructose-bisphosphate)	X05236	Hs.273415	NM_000034	16q22-q24	Cluster Incl. X05236:Human fibroblast mRNA for aldolase A /cds=(146,1240) /gb=X05236 /gi=28596 /ug=Hs.183760 /len=1440	32336_at
CREG (cellular repressor of E1A-stimulated genes)	AF084523	Hs.5710	Hs.5710	1q24	Cluster Incl. AF084523:Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds /cds=(33,695) /gb=AF084523 /gi=3550342 /ug=Hs.5710 /len=1974	35311_at
NME4 (non-metastatic cells 4, protein expressed in)	Y07604	Hs.9235	Hs.9235	16p13.3	Cluster Incl. Y07604:H.sapiens mRNA for nucleoside-diphosphate kinase /cds=(11,574) /gb=Y07604 /gi=1945761 /ug=Hs.9235 /len=879	39089_at
CUTL1 (cut (Drosophila)-like 1 (CCAAT displacement protein))	L12579	Hs.147049	NM_001913	7q22	Cluster Incl. L12579:Human alternatively spliced CUTL1 mRNA, complete cds /cds=(19,2055) /gb=L12579 /gi=457516 /ug=Hs.147049 /len=2855	31822_at

LDHA (lactate dehydrogenase A)	X02152	Hs.2795	NM_005566	11p15.4	Cluster Incl. X02152:Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) /cds=(97,1095) /gb=X02152 /gi=34312 /ug=Hs.2795 /len=1661	41485_at
PTTG1IP (pituitary tumor-transforming 1 interacting protein)	Z50022	Hs.111126	NM_004339	21q22.3	Cluster Incl. Z50022:H.sapiens mRNA for surface glycoprotein /cds=(93,635) /gb=Z50022 /gi=1107702 /ug=Hs.111126 /len=2617	39003_at
H2AV(histone H2A.F/Z variant)	AW007731	Hs.301005	NM_012412	7	Cluster Incl. AW007731:wl68d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512629 /clone_end=3 /gb=AW007731 /gi=5856509 /ug=Hs.9242 /len=659	39092_at
RAB32 (RAB32, member RAS oncogene family)	U59878	Hs.32217	NM_006834	6	Cluster Incl. U59878:Human low-Mr GTP-binding protein (RAB32) mRNA, partial cds /cds=(0,632) /gb=U59878 /gi=1388196 /ug=Hs.32217 /len=980	41523_at

DDAH2 (dimethylarginine dimethylaminohydrolase 2)	AJ012008	Hs.247362	NM_013974	6p21.3	Cluster Incl. AJ012008:Homo sapiens genes encoding RNCC protein, DDAH protein, Ly6-C protein, Ly6-D protein and immunoglobulin receptor /cds=(218,943) /gb=AJ012008 /gi=5304874 /ug=Hs.74276 /len=1200	36131_at
GNG5 (guanine nucleotide binding protein (G protein), gamma 5)	AI541042	Hs.5322	NM_005274	1p22	Cluster Incl. AI541042:pec1.2-1.D12.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI541042 /gi=4458415 /ug=Hs.5322 /len=688	35272_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	Hs.169476	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M33197_5_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3	AFFX-HUMGAPDH/M33197_M_at

					complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	M_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M33197_3_at
CST3 (cystatin C (amyloid angiopathy and cerebral hemorrhage))	AI362017	Hs.135084	NM_000099	20p11.2	Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2014362 /clone_end=3 /gb=AI362017 /gi=4113638 /ug=Hs.135084 /len=778	39689_at
USP5 (ubiquitin specific protease 5 (isopeptidase T))	U47924	Hs.3759	NM_003481	12p13	Cluster Incl. U47924:Human chromosome 12p13 sequence /cds=(373,1122) /gb=U47924 /gi=1633547 /ug=Hs.83848 /len=1843	34003_at

MAPKAPK3 (mitogen-activated protein kinase-activated protein kinase 3)	U09578	Hs.227789	NM_004635	3p21.3	U09578 /FEATURE= /DEFINITION=HSU09578 Homo sapiens MAPKAP kinase (3pK) mRNA, complete cds	1637_at
ARHG (ras homolog gene family, member G (rho G))	X61587	Hs.75082	NM_001665	11p15.5-p15.4	Cluster Incl. X61587:H.sapiens rhoG mRNA for GTPase /cds=(129,704) /gb=X61587 /gi=36035 /ug=Hs.75082 /len=1284	36902_at
TALDO1 (transaldolase 1)	AF010400	Hs.77290	NM_006755	11p15.5-p15.4	Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242	37311_at
HNRPAB (heterogeneous nuclear ribonucleoprotein A/B)	M65028	Hs.81361	NM_004499	5q35	Cluster Incl. M65028:Human hnRNP type A/B protein mRNA, complete cds /cds=(142,996) /gb=M65028 /gi=337450 /ug=Hs.81361 /len=1537	38094_at
FAH (fumarylacetoacetate hydrolase (fumarylacetoacetase))	M55150	Hs.73875	NM_000137	15q23-q25	Cluster Incl. M55150:Human fumarylacetoacetate hydrolase mRNA, complete cds /cds=(56,1315) /gb=M55150	36876_at

					/gi=182392 /ug=Hs.73875 /len=1447	
PRG1 (proteoglycan 1, secretory granule)	X17042	Hs.278687	NM_002727	19q13.2	Cluster Incl. X17042:Human mRNA for hematopoetic proteoglycan core protein /cds=(24,500) /gb=X17042 /gi=32432 /ug=Hs.1908 /len=1182	32227_at
M11S1 (membrane component, chromosome 11, surface marker 1)	Z48042	Hs.278672	NM_005898	11p13	Cluster Incl. Z48042:H.sapiens mRNA encoding GPI-anchored protein p137 /cds=(201,2150) /gb=Z48042 /gi=662993 /ug=Hs.101025 /len=3268	39471_at
ATP6F (ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD)	D89052	Hs.7476	NM_004047	1p32.3	Cluster Incl. D89052:Homo sapiens mRNA for proton-ATPase-like protein, complete cds /cds=(82,699) /gb=D89052 /gi=1694672 /ug=Hs.7476 /len=987	36167_at
ADAM15 (a disintegrin and metalloproteinase domain 15 (metargidin))	U41767	Hs.92208	NM_003815	1q21.3	Cluster Incl. U41767:Human metargidin precursor mRNA, complete cds /cds=(7,2451) /gb=U41767 /gi=1235673 /ug=Hs.92208 /len=2725	38282_at

COX6A1 (cytochrome *c* oxidase subunit VIa polypeptide 1)	AI540925	Hs.180714	NM_004373	12q24.2	Cluster Incl. AI540925:PEC1.2_15_A02.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI540925 /gi=4458298 /ug=Hs.180714 /len=777	41206_r_at
NFIL3 (nuclear factor, interleukin 3 regulated)	X64318	Hs.79334	NM_005384	9q22	Cluster Incl. X64318:H.sapiens E4BP4 gene /cds=(213,1601) /gb=X64318 /gi=30955 /ug=Hs.79334 /len=1904	37544_at
COX8 (cytochrome c oxidase subunit VIII)	AI525665	Hs.81097	NM_004074	11q12-q13	Cluster Incl. AI525665:PT1.3_04_D06.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI525665 /gi=4439800 /ug=Hs.81097 /len=834	38080_at
COMT (catechol-O-methyltransferase)	M58525	Hs.240013	NM_000754	22q11.21	Cluster Incl. :Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds /cds=(204,1019) /gb=M58525 /gi=179954 /ug=Hs.78534 /len=1206	34651_at

SCGF (stem cell growth factor; lymphocyte secreted C-type lectin)	AF020044	Hs.105927	NM_002975	19q13.3	Cluster Incl. AF020044:Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds /cds=(179,1150) /gb=AF020044 /gi=2828595 /ug=Hs.105927 /len=1391	37147_at
P100(staphylococcal nuclease domain containing 1)]	U22055	19	NM_014390	7	Cluster Incl. U22055:Human 100 kDa coactivator mRNA, complete cds /cds=(267,2924) /gb=U22055 /gi=799176 /ug=Hs.79093 /len=3480	37730_at
GPSN2 (glycoprotein, synaptic 2)	AF038958	Hs.306122	NM_004868	19p13.2	Cluster Incl. AF038958:Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds /cds=(76,1002) /gb=AF038958 /gi=3329385 /ug=Hs.109051 /len=1116	38966_at
DDOST (dolichyl-diphosphooligosaccharide-protein glycosyltransferase)	D29643	Hs.34789	NM_005216	1p36.1	Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936 /ug=Hs.89674 /len=1668	38791_at

HDLBP (high density lipoprotein binding protein (vigilin))	M64098	Hs.177516	NM_005336	2q37	Cluster Incl. M64098:Human high density lipoprotein binding protein (HBP) mRNA, complete cds /cds=(154,3960) /gb=M64098 /gi=183891 /ug=Hs.177516 /len=4354	31504_at
LOC57019(hypothetical protein)	AC004382	Hs.4900	NM_020313	16	Cluster Incl. AC004382:Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5 /cds=(0,935) /gb=AC004382 /gi=3252819 /ug=Hs.79402 /len=1659	32600_at
RAB13 (RAB13, member RAS oncogene family)	X75593	Hs.151536	NM_002870	12q13	Cluster Incl. X75593:H.sapiens mRNA for rab 13 /cds=(139,750) /gb=X75593 /gi=452319 /ug=Hs.151536 /len=1238	40210_at
PFN1 (profilin 1)	J03191	Hs.75721	NM_005022	17p13.3	Cluster Incl. J03191:Human profilin mRNA, complete cds /cds=(127,549) /gb=J03191 /gi=190385 /ug=Hs.75721 /len=793	36675_r_at
DXS1357E(accessory proteins BAP31/BAP29)	X81817			X	Cluster Incl. X81817:H.sapiens BAP31 mRNA /cds=(73,813) /gb=X81817	41724_at

					/gi=550342 /ug=Hs.181373 /len=1504	
RAC1 (ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	M29870	Hs.173737	NM_006908	7p22	M29870 /FEATURE= /DEFINITION=HUMRACA Human ras-related C3 botulinum toxin substrate (rac) mRNA, complete cds	2050_s_at
FKBP1A (FK506-binding protein 1A (12kD))	M34539	Hs.179661	NM_000801	20p13	M34539 /FEATURE= /DEFINITION=HUMFKBP Human FK506-binding protein (FKBP) mRNA, complete cds	880_at
YF13H12(protein expressed in thyroid)	D83198	Hs.7486	NM_014297	19	Cluster Incl. D83198:Homo sapiens mRNA expressed in thyroid gland /cds=(341,1024) /gb=D83198 /gi=3893156 /ug=Hs.7486 /len=1154	36170_at
ANXA1 (annexin A1)	X05908	Hs.78225	NM_000700	9q12-q21.2	Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X05908 /gi=34387 /ug=Hs.78225 /len=1399	37403_at

Approved UCL/HGNC/HUGO Human Gene Nomenclature database symbol	AF046889	Hs.153357	NM_001084	7q22	Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735	39801_at
SPN (sialophorin (gpL115, leukosialin, CD43))	J04168	Hs.80738	NM_003123	16p11.2	Cluster Incl. J04168:Human leukosialin mRNA, complete cds /cds=(95,1297) /gb=J04168 /gi=187118 /ug=Hs.80738 /len=2288	36798_g_at
RAGD(Rag D protein)]	W27549	Hs.238679	NM_021244	6	Cluster Incl. W27549:32d11 Homo sapiens cDNA /gb=W27549 /gi=1307353 /ug=Hs.235634 /len=912	32963_s_at
IMPDH2 (IMP (inosine monophosphate) dehydrogenase 2)	L33842	Hs.75432	NM_000884	3p21.2	Cluster Incl. L33842:Homo sapiens (clone FFE-7) type II inosine monophosphate dehydrogenase (IMPDH2) gene, exons 1-13, complete cds /cds=(102,1646) /gb=L33842 /gi=602457 /ug=Hs.75432 /len=1688	36624_at

PSMD9 (proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	AB003177	Hs.5648	NM_002813	12q24.31-q24.32	AB003177 /FEATURE= /DEFINITION=AB003177 Homo sapiens mRNA for proteasome subunit p27, complete cds	1444_at
NSEP1 (nuclease sensitive element binding protein 1)	M85234	Hs.74497	NM_004559	1p34	Cluster Incl. M85234:Human nuclease sensitive element binding protein-1 mRNA, complete cds /cds=(234,1202) /gb=M85234 /gi=337427 /ug=Hs.184712 /len=1474	32340_s_at
LOC95295(hypothetical gene supported by V00599; BC001938; BC007605; BC008791)	V00599			6	V00599 /FEATURE=mRNA /DEFINITION=HSTUB2 Human mRNA fragment encoding beta-tubulin. (from clone D-beta-1)	151_s_at
MAZ (MYC-associated zinc finger protein (purine-binding transcription factor))	M94046	Hs.7647	NM_002383	16p11.2	Cluster Incl. M94046:Human zinc finger protein (MAZ) mRNA /cds=UNKNOWN /gb=M94046 /gi=187393 /ug=Hs.7647 /len=2389	32553_at

HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like))	L24521	Hs.89525	NM_004494	xq25	Cluster Incl. L24521:Human transformation-related protein mRNA, 3 end /cds=(0,1108) /gb=L24521 /gi=403459 /ug=Hs.169225 /len=1240	36446_s_at
KDELR1 (KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1)	X55885	Hs.78040	NM_006801	19q13.3	Cluster Incl. X55885:Human mRNA for a presumptive KDEL receptor /cds=(146,784) /gb=X55885 /gi=34030 /ug=Hs.78040 /len=1086	37386_i_at
ACADVL (acyl-Coenzyme A dehydrogenase, very long chain)	L46590	Hs.82208	NM_000018	17p13-p11	Cluster Incl. L46590:Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds /cds=(88,2055) /gb=L46590 /gi=1008851 /ug=Hs.82208 /len=2224	38376_at
DGKZ (diacylglycerol kinase, zeta (104kD))	U94905	Hs.89981	NM_003646	11p11.2	Cluster Incl. U94905:Human diacylglycerol kinase zeta mRNA, alternatively spliced, complete cds /cds=(125,3478) /gb=U94905 /gi=2183037 /ug=Hs.89981 /len=4094	38003_s_at

SNRPF (small nuclear ribonucleoprotein polypeptide F)	AI032612	Hs.105465	NM_003095	12	Cluster Incl. AI032612:ow17e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1647108 /clone_end=3 /gb=AI032612 /gi=3253738 /ug=Hs.105465 /len=582	41403_at
ATP6S1 (ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1)	D16469	Hs.6551	NM_001183	xq28	Cluster Incl. D16469:Human mRNA for ORF, Xq terminal portion /cds=(1353,2198) /gb=D16469 /gi=758583 /ug=Hs.6551 /len=2823	35770_at
TRIM28 (tripartite motif-containing 28)	X97548	Hs.228059	NM_005762	5	Cluster Incl. X97548:H.sapiens mRNA for TIF1beta zinc finger protein /cds=(361,2868) /gb=X97548 /gi=1524108 /ug=Hs.228059 /len=3035	33425_at
K-ALPHA-1(tubulin, alpha, ubiquitous)	K00558	Hs.334842	NM_006082	12	Cluster Incl. K00558:human alpha-tubulin mRNA, complete cds /cds=(67,1422) /gb=K00558 /gi=340020 /ug=Hs.169476 /len=1596	32272_at
COX7B (cytochrome c oxidase subunit VIIb)	N50520	Hs.75752	NM_001866	xp21.1-q21.33	Cluster Incl. N50520:yy89b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-	36687_at

					280689 /clone_end=3 /gb=N50520 /gi=1191686 /ug=Hs.75752 /len=550	
CHC1 (chromosome condensation 1)	D00591	Hs.84746	NM_001269	1p36.1	D00591 /FEATURE=exons#7-14 /DEFINITION=HUMRCC1 Homo sapiens RCC1 gene, exons 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, complete cds	1196_at
TYMS (thymidylate synthetase)	D00596	Hs.82962	NM_001071	18p11.32	D00596 /FEATURE=cds /DEFINITION=HUMTS1 Homo sapiens gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 6, 7, complete cds	1505_at
GPX1 (glutathione peroxidase 1)	X13710	Hs.76686	NM_000581	3p21.3	Cluster Incl. X13710:H.sapiens unspliced mRNA for glutathione peroxidase /cds=UNKNOWN /gb=X13710 /gi=35387 /ug=Hs.76686 /len=1100	37033_s_at
IGFBP7 (insulin-like growth factor binding protein 7)	L19182	Hs.119206	NM_001553	4q12	L19182 /FEATURE= /DEFINITION=HUMMAC25X Human MAC25 mRNA, complete cds	2062_at

HMG20B (high-mobility group 20B)	AF072836	Hs.32317	NM_006339	19p13.3	Cluster Incl. AF072836:Homo sapiens Sox-like transcriptional factor mRNA, complete cds /cds=(18,1043) /gb=AF072836 /gi=3329481 /ug=Hs.32317 /len=1232	41526_at
R33729_1(hypothetical protein R33729_1)]	AI828168	Hs.10927		19	Cluster Incl. AI828168:wk32h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2414081 /clone_end=3 /gb=AI828168 /gi=5448839 /ug=Hs.10927 /len=759	38969_at
MAN2B1 (mannosidase, alpha, class 2B, member 1)	U60899	Hs.279854	NM_000528	19cen-q13.1	Cluster Incl. U60899:Human lysosomal alpha-mannosidase (manB) gene /cds=(309,3341) /gb=U60899 /gi=2209014 /ug=Hs.234070 /len=3443	34670_at
PSMB4 (proteasome (prosome, macropain) subunit, beta type, 4)	D26600	Hs.89545	NM_002796	1q21	D26600 /FEATURE= /DEFINITION=HUMPSH3 Human mRNA for proteasome subunit HsN3, complete cds	1311_at

CDK2AP1 (CDK2-associated protein 1)	AF006484	Hs.3436	NM_004642	12q24.31	Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor protein (doc-1) mRNA, complete cds /cds=(522,869) /gb=AF006484 /gi=2738496 /ug=Hs.3436 /len=1608	41535_at
H2AFZ (H2A histone family, member Z)	M37583	Hs.119192	NM_002106	4q24	Cluster Incl. M37583:Human histone (H2A.Z) mRNA, complete cds /cds=(106,492) /gb=M37583 /gi=184059 /ug=Hs.119192 /len=873	39337_at
KIAA0095(KIAA0095 gene product)]	D42085	Hs.155314	NM_014669	16	Cluster Incl. D42085:Human mRNA for KIAA0095 gene, complete cds /cds=(66,2525) /gb=D42085 /gi=577316 /ug=Hs.155314 /len=2681	40271_at
RPN2 (ribophorin II)	AL031659	Hs.75722	NM_002951	20q12-q13.1	Cluster Incl. AL031659:dJ343K2.2.1 (ribophorin II (isoform 1)) /cds=(284,2179) /gb=AL031659 /gi=4468296 /ug=Hs.75722 /len=2488	36676_at

SLC29A1 (solute carrier family 29 (nucleoside transporters), member 1	U81375	Hs.25450	NM_004955	6p21.1-p21.2	Cluster Incl. U81375:Human placental equilibrative nucleoside transporter 1 (hENT1) mRNA, complete cds /cds=(178,1548) /gb=U81375 /gi=1845344 /ug=Hs.25450 /len=2162	33901_at
OS-9(amplified in osteosarcoma)	U41635	Hs.76228	NM_006812	12	Cluster Incl. U41635:Human OS-9 precurosor mRNA, complete cds /cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736	36996_at
TIP47(cargo selection protein (mannose 6 phosphate receptor binding protein))	AF057140	Hs.140452	NM_005817	19	Cluster Incl. AF057140:Homo sapiens cargo selection protein TIP47 (TIP47) mRNA, complete cds /cds=(74,1378) /gb=AF057140 /gi=3095185 /ug=Hs.140452 /len=1974	40169_at
AF053356-CDS2(hypothetical protein AF053356-CDS2)	AF053356	Hs.296336	NM_022574	7	Cluster Incl. AF053356:Homo sapiens chromosome 7q22 sequence /cds=(253,1275) /gb=AF053356 /gi=3135305 /ug=Hs.91299 /len=1638	38831_f_at

CS (citrate synthase)	AF047042	Hs.239760	NM_004077	12p11-qter	Cluster Incl. AF047042:Homo sapiens citrate synthase mRNA, complete cds /cds=(0,1400) /gb=AF047042 /gi=3288814 /ug=Hs.239760 /len=1401	41314_at
ATP5I (ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e)	AA426364	Hs.85539	NM_007100	4p	Cluster Incl. AA426364:zv61b06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-758099 /clone_end=3 /gb=AA426364 /gi=2106690 /ug=Hs.85539 /len=401	38751_i_at
KIAA0233(KIAA0233 gene product)	D87071	Hs.79077	NM_014745	16	Cluster Incl. D87071:Human mRNA for KIAA0233 gene, complete cds /cds=(2,6109) /gb=D87071 /gi=1510142 /ug=Hs.79077 /len=6368	37281_at
UQCRFS1 (ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1)	L32977	Hs.3712	NM_006003	19q12-q13	Cluster Incl. L32977:Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRFS1) gene /cds=(90,914) /gb=L32977 /gi=488298 /ug=Hs.3712 /len=1203	34401_at

PSMB7 (proteasome (prosome, macropain) subunit, beta type, 7)	D38048	Hs.118065	NM_002799	9q34.11-q34.12	D38048 /FEATURE= /DEFINITION=D38048 Human mRNA for proteasome subunit z, complete cds	1313_at
YWHAE (tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide)	U54778	Hs.79474	NM_006761	17p13.3	U54778 /FEATURE= /DEFINITION=HSU54778 Human 14-3-3 epsilon mRNA, complete cds	1011_s_at
SMARCA4 (SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4)	U29175	Hs.78202	NM_003072	19p13.2	Cluster Incl. U29175:Human transcriptional activator (BRG1) mRNA, complete cds /cds=(78,5021) /gb=U29175 /gi=902045 /ug=Hs.78202 /len=5247	32579_at
CANX (calnexin)	L10284	Hs.155560	NM_001746	5q35	Cluster Incl. L10284:Homo sapiens integral membrane protein, calnexin, (IP90) mRNA, complete cds /cds=(89,1867) /gb=L10284 /gi=186522 /ug=Hs.155560 /len=4117	40125_at
LIMK2 (LIM domain kinase 2)	AC002073	Hs.278027	NM_005569	22q12.2	Cluster Incl. AC002073:Human PAC clone DJ515N1 from 22q11.2-q22 /cds=(0,2201) /gb=AC002073 /gi=2078469	38618_at

					/ug=Hs.100623 /len=2202	
CAPN4(calpain 4)	X04106	Hs.74451	NM_001749		Cluster Incl. X04106:Human mRNA for calcium dependent protease (small subunit) /cds=(158,964) /gb=X04106 /gi=35327 /ug=Hs.74451 /len=1478	36138_at
DF (D component of complement (adipsin))	M84526	Hs.155597	NM_001928	19	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	40282_s_at
CSF3R (colony stimulating factor 3 receptor (granulocyte))	M59818	Hs.2175	NM_000760	1p35-p34.3	Cluster Incl. M59818:Human granulocyte colony-stimulating factor receptor (G-CSFR-1) mRNA, complete cds /cds=(169,2679) /gb=M59818 /gi=183046 /ug=Hs.2175 /len=2943	34223_at
TNFRSF7 (tumor necrosis factor receptor superfamily, member 7)	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928	38578_at

					/gi=180084 /ug=Hs.180841 /len=1204	
TRB@ (T cell receptor beta locus)	M12886	Hs.303157		7q35	M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	1105_s_at
KIAA0275(KIAA0275 gene product)	D87465	Hs.74583	NM_014767	10	Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(316,1590) /gb=D87465 /gi=1665814 /ug=Hs.74583 /len=5316	36155_at
TGFBR3 (transforming growth factor, beta receptor III (betaglycan, 300kD))	L07594	Hs.79059	NM_003243	1p33-p32	L07594 /FEATURE= /DEFINITION=HUMTGFB3C Human transforming growth factor-beta type III receptor (TGF-beta) mRNA, complete cds	1897_at
IGHM (immunoglobulin heavy constant mu)	X58529	Hs.302063		14q32.33	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480	41166_at

					/ug=Hs.179543 /len=2325	
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
TCL1A (T-cell leukemia/lymphoma 1A)	X82240	Hs.2484	NM_021966	14q32.1	Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=(45,389) /gb=X82240 /gi=624960 /ug=Hs.2484 /len=1312	39318_at
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	41796_at
PFTK1 (PFTAIRE protein kinase 1)	AB020641	Hs.57856	NM_012395	7q21-q22	Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641	36502_at

						/gi=4240156 /ug=Hs.57856 /len=4957	
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33		Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41165_g_at
CBX7 (chromobox homolog 7)	AL031846			22q13.1		Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796	7		Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
BLK (B lymphoid tyrosine kinase)	S76617 /	Hs.2243	NM_001715	8p23-p22		S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]	854_at

CD79A (CD79A antigen (immunoglobulin-associated alpha))	U05259	Hs.79630	NM_001783	19q13.2	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107	38017_at
DGKA (diacylglycerol kinase, alpha (80kD))	X62535	Hs.172690	NM_001345	12q13.3	Cluster Incl. X62535:H.sapiens mRNA for diacylglycerol kinase /cds=(103,2310) /gb=X62535 /gi=30822 /ug=Hs.172690 /len=2564	32716_at
CD19 (CD19 antigen)	M28170	Hs.96023	NM_001770	16p11.2	M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	1096_g_at
SH3BP5 (SH3-domain binding protein 5 (BTK-associated))	AB005047	Hs.109150	NM_004844	1q43	Cluster Incl. AB005047:Homo sapiens mRNA for SH3 binding protein, complete cds /cds=(63,1340) /gb=AB005047 /gi=3116213 /ug=Hs.109150 /len=2570	38968_at
KIAA0226(KIAA0226 gene product)]	D86979	Hs.141296		3	Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(622,2877) /gb=D86979 /gi=1504031	31802_at

					/ug=Hs.141296 /len=5891	
NIFU(nitrogen fixation cluster-like)	U47101	Hs.9908		12	Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819	39165_at
NCOA3 (nuclear receptor coactivator 3	AF012108	Hs.225977	NM_006534	20q12	Cluster Incl. AF012108:Homo sapiens Amplified in Breast Cancer (AIB1) mRNA, complete cds /cds=(200,4462) /gb=AF012108 /gi=2331249 /ug=Hs.225977 /len=6818	33381_at
LEF1 (lymphoid enhancer-binding factor 1)	AL049409	Hs.44865	NM_016269	4q23-q25	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	36021_at
SIAT1 (sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase))	X62822	Hs.2554	NM_003032	3q27-q28	Cluster Incl. X62822:H.sapiens gene encoding beta-galactoside alpha-2,6-sialyltransferase /cds=(310,1530)	41352_at

					/gb=X62822 /gi=29433 /ug=Hs.2554 /len=2699	
BLNK (B-cell linker)	AF068180	Hs.167746		10q23.2-q23.33	Cluster Incl. AF068180:Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds /cds=(153,1523) /gb=AF068180 /gi=3406748 /ug=Hs.167746 /len=1790	38242_at
SIAT1 (sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase))	W30677	Hs.2554	NM_003032	3q27-q28	Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614	34871_at
PSCD1 (pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1)	M85169	Hs.1050	NM_004762	17q25	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	38666_at
LOC54103(hypothetical protein)	AL079277	Hs.12969		7	Cluster Incl. AL079277:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605 /cds=(0,806)	41710_at

					/gb=AL079277 /gi=5102581 /ug=Hs.12969 /len=1414	
	U23852				Cluster Incl. U23852:Human T-lymphocyte specific protein tyrosine kinase p56lck (lck) abberant mRNA, complete cds /cds=(59,1150) /gb=U23852 /gi=775207 /ug=Hs.1765 /len=2129	33238_at
KIAA0922(KIAA0922 protein)	AB023139	Hs.37892	NM_015196	4	Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505	39929_at
	AL049471				Cluster Incl. AL049471:Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012) /cds=UNKNOWN /gb=AL049471 /gi=4500266 /ug=Hs.12702 /len=2905	41690_at
ISG20 (interferon stimulated gene (20kD))	U88964	Hs.183487	NM_002201	15q26	Cluster Incl. U88964:Human HEM45 mRNA, complete cds /cds=(37,582)	33304_at

SYNE-2(synaptic nuclei expressed gene 2)	AL080133	Hs.57749	NM_015180	14	Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	/gb=U88964 /gi=2062679 /ug=Hs.183487 /len=701	41815_at
SETBP1 (SET binding protein 1)	AB022660	Hs.151717	NM_015559	18q21.1	Cluster Incl. AB022660:Homo sapiens mRNA for SET-binding protein (SEB), complete cds /cds=(5,4633) /gb=AB022660 /gi=5478317 /ug=Hs.151717 /len=5744		34990_at
FLJ10140(hypothetical protein FLJ10140)]	AL031588	Hs.250671	NM_018006	22	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438		41660_at

SIT(SHP2 interacting transmembrane adaptor)	AJ010059:	Hs.88012	NM_014450	9	Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010059 /gi=4688891 /ug=Hs.88012 /len=1232	40723_at
SYNE-1B(synaptic nuclear envelope 1)	AB018339	Hs.8182		6	Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
HLA-DOB (major histocompatibility complex, class II, DO beta)	X03066:	Hs.1802	NM_002120	6p21.3	Cluster Incl. X03066:Human mRNA for HLA-D class II antigen DO beta chain /cds=(56,877) /gb=X03066 /gi=32271 /ug=Hs.1802 /len=1322	38570_at
POU2AF1 (POU domain, class 2, associating factor 1)	Z49194	Hs.2407	NM_006235	11q23.1	Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407 /len=3301	36239_at
EZH1 (enhancer of zeste (Drosophila) homolog 1)	AB002386	Hs.194669		17q21.1-q21.3	Cluster Incl. AB002386:Human mRNA for KIAA0388 gene, complete cds /cds=(100,2343) /gb=AB002386	32259_at

					/gi=2224716 /ug=Hs.194669 /len=4606	
SP140(nuclear body protein Sp140)	U36500	Hs.309943	NM_007237	2	Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173653 /ug=Hs.85283 /len=3252	40700_at
MTMR1 (myotubularin related protein 1)	AJ224979	Hs.23200		xq28	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200 /len=2582	34654_at
KIAA0640(SWAP-70 protein	AB014540	Hs.153026		11	Cluster Incl. AB014540:Homo sapiens mRNA for KIAA0640 protein, partial cds /cds=(0,1812) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824	31869_at
CCR7 (chemokine (C-C motif) receptor 7)	L31584	Hs.1652	NM_001838	17q12-q21.2	L31584 /FEATURE=exon /DEFINITION=HUMEBI103 Human G protein-coupled receptor (EBI 1) gene	1097_s_at

					exon 3, complete cds	
SCAP1 (src family associated phosphoprotein 1)	Y11215	Hs.19126	NM_003726	17q21.3	Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524	38862_at
IL24 (interleukin 24)	AA214546	Hs.315463	NM_006850	1q32	Cluster Incl. AA214546:zr92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516	41847_at
ABLIM (actin binding LIM protein)	D31883	Hs.158203	NM_002313	10q25	Cluster Incl. D31883:Human mRNA for KIAA0059 gene, complete cds /cds=(221,1609) /gb=D31883 /gi=505093 /ug=Hs.158203 /len=6754	40155_at
JAK1 (Janus kinase 1 (a protein tyrosine kinase))	AL039831	Hs.50651	NM_002227	1p32.3-p31.3	Cluster Incl. AL039831:DKFZp434D1112_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5866713 /ug=Hs.50651	34877_at

					/len=579	
TLK1 (tousled-like kinase 1)	D50927	Hs.18895	NM_012290	8p22-p12	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927 /gi=1469196 /ug=Hs.18895 /len=4454	32219_at
MGEA5 (meningioma expressed antigen 5 (hyaluronidase))	AB014579	Hs.5734	NM_012215	10q24.1-q24.3	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303	35317_at
AIF1 (allograft inflammatory factor 1)	Y14768	Hs.76364	NM_001623	6p21.3	Cluster Incl. Y14768:Homo sapiens DNA, cosmid clones TN62 and TN82 /cds=(10,744) /gb=Y14768 /gi=3805800 /ug=Hs.890 /len=896	40729_s_at
KIAA0430(KIAA0430 gene product)	AB007890			16	Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=(0,3172) /gb=AB007890 /gi=2887438	31936_s_at

					/ug=Hs.166163 /len=6011	
LCK (lymphocyte-specific protein tyrosine kinase)	M36881	Hs.1765	NM_005356	1p35-p34.3	M36881 /FEATURE=mRNA /DEFINITION=HUMLCKAA Human lymphocyte-specific protein tyrosine kinase (lck) mRNA, complete cds	2059_s_at
GPR18 (G protein-coupled receptor 18)	L42324	Hs.88269		13q32	L42324 /FEATURE=cds /DEFINITION=HUMFRCG Homo sapiens (clone GPCR W) G protein-linked receptor gene (GPCR) gene, 5 end of cds	253_g_at
TC21(oncogene TC21)	AI365215	Hs.206097	NM_012250	11	Cluster Incl. AI365215:qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2029426 /clone_end=3 /gb=AI365215 /gi=4124904 /ug=Hs.206097 /len=918	32827_at
	AI434146				Cluster Incl. AI434146:ti36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2132604 /clone_end=3 /gb=AI434146 /gi=4294137 /ug=Hs.164284 /len=299	36403_s_at

AKAP11 (A kinase (PRKA) anchor protein 11)	AB014529	Hs.232076	NM_016248	13q12.2-13q14.3	Cluster Incl. AB014529:Homo sapiens mRNA for KIAA0629 protein, partial cds /cds=(0,1840) /gb=AB014529 /gi=3327071 /ug=Hs.232076 /len=5883	34657_at
IL4R (interleukin 4 receptor)	X52425	Hs.75545	NM_000418	16p11.2-12.1	X52425 /FEATURE=mRNA /DEFINITION=HSIL4R Human IL-4-R mRNA for the interleukin 4 receptor	404_at
ARHH (ras homolog gene family, member H)	Z35227	Hs.109918	NM_004310	4p13	Cluster Incl. Z35227:H.sapiens TTF mRNA for small G protein /cds=(579,1154) /gb=Z35227 /gi=609016 /ug=Hs.109918 /len=1427	37416_at
E2F5 (E2F transcription factor 5, p130-binding)	U31556	Hs.2331	NM_001951	8p22-q21.3	U31556 /FEATURE= /DEFINITION=HSU31556 Human transcription factor E2F-5 mRNA, complete cds	1044_s_at
TOSO(regulator of Fas-induced apoptosis)]	AF057557	Hs.58831	NM_005449	1	Cluster Incl. AF057557:Homo sapiens anti-Fas-induced apoptosis (TOSO) mRNA, complete cds /cds=(19,1191)	32967_at

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E2F5 (E2F transcription factor 5, p130-binding)	U31556	Hs.2331	NM_001951	8p22-q21.3	Cluster Incl. U31556:Human transcription factor E2F-5 mRNA, complete cds /cds=(38,1075) /gb=U31556 /gi=939728 /ug=Hs.2331 /len=1728	41275_at
PIR121(p53 inducible protein)	L47738	Hs.258503		5	Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881	37579_at
KIAA0543(KIAA0543 protein)	AB011115	Hs.98507		7	Cluster Incl. AB011115:Homo sapiens mRNA for KIAA0543 protein, partial cds /cds=(0,3336) /gb=AB011115 /gi=3043609 /ug=Hs.98507 /len=6443	41077_at
KIAA0769(KIAA0769 gene product)]	AB018312	Hs.19056	NM_014824	11	Cluster Incl. AB018312:Homo sapiens mRNA for KIAA0769 protein, complete cds /cds=(239,2293) /gb=AB018312	32224_at

					/gi=3882258 /ug=Hs.19056 /len=4326	
	AB023183	Hs.52463	Hs.52463	10	Cluster Incl. AB023183:Homo sapiens mRNA for KIAA0966 protein, complete cds /cds=(166,3564) /gb=AB023183 /gi=4589575 /ug=Hs.52463 /len=4924	36089_at
PRDM2 (PR domain containing 2, with ZNF domain)	D45132	Hs.26719	NM_012231	1p36	D45132 /FEATURE= /DEFINITION=HUMHOXY1 Homo sapiens mRNA for zinc-finger DNA-binding protein, complete cds	316_g_at
BCL2 (B-cell CLL/lymphoma 2)	M14745	Hs.79241	NM_000633	18q21.3	M14745 /FEATURE= /DEFINITION=HUMBCL2C Human bcl-2 mRNA	1909_at
KIAA0239(KIAA0239 protein)	D87076	Hs.9729	NM_015288	5	Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,1716) /gb=D87076 /gi=1510152 /ug=Hs.9729 /len=5630	38342_at

DKFZP434L243(DKFZP434L243 protein	AL080140	Hs.21695		3	Cluster Incl. AL080140:Homo sapiens mRNA; cDNA DKFZp434L243 (from clone DKFZp434L243) /cds=(0,2137) /gb=AL080140 /gi=5262585 /ug=Hs.21695 /len=2662	34220_at
IFI41 (interferon-induced protein 41, 30kD)	L22342	Hs.241510	NM_004509		Cluster Incl. L22342:Human nuclear phosphoprotein mRNA, complete cds /cds=(0,746) /gb=L22342 /gi=402204 /ug=Hs.38125 /len=835	35718_at
SLC23A1 (solute carrier family 23 (nucleobase transporters), member 1)	D87075	Hs.82042	NM_005116	20p13	Cluster Incl. D87075:Human mRNA for KIAA0238 gene, partial cds /cds=(0,992) /gb=D87075 /gi=1510150 /ug=Hs.82042 /len=5608	38122_at
PPP2R5C (protein phosphatase 2, regulatory subunit B (B56), gamma isoform)	U37352	Hs.171734	NM_002719	3p21	Cluster Incl. U37352:Human protein phosphatase 2A Balpha1 regulatory subunit mRNA, complete cds /cds=(88,1632) /gb=U37352 /gi=1203811 /ug=Hs.171734 /len=4064	40786_at

MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))	AB023208	Hs.181002	NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
GG2-1(TNF-induced protein)	AF099935	Hs.17839	NM_014350	5	Cluster Incl. AF099935:Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds /cds=(84,680) /gb=AF099935 /gi=3860092 /ug=Hs.17839 /len=1897	33243_at
CBLB (Cas-Br-M (murine) ectropic retroviral transforming sequence b)	U26710	Hs.3144	NM_004351	3p13-q13.2	Cluster Incl. U26710:Human cbl-b mRNA, complete cds /cds=(322,3270) /gb=U26710 /gi=862406 /ug=Hs.3144 /len=3969	35632_at
E2F5 (E2F transcription factor 5, p130-binding)	U15642	Hs.2331	NM_001951	8p22-q21.3	U15642 /FEATURE= /DEFINITION=HSU15642 Human transcription factor E2F-5 mRNA, complete cds	1639_s_at
GGA2(Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2)	AB029003	Hs.155546	NM_015044	16	Cluster Incl. AB029003:Homo sapiens mRNA for KIAA1080 protein, partial cds	40278_at

containing, ARF-binding protein 2)					/cds=(0,1554) /gb=AB029003 /gi=5689496 /ug=Hs.155546 /len=4791	
KIAA0240(KIAA0240 protein)]	D87077	Hs.196275		6	Cluster Incl. D87077:Human mRNA for KIAA0240 gene, partial cds /cds=(0,2953) /gb=D87077 /gi=1510154 /ug=Hs.196275 /len=6060	38892_at
KIAA0542(KIAA0542 gene product)	AB011114	Hs.62209		22	Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, complete cds /cds=(393,3299) /gb=AB011114 /gi=3043607 /ug=Hs.62209 /len=5280	36545_s_at
DKFZP586F2423(hypothetical protein DKFZp586F2423)	AL080209:	Hs.13659		7	Cluster Incl. AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4241	39692_at
GPR18 (G protein-coupled receptor 18)	L42324	Hs.88269		13q32	L42324 /FEATURE=cds /DEFINITION=HUMFRCG Homo sapiens (clone GPCR W) G protein-linked receptor	252_at

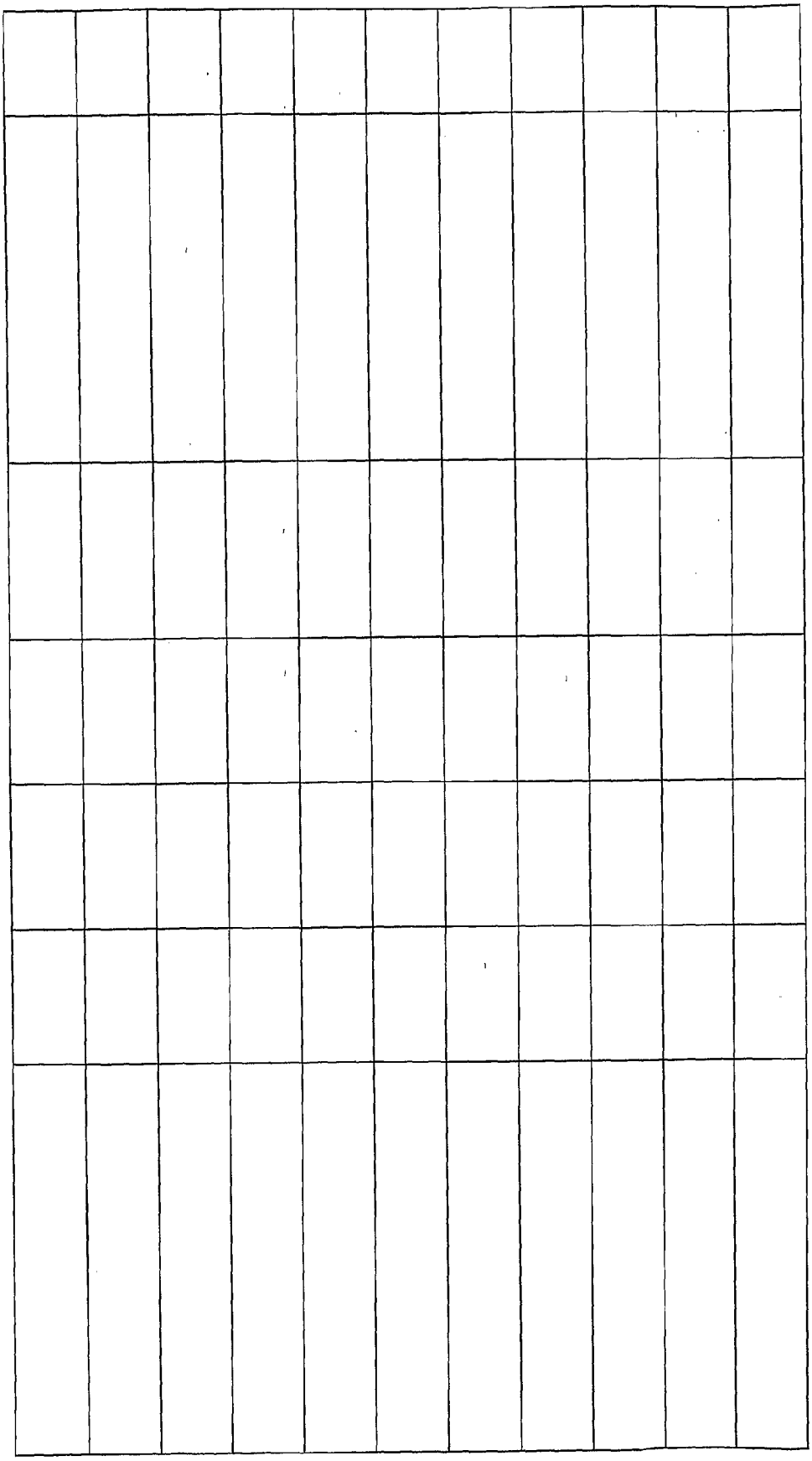
					gene (GPCR) gene, 5 end of cds	
LIG1 (ligase I, DNA, ATP-dependent)	AL039458	Hs.4193		3p14	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N0910 /clone_end=3 /gb=AL039458 /gi=5408506 /ug=Hs.4193 /len=849	34800_at
KIAA0136(DNA segment, Chr 16, Johns Hopkins University 32, expressed)	D50926	Hs.70359		21q22.13	Cluster Incl. D50926:Human mRNA for KIAA0136 gene, partial cds /cds=(0,2854) /gb=D50926 /gi=1469194 /ug=Hs.70359 /len=4197	36845_at
SGF3G (interferon-stimulated transcription factor 3, gamma (48kD))	M87503	Hs.1706	NM_006084	14q11.2	Cluster Incl. M87503:Human IFN-responsive transcription factor subunit mRNA, complete cds /cds=(34,1215) /gb=M87503 /gi=184652 /ug=Hs.1706 /len=1584	38517_at

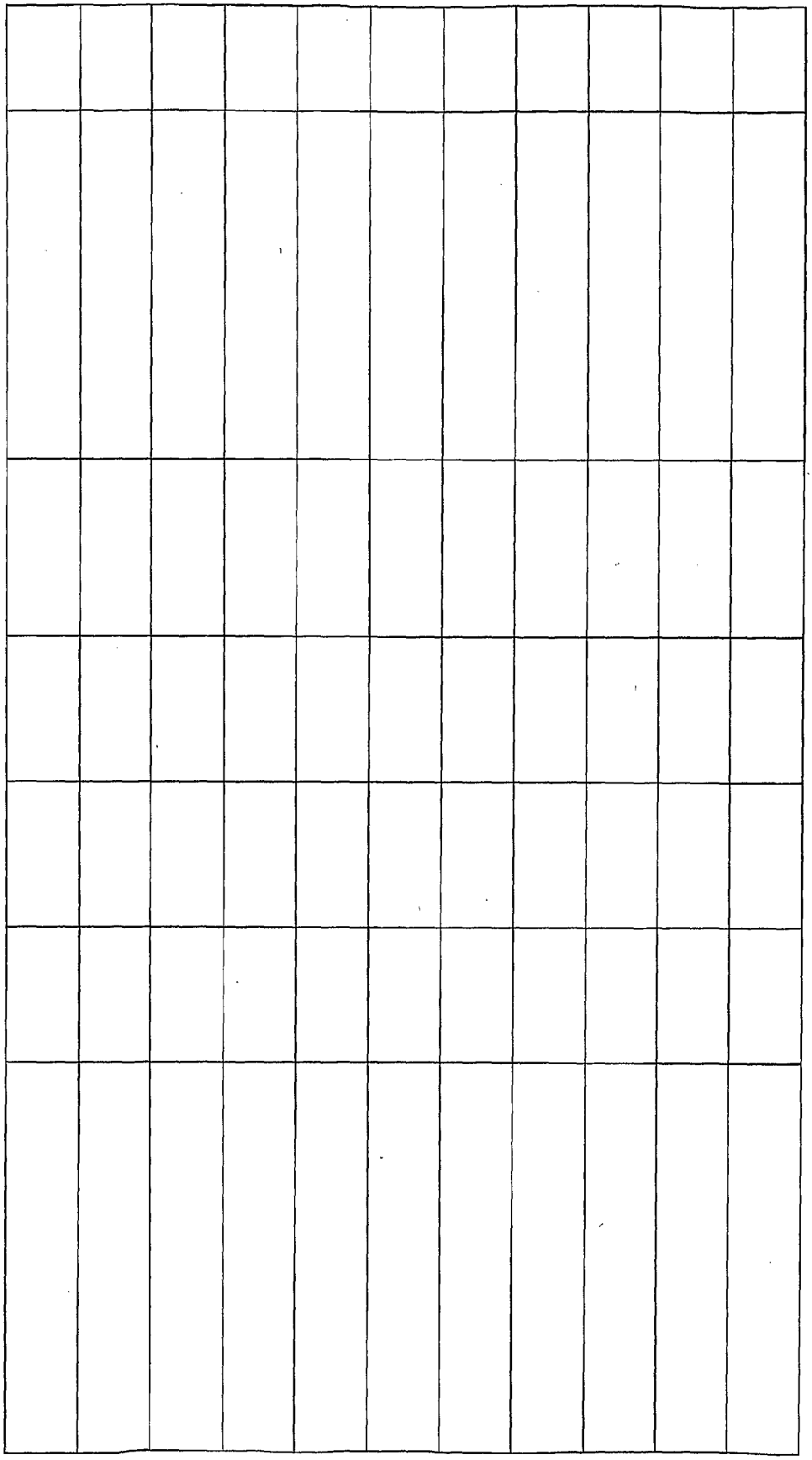
KIAA0441(KIAA0441 gene product)	AB007901			6	Cluster Incl. AB007901:Homo sapiens KIAA0441 mRNA, complete cds /cds=(168,2261) /gb=AB007901 /gi=2662162 /ug=Hs.32511 /len=5597	39658_at
P2Y10(putative purinergic receptor)	AF000545	Hs.296433	NM_014499	X	AF000545 /FEATURE=cds /DEFINITION=HSAF000545 Homo sapiens putative purinergic receptor P2Y10 gene, complete cds	358_at
PPP3CC (protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma))	S46622	Hs.75206	NM_005605	8	Cluster Incl. S46622:calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] /cds=(286,1794) /gb=S46622 /gi=258000 /ug=Hs.75206 /len=2134	32541_at
MGC12335(hypothetical protein MGC12335)	AL022724	Hs.97411	NM_032744	6	Cluster Incl. AL022724:Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs /cds=(94,861) /gb=AL022724 /gi=4468306	34043_at

					/ug=Hs.97411 /len=1037	
SP100 (nuclear antigen Sp100)	M60618	Hs.77617	NM_003113	2q37.1	Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complete cds /cds=(31,1473) /gb=M60618 /gi=178688 /ug=Hs.77617 /len=1879	37352_at
KIAA0746(KIAA0746 protein)]	AB018289	Hs.49500		4	Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein, partial cds /cds=(0,3091) /gb=AB018289 /gi=3882212 /ug=Hs.49500 /len=4086	41585_at
RBL2 (retinoblastoma-like 2 (p130))	X76061	Hs.79362	NM_005611	16q12.2	Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835	32597_at
APOC4 (apolipoprotein C-IV)	U32576	Hs.110675	NM_001646	19q13.2	Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, complete cds /cds=(40,423) /gb=U32576	34454_r_at

					/gi=975892 /ug=Hs.110675 /len=613	
STK10 (serine/threonine kinase 10)	AB015718	Hs.16134	NM_005990	5q35.1	Cluster Incl. AB015718:Homo sapiens lok mRNA for protein kinase, complete cds /cds=(50,2956) /gb=AB015718 /gi=4001687 /ug=Hs.16134 /len=4221	40420_at
MAP3K5 (mitogen-activated protein kinase kinase kinase 5)	U67156	Hs.151988	NM_005923	6q22.33	U67156 /FEATURE= /DEFINITION=HSU67156 Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds	1327_s_at
PRKCB1 (protein kinase C, beta 1)	X07109	Hs.77202	NM_002738	16p11.2	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II /NOTE=replacement of probe set 1216_at	160029_at
BIRC3 (baculoviral IAP repeat-containing 3)	U45878	Hs.127799	NM_001165	11q22	U45878 /FEATURE= /DEFINITION=HSU45878 Human inhibitor of apoptosis protein 1 mRNA, complete cds	1717_s_at

SLC7A6 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 6)	D87432	Hs.10315	NM_003983	16q22.1-q22.3	Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(261,1808) /gb=D87432 /gi=1665758 /ug=Hs.10315 /len=6296	39533_at
KIAA1093(KIAA1093 protein)	AB029016	Hs.117333		22	Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial cds /cds=(0,3613) /gb=AB029016 /gi=5689522 /ug=Hs.117333 /len=4159	37487_at





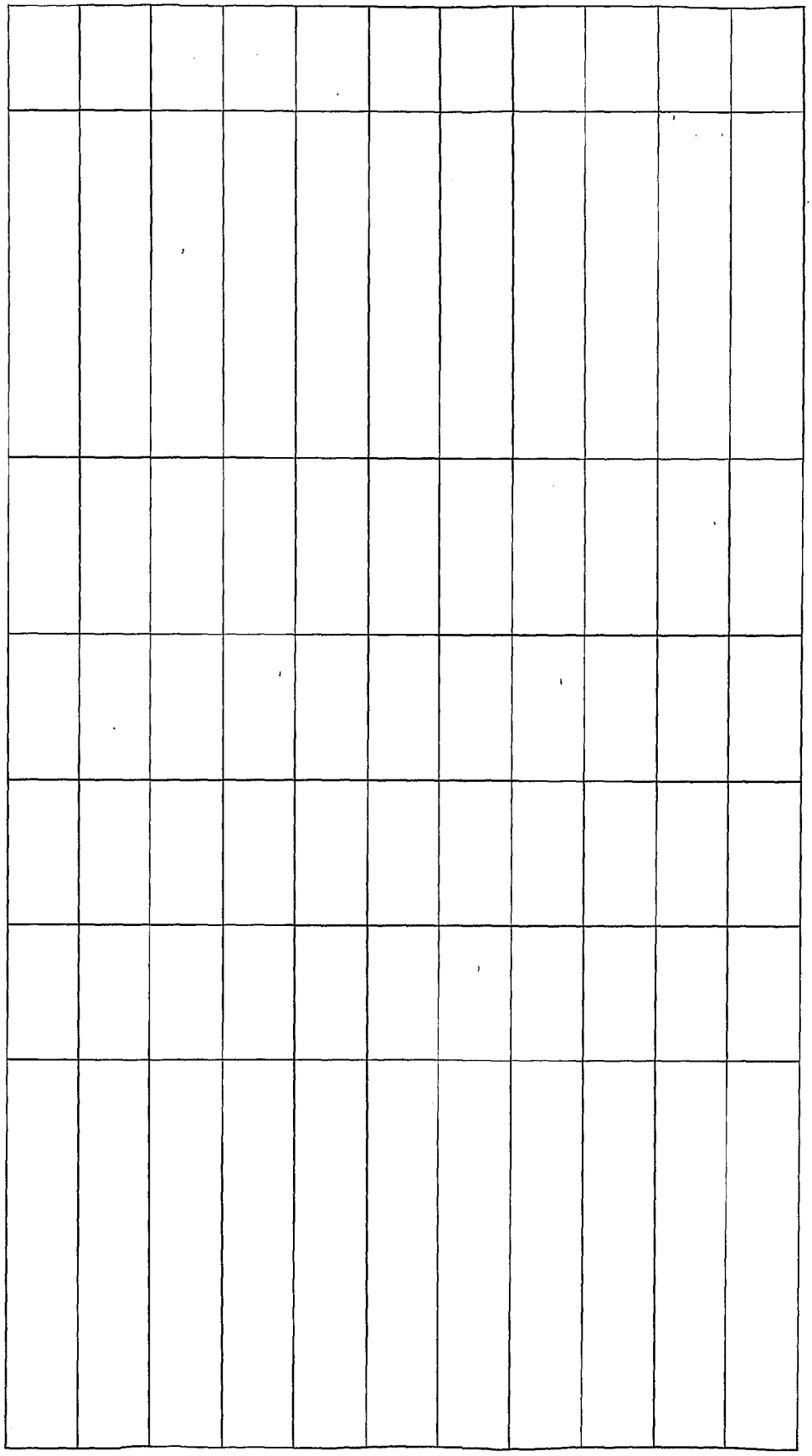


Table 10:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
GATA2 (GATA-binding protein 2)	M77810	Hs.334695	NM_002050	3q21	M77810 /FEATURE= /DEFINITION=HUMGATA2A Human transcription factor GATA-2 (GATA-2) mRNA, complete cds	1072_g_at
MYL6 (myosin, light polypeptide 6, alkali, smooth muscle and non-muscle)	M22919	Hs.77385	NM_021019	12	Cluster Incl. M22919:Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds /cds=(42,353) /gb=M22919 /gi=189016 /ug=Hs.77385 /len=1259	33994_g_at
PRG2 (proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein))	Z26248	Hs.99962	NM_002728	11q12	Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=940510 /ug=Hs.99962 /len=1637	39179_at

					/ug=Hs.99962 /len=1637	
CLC (Charot-Leyden crystal protein)	L01664	Hs.132004	NM_013246	11q13.3	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	36809_at
ST7 (suppression of tumorigenicity 7)	W02490	Hs.301974	NM_013437	8q22.2-q23.1	Cluster Incl. W02490:za48b02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-295755 /clone_end=5 /gb=W02490 /gi=1274488 /ug=Hs.5814 /len=623	40039_g_at
TTF2 (transcription termination factor, RNA polymerase II)	AF073771	Hs.142157	NM_003594	1p22	Cluster Incl. AF073771:Homo sapiens RNA polymerase II termination factor mRNA, complete cds /cds=(20,3508) /gb=AF073771 /gi=3702845 /ug=Hs.142157 /len=3591	37870_at
TALDO1 (transaldolase 1)	AF010400	Hs.77290	NM_006755	11p15.5-p15.4	Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400	37311_at

					/gi=2612878 /ug=Hs.77290 /len=1242	
PGD (phosphogluconate dehydrogenase)	U30255	Hs.75888	NM_002631	1p36.3-p36.13	Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324 /ug=Hs.75888 /len=1536	36963_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	U34995	Hs.169476	NM_002046	12p13	Cluster Incl. U34995:Human normal keratinocyte substraction library mRNA, clone H22a, complete sequence /cds=UNKNOWN /gb=U34995 /gi=1497857 /ug=Hs.195188 /len=1626	35905_s_at
RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin))	X55988	Hs.728	NM_002934	14q24-q31	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	36766_at
ICA1 (islet cell autoantigen 1 (69kD))	U38260	Hs.167927	NM_004968	7p22	Cluster Incl. U38260:Human islet cell autoantigen ICAp69 mRNA, complete cds /cds=(169,942) /gb=U38260 /gi=1675205	32634_s_at

					/ug=Hs.167927 /len=1415	
M6PR (mannose-6-phosphate receptor (cation dependent))	X56253	Hs.75709	NM_002355	12p13	Cluster Incl. X56253:Human MPR46 gene for 46kd mannose 6-phosphate receptor /cds=(168,1001) /gb=X56253 /gi=34727 /ug=Hs.75709 /len=2455	32547_at
GCDH (glutaryl-Coenzyme A dehydrogenase)	AD000092	Hs.184141	NM_000159	19p13.2	AD000092 /FEATURE=cds#4 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence	1749_at
ACTB (actin, beta)	X00351	Hs.288061	NM_001101	7p15-p12	Homo sapiens /REF=X00351 /DEF=Human mRNA for beta-actin /LEN=1761 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HSAC0
PMS2L11 (postmeiotic segregation increased 2-like 11)	U38980	Hs.306174		7q	U38980 /FEATURE= /DEFINITION=U38980 Human PMS2	179_at

like 11)					related (hPMSR6) mRNA, complete cds	
NCF4 (neutrophil cytosolic factor 4 (40kD))	AL008637	Hs.196352	NM_000631	22q13.1	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136	38894_g_at
CSF2RB (colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage))	AL008637	Hs.285401	NM_000395	22q13.1	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136	
TMSB4X (thymosin, beta 4, X chromosome)	M17733	Hs.75968	NM_021109	xq21.3-q22	Cluster Incl. M17733:Human thymosin beta-4 mRNA, complete cds /cds=(77,211)	31557_at

					/gb=M17733 /gi=339688 /ug=Hs.75968 /len=556	
MTX1 (metaxin 1)	U46920	Hs.247551	NM_002455	1q21	Cluster Incl. U46920:Human metaxin (MTX) gene, complete cds /cds=(0,953) /gb=U46920 /gi=1326107 /ug=Hs.181246 /len=1065	40890_at
	AA524802				Cluster Incl. AA524802:nh33h11.s1 Homo sapiens cDNA /clone=IMAGE-954213 /gb=AA524802 /gi=2265730 /ug=Hs.203907 /len=500	32877_i_at
CFL1 (cofilin 1 (non-muscle))	X95404	Hs.180370	NM_005507	11q13	Cluster Incl. X95404:H.sapiens mRNA for non-muscle type cofilin /cds=(51,551) /gb=X95404 /gi=1177470 /ug=Hs.180370 /len=1059	33659_at
DEFA1 (defensin, alpha 1, myeloid-related sequence)	AL036554	Hs.274463	NM_004084	8p23.2-p23.1	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5	31793_at

					/gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	AI126134	Hs.100000	NM_002964	1q21	Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at
	AC005764				Cluster Incl. AC005764:Homo sapiens chromosome 19, cosmid R31343 /cds=(0,1262) /gb=AC005764 /gi=3694626 /ug=Hs.126496 /len=1263	35512_at
DAPK2 (death-associated protein kinase 2)	AF052941	Hs.129208	NM_014326	15	Cluster Incl. AF052941:Homo sapiens DAP-kinase related protein 1 mRNA, complete cds /cds=(31,1143) /gb=AF052941 /gi=3560542 /ug=Hs.129208 /len=1742	34912_at
DEFA3 (defensin, alpha 3, neutrophil-specific)	L12691	Hs.294176	NM_005217	8pter-p23.3	Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364	31506_s_at

					/ug=Hs.178741 /len=452	
MTHFS (5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase))	L38928	Hs.118131	NM_006441	15	Cluster Incl. L38928:Homo sapiens 5,10-methenyltetrahydrofolate synthetase mRNA, complete cds /cds=(13,624) /gb=L38928 /gi=886296 /ug=Hs.118131 /len=857	39064_at
B2M (beta-2-microglobulin)	V00567	Hs.75415	NM_004048	15q21-q22.2	V00567 /FEATURE=cds /DEFINITION=HSMGLO Human messenger RNA fragment for the beta-2 microglobulin	428_s_at
ACTB (actin, beta)	X00351	Hs.288061	NM_001101	7p15-p12	Homo sapiens /REF=X00351 /DEF=Human mRNA for beta-actin /LEN=1761 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HSAC0
ADAM8 (a disintegrin and metalloproteinase domain 8)	D26579	Hs.86947	NM_001109	10q26.3	Cluster Incl. D26579:Homo sapiens mRNA for transmembrane protein, complete cds /cds=(9,2483) /gb=D26579 /gi=1864004	40712_at

					/ug=Hs.86947 /len=3236	
CHRNE (cholinergic receptor, nicotinic, epsilon polypeptide)	X66403	Hs.278295	NM_000080	17p13-p12	Cluster Incl. X66403:H.sapiens mRNA for acetylcholine receptor (epsilon subunit) /cds=(11,1492) /gb=X66403 /gi=560152 /ug=Hs.112028 /len=2457	39834_at
BRCA1 (breast cancer 1, early onset)	L78833	Hs.194143	NM_007294	17q21	L78833 /FEATURE=exon#36 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds	605_at
OAZ1 (ornithine decarboxylase antizyme 1)	D78361	Hs.125078		19p13.3	D78361 /FEATURE= /DEFINITION=HUMODAZ Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2	1315_at
DOC2B (double C2-like domains, beta)	D70830	Hs.54402	NM_003585	17	Cluster Incl. D70830:Homo sapiens mRNA for Doc2 beta, complete cds /cds=(160,1398) /gb=D70830 /gi=1235721 /ug=Hs.54402 /len=2043	32422_at

LIG3 (ligase III, DNA, ATP-dependent)	X84740	Hs.100299	NM_002311	17q11.2-q12	Cluster Incl. X84740:H.sapiens mRNA for DNA ligase III /cds=(333,3101) /gb=X84740 /gi=860962 /ug=Hs.100299 /len=3400	41099_at
S100A9 (S100 calcium-binding protein A9 (calgranulin B))	W72424	Hs.112405	NM_002965	1q21	Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	41471_at
MPB1 (MYC promoter-binding protein 1)	M55914	Hs.284127	NM_005945	1pter-p35	M55914 /FEATURE= /DEFINITION=HUMCMYCQ Human c-myc binding protein (MBP-1) mRNA, complete cds	2035_s_at
MAD (MAX dimerization protein)	L06895	Hs.109012	NM_002357	2p13-p12	L06895 /FEATURE= /DEFINITION=HUMMAD Homo sapiens antagonizer of myc transcriptional activity (Mad) mRNA, complete cds	1774_at

GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGA
RAB31 (RAB31, member RAS oncogene family)	U59877	Hs.223025	NM_006868	18p11.3	Cluster Incl. U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds /cds=(60,644) /gb=U59877 /gi=1388194 /ug=Hs.223025 /len=907	33371_s_at
ABCC5 (ATP-binding cassette, sub-family C (CFTR/MRP), member 5)	U83661	Hs.108660	NM_005688	3q27	U83661 /FEATURE= /DEFINITION=HSU83661 Homo sapiens multidrug resistance protein 5 (MRP5) mRNA, complete cds	1933_g_at
PABPC2 (poly(A)-binding protein, cytoplasmic 2)	Z48501	Hs.172182			Cluster Incl. Z48501:H.sapiens mRNA for polyadenylate binding protein II /cds=(0,1568) /gb=Z48501 /gi=693936 /ug=Hs.172182 /len=1569	31951_s_at

HBB (hemoglobin, beta)	L48215	Hs.155376	NM_000518	11p15.5	Cluster Incl. L48215:Homo sapiens beta-globin (HBB) gene, with a to c allele 28 bp 5 to exon 1, (J00179 bases 61971-63802) /cds=(50,493) /gb=L48215 /gi=1066772 /ug=Hs.155376 /len=626	32052_at
P8(nuclear proten 1)	W47047	Hs.8603	NM_012385	16	Cluster Incl. W47047:zc38g10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-324642 /clone_end=5 /gb=W47047 /gi=1331686 /ug=Hs.166194 /len=441	36423_at
	M64936				M64936 /FEATURE= /DEFINITION=HUMRIRT Homo sapiens retinoic acid-inducible endogenous retroviral DNA	1090_f_at
	M64936				Cluster Incl. M64936:Homo sapiens retinoic acid-inducible endogenous retroviral DNA /cds=UNKNOWN /gb=M64936 /gi=337422 /ug=Hs.55322 /len=3307	36727_at

Human BRCA2 region	U50534	Hs.181304	NM_023037	13	U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence CG003	1529_at
	AL049675				Cluster Incl. AL049675:Human gene from PAC 886K2, chromosome 1 /cds=UNKNOWN /gb=AL049675 /gi=4678768 /ug=Hs.15535 /len=1074	32048_at
CAMK2B (calcium/calmodulin-dependent protein kinase (CaM kinase) II beta)	AF112471	Hs.4884	NM_001220	7p14.3-p14.1	Cluster Incl. AF112471:Homo sapiens calcium/calmodulin-dependent protein kinase II beta subunit mRNA, alternatively spliced, complete cds /cds=(46,1599) /gb=AF112471 /gi=4139267 /ug=Hs.4884 /len=1750	34847_s_at
HBB (hemoglobin, beta)	M25079	Hs.155376	NM_000518	11p15.5	Cluster Incl. M25079:Human sickle cell beta-globin mRNA, complete cds /cds=(0,443) /gb=M25079 /gi=179408 /ug=Hs.234764 /len=468	31687_f_at

HSPC022(HSPC022 protein)	W68830	Hs.301175	NM_014029	22	Cluster Incl. W68830:zd37g06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-342874 /clone_end=5 /gb=W68830 /gi=1377739 /ug=Hs.173466 /len=614	32736_at
B2M (beta-2-microglobulin)	AB021288	Hs.75415	NM_004048	15q21-q22.2	Cluster Incl. AB021288:Homo sapiens mRNA for beta 2-microglobulin, complete cds /cds=(13,372) /gb=AB021288 /gi=4038732 /ug=Hs.75415 /len=925	34644_at
HMG17 (high-mobility group (nonhistone chromosomal) protein 17)	X13546	Hs.181163	NM_005517	1p36.1	Cluster Incl. X13546:Human HMG-17 gene for non-histone chromosomal protein HMG-17 /cds=(107,379) /gb=X13546 /gi=32328 /ug=Hs.181163 /len=1198	41231_f_at
GDF1 (growth differentiation factor 1)	M62302	Hs.336964	NM_001492	19p12	M62302 /FEATURE= /DEFINITION=HUMGDF1 Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds	887_at
EPX (eosinophil peroxidase)	X14346	Hs.46295	NM_000502	17q23.1	Cluster Incl. X14346:Human mRNA for eosinophil peroxidase /cds=(0,2108)	34587_at

					/gb=X14346 /gi=31182 /ug=Hs.46295 /len=2558	
VCL (vinculin)	M33308	Hs.75350	NM_003373	10q22.1-q23	Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102	36601_at
CLIC2 (chloride intracellular channel 2)	Y12696	Hs.54570	NM_001289	xq28	Cluster Incl. Y12696:H.sapiens mRNA homologous to the p64 bovine chloride channel peptide /cds=(221,952) /gb=Y12696 /gi=2584784 /ug=Hs.54570 /len=1219	40013_at
RPL41 (ribosomal protein L41)	Z12962	Hs.324406	NM_021104	12q	Homo sapiens /REF=Z12962 /DEF=Cluster Incl. :H.sapiens mRNA for homologue to yeast ribosomal protein L41 /cds=(83,160) /gb= /gi=36135 /ug=Hs.108124 /len=468 /LEN=468	32466_at
TNA (tetranectin (plasminogen-binding protein))	X64559	Hs.65424	NM_003278	3p22-p21.3	Cluster Incl. X64559:H.sapiens mRNA for tetranectin /cds=(93,701) /gb=X64559	36569_at

					/gi=37408 /ug=Hs.65424 /len=848	
MYC (v-myc avian myelocytomatosis viral oncogene homolog)	M13929	Hs.79070	NM_002467	8q24.12-q24.13	M13929 /FEATURE=mRNA /DEFINITION=HUMMYCPOA Human c-myc-P64 mRNA, initiating from promoter P0, (HLmyc2.5) partial cds	1827_s_at
FCGR2A (Fc fragment of IgG, low affinity IIa, receptor for (CD32))	M31932	Hs.78864	NM_021642	1q23	Cluster Incl. M31932:Human IgG low affinity Fc fragment receptor (FcRIIa) mRNA, complete cds /cds=(7,960) /gb=M31932 /gi=182473 /ug=Hs.78864 /len=2372	37687_i_at
RPS3A (ribosomal protein S3A)	M84711	Hs.77039	NM_001006	4q31.2-q31.3	M84711 /FEATURE= /DEFINITION=HUMFTE1A Human v-fos transformation effector protein (Fte-1), mRNA complete cds	1653_at
	H12458				H12458 /FEATURE= /DEFINITION=H12458 yj12d03.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148517 3 similar to	2090_i_at

						SP:WNT6_MOUSE P22727 WNT-6 PROTEIN ;, mRNA sequence	
IRF5 (interferon regulatory factor 5)	U51127	Hs.334450	NM_002200	7q32		U51127 /FEATURE= /DEFINITION=HSU51127 Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds	477_at
H3F3A (H3 histone, family 3A)	M11353	Hs.181307	NM_002107	1q41		M11353 /FEATURE= /DEFINITION=HUMHISH3C Human H3.3 histone class C mRNA, complete cds	254_at
MAPT (microtubule-associated protein tau)		Hs.101174	NM_005910	17q21.1		Microtubule-Associated Protein Tau, Alt. Splice 5, Exon 4a	331_at
CML1(kidney- and liver-specific gene)	AB013094	Hs.14637	NM_003960	2		Cluster Incl. AB013094:Homo sapiens TSC501 mRNA, complete cds /cds=(168,851) /gb=AB013094 /gi=3721765 /ug=Hs.14637 /len=960	38128_at

HCLS1 (hematopoietic cell-specific Lyn substrate 1)	X16663	Hs.14601	NM_005335	3q13	Cluster Incl. X16663:Human HS1 gene for heamatopoietic lineage cell specific protein /cds=(42,1502) /gb=X16663 /gi=32054 /ug=Hs.14601 /len=1950	31820_at
KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2)	U04270	Hs.188021	NM_000238	7q35-q36	Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) mRNA, complete cds /cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.188021 /len=4070	38858_at
FTL (ferritin, light polypeptide)	AL031670	Hs.111334	NM_000146	19q13.3-q13.4	Cluster Incl. AL031670:dJ681N20.2 (ferritin, light polypeptide-like 1) /cds=(200,727) /gb=AL031670 /gi=4469083 /ug=Hs.111334 /len=978	35083_at
ALOX5AP (arachidonate 5-lipoxygenase-activating protein)	AI806222	Hs.100194	NM_001629	13q12	Cluster Incl. AI806222:wf26e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2356746 /clone_end=3 /gb=AI806222 /gi=5392788 /ug=Hs.100194 /len=563	37099_at

MLLT7 (myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 7)	Y11284	Hs.239663	NM_005938	xq13.1	Cluster Incl. Y11284:Homo sapiens AFX1 gene, exon 1 (and joined CDS) /cds=(244,1758) /gb=Y11284 /gi=2879783 /ug=Hs.239663 /len=3162	36238_at
RPS4X (ribosomal protein S4, X-linked)	M58458	Hs.108124	NM_001007	xq13.1	Cluster Incl. M58458:Human ribosomal protein S4 (RPS4X) isoform mRNA, complete cds /cds=(35,826) /gb=M58458 /gi=337509 /ug=Hs.75344 /len=888	34643_at
TLN1 (talin 1)	AB028950	Hs.18420	NM_006289	9p13	Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027 protein, partial cds /cds=(0,5088) /gb=AB028950 /gi=5689390 /ug=Hs.18420 /len=5542	32166_at
BPHL (biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen))	X81372	Hs.7298	NM_004332	6p25	Cluster Incl. X81372:H.sapiens mRNA for biphenyl hydrolase-related protein /cds=(212,1036) /gb=X81372 /gi=984662 /ug=Hs.184552 /len=1508	40912_s_at
RPA2 (replication protein A2 (32kD))	J05249	Hs.79411	NM_002946	1p35	J05249 /FEATURE= /DEFINITION=HUMREPA Human	1119_at

					replication protein A 32-kDa subunit mRNA, complete cds	
NCF4 (neutrophil cytosolic factor 4 (40kD))	AL008637	Hs.196352	NM_000631	22q13.1	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136	38893_at
CAT (catalase)	AL035079	Hs.76359	NM_001752	11p13	Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079 /gi=4775614 /ug=Hs.76359 /len=2287	37009_at
	L43366				L43366 /FEATURE=mRNA /DEFINITION=HUMCADF Homo sapiens (clone jj1b) cadherin mRNA fragment	637_at
TKT (transketolase (Wernicke-Korsakoff syndrome))	L12711	Hs.89643	NM_001064	3p14.3	Cluster Incl. L12711:Homo sapiens transketolase (tk) mRNA, complete cds	38789_at

syndrome))					/cds=(98,1969) /gb=L12711 /gi=388890 /ug=Hs.89643 /len=2069	
STAT6 (signal transducer and activator of transcription 6, interleukin-4 induced)	U16031	Hs.181015	NM_003153	12q13	U16031 /FEATURE= /DEFINITION=HSU16031 Human transcription factor IL-4 Stat mRNA, complete cds	845_at
PLOD (procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI))	L06419	Hs.75093	NM_000302	1p36.3-p36.2	Cluster Incl. L06419:Homo sapiens lysyl hydroxylase (PLOD) mRNA, complete cds /cds=(200,2383) /gb=L06419 /gi=190073 /ug=Hs.75093 /len=3115	36184_at
LRP3 (low density lipoprotein receptor-related protein 3)	AB009462	Hs.143641	NM_002333	19q13.1	Cluster Incl. AB009462:Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds /cds=(226,2538) /gb=AB009462 /gi=3413957 /ug=Hs.143641 /len=2601	31815_r_at
BLCAP (bladder cancer associated protein)	AL049288	Hs.5300	NM_006698	20q11.2-q12	Cluster Incl. AL049288:Homo sapiens mRNA; cDNA DKFZp564M053 (from clone DKFZp564M053) /cds=UNKNOWN	35267_g_at

						/gb=AL049288 /gi=4500049 /ug=Hs.5300 /len=2018	
WBSCR1 (Williams-Beuren syndrome chromosome region 1)	D26068	Hs.180900	NM_022170	7q11.23		Cluster Incl. D26068:Human mRNA for KIAA0038 gene, partial cds /cds=(0,694) /gb=D26068 /gi=436225 /ug=Hs.180900 /len=2477	41212_r_at
PPP6C (protein phosphatase 6, catalytic subunit)	X92972	Hs.80324	NM_002721	xq22.3		Cluster Incl. X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21,936) /gb=X92972 /gi=5701862 /ug=Hs.80324 /len=1292	37581_at
UNRIP(unr-interacting protein)	AB024327	Hs.3727	NM_007178	12		Cluster Incl. AB024327:Homo sapiens pt-wd mRNA for WD-40 repeat protein, complete cds /cds=(300,1352) /gb=AB024327 /gi=4519416 /ug=Hs.3727 /len=1850	34402_at
EP300 (E1A binding protein p300)	U01877	Hs.25272	NM_001429	22q13.2		Cluster Incl. U01877:Human p300 protein mRNA, complete cds /cds=(1199,8443) /gb=U01877 /gi=495300 /ug=Hs.25272	33896_at

					/len=9046	
DKFZP434D1335(DKFZP434D1335 protein)	AI920820	Hs.8258		19	Cluster Incl. AI920820:wn82e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2452362 /clone_end=3 /gb=AI920820 /gi=5656784 /ug=Hs.8258 /len=519	38400_at
GCGR (glucagon receptor)	L20316	Hs.208	NM_000160	17q25	Cluster Incl. L20316:Human glucagon receptor mRNA, complete cds /cds=(277,1710) /gb=L20316 /gi=405189 /ug=Hs.208 /len=2034	32886_at
KIAA0842(KIAA0842 protein)	AB020649	Hs.74569		1	Cluster Incl. AB020649:Homo sapiens mRNA for KIAA0842 protein, partial cds /cds=(0,3062) /gb=AB020649 /gi=4240172 /ug=Hs.74569 /len=3896	36150_at
USP7 (ubiquitin specific protease 7 (herpes virus-associated))	Z72499	Hs.78683	NM_003470	16p13.3	Cluster Incl. Z72499:H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP) /cds=(199,3507) /gb=Z72499 /gi=1545951 /ug=Hs.78683	37672_at

					/len=4022	
UGTREL7(UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter)	D87449	Hs.82635	NM_015139	1	Cluster Incl. D87449:Human mRNA for KIAA0260 gene, partial cds /cds=(0,1153) /gb=D87449 /gi=1665786 /ug=Hs.82635 /len=5918	37888_at
MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))	AB023208	Hs.181002	NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
PPP1R8 (protein phosphatase 1, regulatory (inhibitor) subunit 8)	U14575	Hs.78961	NM_002713	1p35	Cluster Incl. U14575:Human (ard-1) mRNA, complete cds /cds=(935,1318) /gb=U14575 /gi=559771 /ug=Hs.78961 /len=2401	37705_at
LNK(linker of T-cell receptor pathways)	AF055581	Hs.13131	NM_005475	12	Cluster Incl. AF055581:Homo sapiens adaptor protein Lnk mRNA, complete cds /cds=(357,2084) /gb=AF055581	39428_at

					/gi=3845720 /ug=Hs.13131 /len=5403	
DYRK1A (dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A)	D86550	Hs.75842	NM_001396	21q22.13	D86550 /FEATURE= /DEFINITION=D86550 Human mRNA for serine/threonine protein kinase, complete cds	1512_at
ZNF24 (zinc finger protein 24 (KOX 17))	AF016052	Hs.183593	NM_006965	18q12	Cluster Incl. AF016052:Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds /cds=(165,1271) /gb=AF016052 /gi=2394173 /ug=Hs.183593 /len=2976	33306_at
FLJ11126(hypothetical protein FLJ11126)	AA034074	Hs.226396	NM_018332	16	Cluster Incl. AA034074:zi06c05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-429992 /clone_end=5 /gb=AA034074 /gi=1505901 /ug=Hs.226396 /len=655	33394_at
EIF2S3 (eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD))	L19161	Hs.211539	NM_001415	xp22.2-p22.1	Cluster Incl. L19161:Human translation initiation factor eIF-2 gamma subunit mRNA, complete cds /cds=(0,1418) /gb=L19161 /gi=306899 /ug=Hs.211539	35934_at

					/len=1440	
UBE2N (ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13))	D83004	Hs.75355	NM_003348	12	D83004 /FEATURE= /DEFINITION=D83004 Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds	1660_at
RNF6 (ring finger protein (C3H2C3 type) 6)	AJ010346	Hs.32597	NM_005977	13q12.2	Cluster Incl. AJ010346:Homo sapiens mRNA for RING-H2 protein RNF6, alternative exon 1a /cds=(360,2417) /gb=AJ010346 /gi=4583651 /ug=Hs.32597 /len=3503	35656_at
KIAA0138(KIAA0138 gene product)	D50928	Hs.159384	NM_014649	19	Cluster Incl. D50928:Human mRNA for KIAA0138 gene, complete cds /cds=(36,2897) /gb=D50928 /gi=1469198 /ug=Hs.159384 /len=3233	32099_at
FGFR1 (fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome))	X66945	Hs.748	NM_000604	8p11.2-p11.1	X66945 /FEATURE=cds /DEFINITION=HSNSAMTK H.sapiens N-	424_s_at

related tyrosine kinase 2, Pfeiffer syndrome))					sam mRNA for fibroblast growth factor receptor	
C6orf5 (chromosome 6 open reading frame 5)	AL050289	Hs.7446	NM_015524	6q21	Cluster Incl. AL050289:Homo sapiens mRNA; cDNA DKFZp586G0522 (from clone DKFZp586G0522) /cds=(179,1876) /gb=AL050289 /gi=4886510 /ug=Hs.7446 /len=2364	36139_at
EP300 (E1A binding protein p300)	U01877	Hs.25272	NM_001429	22q13.2	U01877 /FEATURE= /DEFINITION=HSU01877 Human p300 protein mRNA, complete cds	551_at
BRAP (BRCA1 associated protein)	AL042733	Hs.122764	NM_006768	12q24	Cluster Incl. AL042733:DKFZp434B2222_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434B2222 /clone_end=3 /gb=AL042733 /gi=5422182 /ug=Hs.30982 /len=782	41512_at
TGFBR2 (transforming growth factor, beta receptor II (70-80kD))	D50683	Hs.82028	NM_003242	3p22	D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens	1814_at

receptor II (70-80kD))					mRNA for TGF-betaIIR alpha, complete cds	
KIAA0553(KIAA0553 protein)	AB011125	Hs.105749		17	Cluster Incl. AB011125:Homo sapiens mRNA for KIAA0553 protein, partial cds /cds=(0,3289) /gb=AB011125 /gi=3043629 /ug=Hs.105749 /len=5574	38668_at
TGFBR2 (transforming growth factor, beta receptor II (70-80kD))	D50683	Hs.82028	NM_003242	3p22	D50683 /FEATURE= /DEFINITION=D50683 Homo sapiens mRNA for TGF-betaIIR alpha, complete cds	1815_g_at
SFPQ (splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated))	X70944	Hs.180610	NM_005066	1pter-p32.3	Cluster Incl. X70944:H.sapiens mRNA for PTB-associated splicing factor /cds=(85,2208) /gb=X70944 /gi=38457 /ug=Hs.180610 /len=3071	40638_at
CHRAC17(DNA polymerase epsilon, subunit 3)	AF070640	Hs.108112	NM_017443	9	Cluster Incl. AF070640:Homo sapiens clone 24781 mRNA sequence /cds=UNKNOWN /gb=AF070640	38702_at

					/gi=3283913 /ug=Hs.108112 /len=1583	
SF3B4 (splicing factor 3b, subunit 4, 49kD)	L35013	Hs.25797	NM_005850	1q12-q21	Cluster Incl. L35013:Human spliceosomal protein (SAP 49) gene, complete cds /cds=(0,1274) /gb=L35013 /gi=556216 /ug=Hs.25797 /len=1275	33909_at
COL6A2 (collagen, type VI, alpha 2)	M20777	Hs.159263		21q22.3	Cluster Incl. M20777:Homo sapiens, alpha-2 (VI) collagen /cds=UNKNOWN /gb=M20777 /gi=180910 /ug=Hs.159263 /len=1005	32098_at
GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))	M63904	Hs.73797	NM_002068	19p13.3	Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	40365_at
KIAA0602(KIAA0602 protein)	AB011174	Hs.37656		14	Cluster Incl. AB011174:Homo sapiens mRNA for KIAA0602 protein, partial cds /cds=(0,2889) /gb=AB011174 /gi=3043727 /ug=Hs.37656 /len=3428	34406_at

KIAA0997(KIAA0997 protein)	AI970189	Hs.24083	NM_014950	14	Cluster Incl. AI970189:wr08d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2480929 /clone_end=3 /gb=AI970189 /gi=5767015 /ug=Hs.24083 /len=659	34751_at
TAF2I (TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD)	X83928	Hs.83126	NM_005643	6	X83928 /FEATURE=cds /DEFINITION=HSTAFII28 H.sapiens mRNA for transcription factor TFIID subunit TAFII28	131_at
MGC4175(hypothetical protein MGC4175)	AI656421	Hs.322404	NM_024315	7	Cluster Incl. AI656421:tt50h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2244259 /clone_end=3 /gb=AI656421 /gi=4740400 /ug=Hs.5671 /len=566	41809_at
RY1(putative nucleic acid binding protein RY-1)	X76302	Hs.54649		2	Cluster Incl. X76302:H.sapiens RY-1 mRNA for putative nucleic acid binding protein /cds=(0,493) /gb=X76302 /gi=431952 /ug=Hs.54649 /len=1402	35286_r_at
CDKN1A (cyclin-dependent kinase inhibitor 1A (p21, Cip1))	U03106	Hs.179665	NM_000389	6p21.2	U03106 /FEATURE= /DEFINITION=HSU03106 Human wild-	2031_s_at

(p21, Cip1))					type p53 activated fragment-1 (WAF1) mRNA, complete cds	
WEE1 (wee1+ (S. pombe) homolog)	W28575	Hs.75188	NM_003390	11p15.3-p15.1	Cluster Incl. W28575:51f12 Homo sapiens cDNA /gb=W28575 /gi=1308730 /ug=Hs.8151 /len=906	38102_at
KIAA0143(KIAA0143 protein)	D63477	Hs.84087		8	Cluster Incl. D63477:Human mRNA for KIAA0143 gene, partial cds /cds=(0,2658) /gb=D63477 /gi=1469867 /ug=Hs.84087 /len=5286	38472_at
SLBP (stem-loop (histone) binding protein)	U75679	Hs.75257	NM_006527	4p16.3	Cluster Incl. U75679:Human histone stem-loop binding protein (SLBP) mRNA, complete cds /cds=(115,927) /gb=U75679 /gi=1732076 /ug=Hs.75257 /len=1725	36913_at
KRN1 (keratin, cuticle, ultrahigh sulphur 1)	X63755	Hs.2743	NM_005553	11q13.5	Cluster Incl. X63755:H.sapiens mRNA for high-sulphur keratin /cds=(238,747) /gb=X63755 /gi=32471 /ug=Hs.2743 /len=1024	34555_at

COPB (coatomer protein complex, subunit beta)	X82103	Hs.3059	NM_016451	11pter-p15.5	Cluster Incl. X82103:H.sapiens mRNA for beta-COP /cds=(0,911) /gb=X82103 /gi=620109 /ug=Hs.3059 /len=1183	34326_at
TAF2I (TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD)	X83928	Hs.83126	NM_005643	6	Cluster Incl. X83928:H.sapiens mRNA for transcription factor TFIID subunit TAFII28 /cds=(92,727) /gb=X83928 /gi=791056 /ug=Hs.83126 /len=925	38426_at
ZFX (zinc finger protein, X-linked)	X59739	Hs.2074	NM_003410	xp21.3	Cluster Incl. X59739:Human ZFX mRNA for put. transcription activator, isoform 2 /cds=(78,2492) /gb=X59739 /gi=38021 /ug=Hs.2074 /len=5527	38931_at
GOLPH1 (golgi phosphoprotein 1)	AF020762	Hs.6831	NM_022735	1q41	Cluster Incl. AF020762:Homo sapiens clone 1400 unknown protein mRNA, partial cds /cds=(0,805) /gb=AF020762 /gi=2738926 /ug=Hs.6831 /len=1319	36827_at
PTP4A2 (protein tyrosine phosphatase type IVA, member 2)	U14603	Hs.82911	NM_003479	1p35	Cluster Incl. U14603:Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence /cds=(423,926)	38415_at

					/gb=U14603 /gi=894158 /ug=Hs.82911 /len=1526	
KIAA0863(KIAA0863 protein)	AB020670	Hs.131915	NM_014913	18	Cluster Incl. AB020670:Homo sapiens mRNA for KIAA0863 protein, complete cds /cds=(185,3580) /gb=AB020670 /gi=4240214 /ug=Hs.131915 /len=4313	37837_at
UBE2D3 (ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5))	U39318	Hs.118797	NM_003340	4q24-q26	Cluster Incl. U39318:Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds /cds=(45,488) /gb=U39318 /gi=1145690 /ug=Hs.118797 /len=724	39083_at
NTPBP(XPA binding protein 1; putative ATP(GTP)-binding protein)	AJ010842	Hs.18259	NM_007266	2	Cluster Incl. AJ010842:Homo sapiens mRNA for putative ATP(GTP)-binding protein, partial /cds=(0,1077) /gb=AJ010842 /gi=3646129 /ug=Hs.18259 /len=1722	41756_at

UBE2N (ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13))	D83004	Hs.75355	NM_003348	12	Cluster Incl. D83004:Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds /cds=(63,521) /gb=D83004 /gi=1181557 /ug=Hs.75355 /len=1203	36604_at
NCOR2 (nuclear receptor co-repressor 2)	U37146	Hs.287994	NM_006312	12q24	Cluster Incl. U37146:Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds /cds=(495,4982) /gb=U37146 /gi=1045654 /ug=Hs.120980 /len=5970	39358_at
LGALS2 (lectin, galactoside-binding, soluble, 2 (galectin 2) (NOTE: redefinition of symbol))	AL022315	Hs.113987	NM_006498	22q13.1	Cluster Incl. AL022315:dJ1177I5.3 (Lectin, Galactose-binding, soluble, 2 (Galectin 2, S-Lac Lectin 2, HL14)) /cds=(80,478) /gb=AL022315 /gi=3820991 /ug=Hs.113987 /len=494	37456_at
ERPROT213-21(protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein)	U94836	Hs.6430	NM_006387	19	Cluster Incl. U94836:Human ERPROT 213-21 mRNA, complete cds /cds=(88,2742) /gb=U94836 /gi=2058690	41836_at

endoplasmic reticulum protein)					/ug=Hs.6430 /len=4003	
FMR1 (fragile X mental retardation 1)	X69962	Hs.89764	NM_002024	xq27.3	Cluster Incl. X69962:H.sapiens FMR-1 mRNA /cds=(219,2117) /gb=X69962 /gi=296587 /ug=Hs.89764 /len=4362	37994_at
SUPV3L1 (suppressor of var1 (S.cerevisiae) 3-like 1)	AF042169	Hs.106469	NM_003171	10q22.1	Cluster Incl. AF042169:Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complete cds /cds=(0,2360) /gb=AF042169 /gi=2801554 /ug=Hs.106469 /len=2361	41408_at
NUFIP1 (nuclear fragile X mental retardation protein interacting protein 1)	AL049842	Hs.120247	NM_012345	13q14	Cluster Incl. AL049842:Human DNA sequence from clone 129L7 on chromosome 6q12-13. Contains the gene for a PUTATIVE novel protein, ESTs, an STS, GSSs and a taga repeat polymorphism /cds=(9,749) /gb=AL049842 /gi=5419768 /ug=Hs.120247 /len=1679	37518_at

GNE(UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase)	AJ238764	Hs.5920	NM_005476	9	Cluster Incl. AJ238764:Homo sapiens mRNA for UDP-N-acetylglucosamine-2-epimerase_/ N-acetylmannosamine kinase /cds=(41,2209) /gb=AJ238764 /gi=4775361 /ug=Hs.5920 /len=3649	36515_at
SAS10(disrupter of silencing 10)	AI126004	Hs.322901	NM_020368	4	Cluster Incl. AI126004:qc50e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1713070 /clone_end=3 /gb=AI126004 /gi=3594518 /ug=Hs.87627 /len=611	33150_at
UBE3A (ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome))	U84404	Hs.180686	NM_000462	15q11-q13	Cluster Incl. U84404:Human E6-associated protein E6-AP/ubiquitin-protein ligase (UBE3A) mRNA, alternatively spliced, complete cds /cds=(586,3144) /gb=U84404 /gi=1872513 /ug=Hs.180686 /len=3168	41205_at
TRAM(translocating chain-associating membrane protein)	X63679	Hs.4147	NM_014294	8	Cluster Incl. X63679:H.sapiens mRNA for TRAMP protein /cds=(121,1245) /gb=X63679 /gi=37264 /ug=Hs.4147	34796_at

					/len=1267	
PRCC (papillary renal cell carcinoma (translocation-associated))	X99720	Hs.9629	NM_005973	1q21.1	Cluster Incl. X99720:H.sapiens TPRC gene /cds=(212,1687) /gb=X99720 /gi=1869817 /ug=Hs.9629 /len=2053	39149_at
HBOA(histone acetyltransferase)	AI951946	Hs.21907	NM_007067	X	Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523	41338_at
SNRPA1 (small nuclear ribonucleoprotein polypeptide A')	X13482	Hs.80506	NM_003090	22q	Cluster Incl. X13482:Human mRNA for U2 snRNP-specific A protein /cds=(56,823) /gb=X13482 /gi=37546 /ug=Hs.80506 /len=1033	37585_at
ZFR(zinc finger RNA binding protein)	AI743507	Hs.173518	NM_016107	5	Cluster Incl. AI743507:wf72a06.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-2361106 /clone_end=3 /gb=AI743507 /gi=5111795 /ug=Hs.173518 /len=733	40610_at

RAGA(Ras-related GTP-binding protein)	U41654	Hs.57304	NM_006570	9	Cluster Incl. U41654:Human adenovirus protein E3-14.7k interacting protein 1 (FIP-1) mRNA, complete cds /cds=(243,1184) /gb=U41654 /gi=2058395 /ug=Hs.57304 /len=1610	35316_at
RAC1 (ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1))	D25274	Hs.173737	NM_006908	7p22	Cluster Incl. D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN /gb=D25274 /gi=464185 /ug=Hs.173737 /len=1232	40864_at
	AB015202				Cluster Incl. AB015202:Homo sapiens gene for hippocalcin /cds=(235,816) /gb=AB015202 /gi=4417205 /ug=Hs.114215 /len=1584	41602_at
PFDN4 (prefoldin 4)	U41816	Hs.91161	NM_002623	20q13	Cluster Incl. U41816:Human C-1 mRNA, complete cds /cds=(11,403) /gb=U41816 /gi=1620560 /ug=Hs.91161 /len=1203	41003_at
YY1 (YY1 transcription factor)	M77698	Hs.97496	NM_003403	14q	M77698 /FEATURE= /DEFINITION=HUMKRP Homo sapiens	891_at

					GLI-Krupple related protein (YY1) mRNA, complete cds	
REM(GTPase GES; REM protein)	AF084465	Hs.247729	NM_014012	20	Cluster Incl. AF084465:Homo sapiens Ras-like GTP-binding protein REM mRNA, complete cds /cds=(72,968) /gb=AF084465 /gi=3462895 /ug=Hs.87062 /len=976	34008_at
CLTC (clathrin, heavy polypeptide (Hc))	D21260	Hs.178710	NM_004859	17q11-qter	Cluster Incl. D21260:Human mRNA for KIAA0034 gene, complete cds /cds=(172,5199) /gb=D21260 /gi=434760 /ug=Hs.178710 /len=6111	41159_at
	AL049229				Cluster Incl. AL049229:Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone DKFZp564O1016) /cds=UNKNOWN /gb=AL049229 /gi=4499961 /ug=Hs.15787 /len=1767	32082_at
BAG5 (BCL2-associated athanogene 5)	AB020680	Hs.5443	NM_004873	14	Cluster Incl. AB020680:Homo sapiens mRNA for KIAA0873 protein, partial cds	36463_at

					/cds=(0,1400) /gb=AB020680 /gi=4240234 /ug=Hs.5443 /len=4119	
HSPA9B (heat shock 70kD protein 9B (mortalin-2))	L15189	Hs.3069	NM_004134	5q31.1	Cluster Incl. L15189:Homo sapiens mitochondrial HSP75 mRNA, complete cds /cds=(29,2068) /gb=L15189 /gi=292058 /ug=Hs.3069 /len=2131	41510_s_at
PPP2CA (protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform)	M60483	Hs.91773	NM_002715	5q23-q31	M60483 /FEATURE=mRNA /DEFINITION=HUMPP2AA Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds	237_s_at
TERF1 (telomeric repeat binding factor (NIMA-interacting) 1)	U74382	Hs.194562	NM_003218	8q13	U74382 /FEATURE= /DEFINITION=HSU74382 Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete cds	1329_s_at
KIAA0685(KIAA0685 gene product)	AI677689	Hs.296406	NM_014678	22	Cluster Incl. AI677689:wd33c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2329930 /clone_end=3 /gb=AI677689	40222_s_at

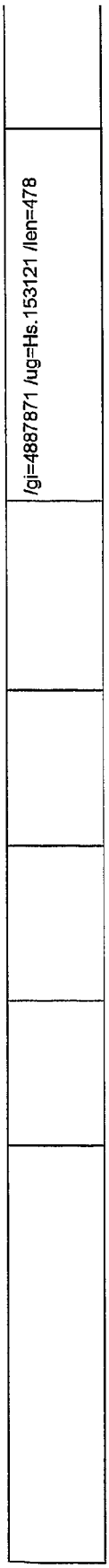

/gi=4887871 /ug=Hs.153121 /len=478

Table 11:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
NCOA1 (nuclear receptor coactivator 1	AJ000882	Hs.74002	NM_003743	2p23	Cluster Incl. AJ000882:Homo sapiens mRNA for steroid receptor coactivator 1e /cds=(201,4400) /gb=AJ000882 /gi=2924310 /ug=Hs.74002 /len=4709	36118_at
NCOA1 (nuclear receptor coactivator 1	U59302	Hs.74002	NM_003743	2p23	U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	484_at
FCGR2B (Fc fragment of IgG, low affinity IIb, receptor for (CD32)	M28696	Hs.278443	NM_004001	1q23	Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-RII) mRNA, complete cds /cds=(41,916) /gb=M28696 /gi=184843 /ug=Hs.233450	34663_at

					/len=1416		
RBL2 (retinoblastoma-like 2 (p130))	X76061	Hs.79362	NM_005611	16q12.2	Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835	32597_at	
	AI749193				Cluster Incl. AI749193:al40e04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2374494 /clone_end=3 /gb=AI749193 /gi=5127457 /ug=Hs.17639 /len=544	40623_at	
ITGB7 (integrin, beta 7	M68892	Hs.1741	NM_000889	12q13.13	M68892 /FEATURE= /DEFINITION=HUMINTB7 Human integrin beta-7 subunit mRNA, complete cds	2019_s_at	
ITGB7 (integrin, beta 7)	U50534	Hs.1741	NM_000889	12q13.13	U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence CG003	1529_at	

KIAA0476(KIAA0476 gene product	AB007945	Hs.6684	NM_014856	1	Cluster Incl. AB007945:Homo sapiens mRNA for KIAA0476 protein, complete cds /cds=(568,4728) /gb=AB007945 /gi=3413913 /ug=Hs.6684 /len=5525	35786_at
KIAA0240(KIAA0240 protein	D87077	Hs.196275		6	Cluster Incl. D87077:Human mRNA for KIAA0240 gene, partial cds /cds=(0,2953) /gb=D87077 /gi=1510154 /ug=Hs.196275 /len=6060	38892_at
UCP2 (uncoupling protein 2 (mitochondrial, proton carrier	U94592	Hs.80658	NM_003355	11q13	Cluster Incl. U94592:Human uncoupling protein homolog (UCPH) mRNA, complete cds /cds=(314,1243) /gb=U94592 /gi=2052354 /ug=Hs.80658 /len=1888	37591_at
ADAM19 (a disintegrin and metalloproteinase domain 19 (meltrin beta))	AL049415	Hs.278679	NM_023038	5q32-q33	Cluster Incl. AL049415:Homo sapiens mRNA; cDNA DKFZp586N2119 (from clone DKFZp586N2119) /cds=UNKNOWN /gb=AL049415 /gi=4500196 /ug=Hs.204290 /len=1232	33812_at

CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at
CD37 (CD37 antigen)	X14046	Hs.153053	NM_001774	19p13-q13.4	Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908) /gb=X14046 /gi=29793 /ug=Hs.153053 /len=1125	31870_at
IRF6 (interferon regulatory factor 6	AL022398	Hs.11801	NM_006147	1q32.3-q41	Cluster Incl. AL022398:dJ434O14.3.1 (putative protein) (isoform 1) /cds=(0,988) /gb=AL022398 /gi=3355547 /ug=Hs.87684 /len=1241	40721_g_at
KIAA1002(KIAA1002 protein	AB023219	Hs.20340			Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete cds /cds=(800,3322) /gb=AB023219 /gi=4589647 /ug=Hs.102483 /len=4331	41366_at
TGFBR3 (transforming growth factor, beta receptor III (betaglycan, 300kD)	L07594	Hs.79059	NM_003243	1p33-p32	L07594 /FEATURE= /DEFINITION=HUMTGFB3C Human	1897_at

receptor III (betaglycan, 300kD)					transforming growth factor-beta type III receptor (TGF-beta) mRNA, complete cds	
LAMA5 (laminin, alpha 5	AB011105	Hs.11669	NM_005560	20q13.2-q13.3	Cluster Incl. AB011105:Homo sapiens mRNA for KIAA0533 protein, partial cds /cds=(0,4939) /gb=AB011105 /gi=3043589 /ug=Hs.11669 /len=5117	41610_at
FLJ10140(hypothetical protein FLJ10140	AL031588	Hs.250671	NM_018006	22	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	41660_at
PRKCB1 (protein kinase C, beta 1	X07109	Hs.77202	NM_002738	16p11.2	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II /NOTE=replacement of probe set 1216_at	160029_at
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds	41796_at

					/cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	
C9ORF10(C9orf10 protein)	D80005	Hs.76666	NM_014612	9	Cluster Incl. D80005:Human mRNA for KIAA0183 gene, partial cds /cds=(0,3190) /gb=D80005 /gi=1136425 /ug=Hs.76666 /len=4905	37031_at
TMEM5 (transmembrane protein 5)	AB015633	Hs.112986		1	Cluster Incl. AB015633:Homo sapiens mRNA for type II membrane protein, complete cds, clone-HP10481 /cds=(104,1435) /gb=AB015633 /gi=4586843 /ug=Hs.112986 /len=1451	37445_at
TUCAN(tumor up-regulated CARD-containing antagonist of caspase nine)	AB023172			19	Cluster Incl. AB023172:Homo sapiens mRNA for KIAA0955 protein, complete cds /cds=(313,1608) /gb=AB023172 /gi=4589553 /ug=Hs.10031 /len=5059	41100_at
PFTK1 (PFTAIRE protein kinase 1	AB020641	Hs.57856	NM_012395	7q21-q22	Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641	36502_at

					/gi=4240156 /ug=Hs.57856 /len=4957	
IRF6 (interferon regulatory factor 6	AL022398	Hs.11801	NM_006147	1q32.3-q41	Cluster Incl. AL022398:dJ434O14.3.3 (novel protein) (isoform 3) /cds=(290,1885) /gb=AL022398 /gi=3355547 /ug=Hs.87684 /len=2058	40719_at
M17S2 (membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen	D30756	Hs.277721	NM_005899	17q21.1	Cluster Incl. D30756:Human mRNA for KIAA0049 gene, complete cds /cds=(140,3040) /gb=D30756 /gi=488500 /ug=Hs.233745 /len=4654	33444_at
DKFZP564K0822(hypothetical protein DKFZp564K0822	W25986	Hs.4750	NM_030796	7	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
KIAA0430(KIAA0430 gene produc	AB007890			16	Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=(0,3172) /gb=AB007890 /gi=2887438 /ug=Hs.166163 /len=6011	31936_s_at

KIAA1696(KIAA1696 protein)	N98667	Hs.106826	NM_016621	11	Cluster Incl. N98667:yy66d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-278505 /clone_end=5 /gb=N98667 /gi=1270089 /ug=Hs.106826 /len=549	39551_at
GABBR1 (gamma-aminobutyric acid (GABA) B receptor, 1	AJ225028	Hs.167017	NM_001470	6p21.3	Cluster Incl. AJ225028:Homo sapiens mRNA for GABA-B R1a receptor /cds=(234,3119) /gb=AJ225028 /gi=3892593 /ug=Hs.167017 /len=4434	32623_at
OGDH (oxoglutarate dehydrogenase (lipoamide)	D10523	Hs.168669	NM_002541	7p14-p13	Cluster Incl. D10523:Human mRNA for 2-oxoglutarate dehydrogenase, complete cds /cds=(57,3065) /gb=D10523 /gi=531240 /ug=Hs.168669 /len=4122	40470_at
CBX7 (chromobox homolog 7	AL031846			22q13.1	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at

SP140(nuclear body protein Sp140	U36500	Hs.309943	NM_007237	2	Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173653 /ug=Hs.85283 /len=3252	40700_at
13CDNA73(putative gene product	U50534	Hs.181304	NM_023037	13	U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence CG003	1530_g_at
SIAT1 (sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase	X62822	Hs.2554	NM_003032	3q27-q28	Cluster Incl. X62822:H.sapiens gene encoding beta-galactoside alpha-2,6-sialyltransferase /cds=(310,1530) /gb=X62822 /gi=29433 /ug=Hs.2554 /len=2699	41352_at
MAP3K5 (mitogen-activated protein kinase kinase kinase 5)	U67156	Hs.151988	NM_005923	6q22.33	U67156 /FEATURE= /DEFINITION=HSU67156 Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds	1327_s_at

KIAA0747(KIAA0747 protein)	AB018290	Hs.8309	NM_015292	12	Cluster Incl. AB018290:Homo sapiens mRNA for KIAA0747 protein, partial cds /cds=(0,3219) /gb=AB018290 /gi=3882214 /ug=Hs.8309 /len=4026	38424_at
PRKCB1 (protein kinase C, beta 1	X07109	Hs.77202	NM_002738	16p11.2	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II	1217_g_at
KIAA0274(KIAA0274 gene product	D87464	Hs.10037	NM_014845	6	Cluster Incl. D87464:Human mRNA for KIAA0274 gene, complete cds /cds=(124,2847) /gb=D87464 /gi=1665812 /ug=Hs.10037 /len=3010	41101_at
KIAA0660(ras-GTPase-activating protein (GAP<120>) SH3-domain-binding protein 2	AB014560	Hs.6727	NM_012297	4	Cluster Incl. AB014560:Homo sapiens mRNA for KIAA0660 protein, complete cds /cds=(120,1568) /gb=AB014560 /gi=3327133 /ug=Hs.6727 /len=4210	35793_at
FCER2 (Fc fragment of IgE, low affinity II, receptor for (CD23A)	M15059	Hs.1416	NM_002002	19p13.3	Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds (H107 epitope) /cds=(213,1178)	34960_g_at

						/gb=M15059 /gi=182447 /ug=Hs.1416 /len=1530	
HLA-DMB (major histocompatibility complex, class II, DM beta	U15085	Hs.1162	NM_002118	6p21.3		Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	41609_at
KIAA1093(KIAA1093 protein	AB029016	Hs.117333		22		Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial cds /cds=(0,3613) /gb=AB029016 /gi=5689522 /ug=Hs.117333 /len=4159	37487_at
IGHM (immunoglobulin heavy constant mu)	X58529	Hs.302063		14q32.33		Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325	41166_at
KIAA0649(KIAA0649 gene product	AB014549	Hs.26163	NM_014811	9		Cluster Incl. AB014549:Homo sapiens mRNA for KIAA0649 protein, complete cds /cds=(549,4178) /gb=AB014549	39580_at

					/gi=3327111 /ug=Hs.26163 /len=4932	
KIAA0494(KIAA0494 gene product	AB007963	Hs.62515	NM_014774	1	Cluster Incl. AB007963:Homo sapiens mRNA for KIAA0494 protein, complete cds /cds=(977,2464) /gb=AB007963 /gi=3413937 /ug=Hs.62515 /len=5766	41830_at
CLOCK (clock (mouse) homolog	AB002332	Hs.50722	NM_004898	4q12	Cluster Incl. AB002332:Human mRNA for KIAA0334 gene, complete cds /cds=(251,2791) /gb=AB002332 /gi=2224608 /ug=Hs.50722 /len=5715	36080_at
JIK(STE20-like kinase)	AA576724	Hs.12040	NM_016281	12	Cluster Incl. AA576724:nm81b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1074607 /clone_end=3 /gb=AA576724 /gi=2354198 /ug=Hs.12040 /len=580	41646_at
SETBP1 (SET binding protein 1)	AB022660	Hs.151717	NM_015559	18q21.1	Cluster Incl. AB022660:Homo sapiens mRNA for SET-binding protein (SEB), complete cds /cds=(5,4633) /gb=AB022660 /gi=5478317	34990_at

						/ug=Hs.151717 /len=5744	
STAT6 (signal transducer and activator of transcription 6, interleukin-4 induced	AF067575	Hs.181015	NM_003153	12q13		Cluster Incl. AF067575:untitled /cds=(21,2564) /gb=AF067575 /gi=3789867 /ug=Hs.181015 /len=3725	41222_at
DOC2B (double C2-like domains, beta)	D70830	Hs.54402	NM_003585	17		Cluster Incl. D70830:Homo sapiens mRNA for Doc2 beta, complete cds /cds=(160,1398) /gb=D70830 /gi=1235721 /ug=Hs.54402 /len=2043	32422_at
	AA868268					Cluster Incl. AA868268:ak40a05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1408400 /clone_end=3 /gb=AA868268 /gi=2963713 /ug=Hs.170267 /len=570	40574_at
	AB018272					Cluster Incl. AB018272:Homo sapiens mRNA for KIAA0729 protein, partial cds /cds=(0,3591) /gb=AB018272 /gi=3882178 /ug=Hs.180948 /len=4143	41218_at

TNFRSF7 (tumor necrosis factor receptor superfamily, member 7	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	38578_at
PLCG2 (phospholipase C, gamma 2 (phosphatidylinositol-specific	M37238	Hs.75648	NM_002661	16q24.1	M37238 /FEATURE=mRNA /DEFINITION=HUMPLC Human phospholipase C mRNA, complete cds	1085_s_at
	H24861				Cluster Incl. H24861:yl42e11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-160940 /clone_end=5 /gb=H24861 /gi=893760 /ug=Hs.90145 /len=517	33168_at
KIAA0543(KIAA0543 protein	AB011115	Hs.98507	H12985S1	7	Cluster Incl. AB011115:Homo sapiens mRNA for KIAA0543 protein, partial cds /cds=(0,3336) /gb=AB011115 /gi=3043609 /ug=Hs.98507 /len=6443	41077_at
HSD17B4 (hydroxysteroid (17-beta) dehydrogenase 4)	X87176	Hs.75441	NM_000414	5q21	Cluster Incl. X87176:H.sapiens mRNA for 17-beta-hydroxysteroid dehydrogenase /cds=(48,2258) /gb=X87176 /gi=1050516	36626_at

					/ug=Hs.75441 /len=2593	
TLK1 (tousled-like kinase 1)	D50927	Hs.18895	NM_012290	8p22-p12	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927 /gi=1469196 /ug=Hs.18895 /len=4454	32219_at
CASK (calcium/calmodulin-dependent serine protein kinase (MAGUK family)	AF035582	Hs.151469	NM_003688	xp11.4	Cluster Incl. AF035582:Homo sapiens CASK mRNA, complete cds /cds=(15,2708) /gb=AF035582 /gi=2661105 /ug=Hs.151469 /len=3919	31854_at
TRIAD3(TRIAD3 protein	AA650210	Hs.66228	NM_019011	7	Cluster Incl. AA650210:ns88b12.s1 Homo sapiens cDNA /clone=IMAGE-1190687 /gb=AA650210 /gi=2577538 /ug=Hs.116406 /len=528	37476_at
SCAP1 (src family associated phosphoprotein 1	Y11215	Hs.19126	NM_003726	17q21.3	Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524	38862_at

KIAA0746(KIAA0746 protein	AB018289	Hs.49500		4	Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein, partial cds /cds=(0,3091) /gb=AB018289 /gi=3882212 /ug=Hs.49500 /len=4086	41585_at
DKFZP586F2423(hypothetical protein DKFZp586F2423	AL080209	Hs.13659		7	Cluster Incl. AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4241	39692_at
DKFZP434C171(DKFZP434C171 protein	AL080169	Hs.209100	NM_015621	5	Cluster Incl. AL080169:Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171) /cds=(0,544) /gb=AL080169 /gi=5262637 /ug=Hs.209100 /len=2595	34183_at
ATRX (alpha thalassemia/mental retardation syndrome X-linked (RAD54 (S. cerevisiae) homolog)	U72936	Hs.96264	NM_000489	xq13.1-q21.1	Cluster Incl. U72936:Human putative DNA dependent ATPase and helicase (ATRX) mRNA, alternatively spliced product 1, complete cds /cds=(945,7811) /gb=U72936 /gi=1778306 /ug=Hs.96264	39147_g_at

					/len=10448	
MAPK3 (mitogen-activated protein kinase 3)	X60188	Hs.861		16p12-p11.2	X60188 /FEATURE=mRNA /DEFINITION=HSERK1 Human ERK1 mRNA for protein serine/threonine kinase	1000_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41165_g_at
	W30677				Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614	34871_at
AP1G2 (adaptor-related protein complex 1, gamma 2 subunit)	AI741833	Hs.8991	NM_003917	14q11.2-14q21.3	Cluster Incl. AI741833:wg29e04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2366526 /clone_end=3 /gb=AI741833 /gi=5110121 /ug=Hs.8991 /len=658	38798_s_at

CDC4L (cell division cycle 4-like)	M83822	Hs.62354		4	Cluster Incl. M83822:Human beige-like protein (BGL) mRNA, partial cds /cds=(0,5758) /gb=M83822 /gi=1580780 /ug=Hs.62354 /len=7332	35371_at
DKFZP564B116(DKFZP564B116 protein	AL050018	Hs.7387		6	Cluster Incl. AL050018:Homo sapiens mRNA; cDNA DKFZp564B116 (from clone DKFZp564B116) /cds=(0,1151) /gb=AL050018 /gi=4884085 /ug=Hs.7387 /len=2335	36875_at
CSK (c-src tyrosine kinase)	X59932	Hs.77793	NM_004383	15q23-q25	X59932 /FEATURE=mRNA /DEFINITION=HSCSRCKIN Human mRNA for C-SRC-kinase	1768_s_at
LOC54103(hypothetical protein	AL079277	Hs.12969		7	Cluster Incl. AL079277:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605 /cds=(0,806) /gb=AL079277 /gi=5102581 /ug=Hs.12969 /len=1414	41710_at

DKFZP586A0522(DKFZP586A0522 protein	AL050159	Hs.288771	NM_014033	12	Cluster Incl. AL050159:Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522) /cds=(0,732) /gb=AL050159 /gi=4884371 /ug=Hs.108740 /len=1846	38717_at
DGKA (diacylglycerol kinase, alpha (80kD)	X62535	Hs.172690	NM_001345	12q13.3	Cluster Incl. X62535:H.sapiens mRNA for diacylglycerol kinase /cds=(103,2310) /gb=X62535 /gi=30822 /ug=Hs.172690 /len=2564	32716_at
	AL049701				Cluster Incl. AL049701:Human gene from PAC 433G19, chromosome 1 /cds=(0,370) /gb=AL049701 /gi=4678835 /ug=Hs.107325 /len=648	34446_at
IFI41 (interferon-induced protein 41, 30kD)	L22342	Hs.241510	NM_004509		Cluster Incl. L22342:Human nuclear phosphoprotein mRNA, complete cds /cds=(0,746) /gb=L22342 /gi=402204 /ug=Hs.38125 /len=835	35718_at

	AF038199				Cluster Incl. AF038199:Homo sapiens clone 23728 mRNA sequence /cds=UNKNOWN /gb=AF038199 /gi=2795920 /ug=Hs.153106 /len=1112	38154_at
HLA-DOB (major histocompatibility complex, class II, DO beta	X03066	Hs.1802	NM_002120	6p21.3	Cluster Incl. X03066:Human mRNA for HLA-D class II antigen DO beta chain /cds=(56,877) /gb=X03066 /gi=32271 /ug=Hs.1802 /len=1322	38570_at
GTF2E2 (general transcription factor IIE, polypeptide 2 (beta subunit, 34kD)	X63469	Hs.77100	NM_002095	8p21-p12	Cluster Incl. X63469:H.sapiens mRNA for transcription factor TFIIE beta /cds=(242,1117) /gb=X63469 /gi=37069 /ug=Hs.77100 /len=1515	37295_at
NIFU(nitrogen fixation cluster-like	U47101	Hs.9908		12	Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819	39165_at

LY117 (lymphocyte antigen 117)	AF031137	Hs.88411	NM_007161	6p21.3	Cluster Incl. AF031137:Homo sapiens 1C7 precursor, mRNA, alternatively spliced, complete cds /cds=(264,869) /gb=AF031137 /gi=2623874 /ug=Hs.88411 /len=1041	37968_at
ENTPD6 (ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	AL035252	Hs.12330	NM_001247	20q11.2	Cluster Incl. AL035252:Human DNA sequence from clone 738P15 on chromosome 20p11.2-11.22. Contains a putative new gene, the CD39L2 for nucleoside phosphatase D39-like 2, and the (putative?) IL-6SAG gene in the CD39L2 3 UTR. Contains ESTs, an STS, GSSs and a putative CpG island /cds=(147,1601) /gb=AL035252 /gi=4490906 /ug=Hs.12330 /len=2729	39876_at
ATRX (alpha thalassemia/mental retardation syndrome X-linked (RAD54 (S. cerevisiae) homolog	U72936	Hs.96264	NM_000489	xq13.1-q21.1	U72936 /FEATURE= /DEFINITION=HSU72936 Homo sapiens putative DNA dependent ATPase and helicase (ATRX) mRNA, alternatively spliced product 1, complete cds	818_s_at

MAN2A1 (mannosidase, alpha, class 2A, member 1	D63998	Hs.32965	NM_002372	5q21-q22	Cluster Incl. D63998:Human mRNA for golgi alpha-mannosidaseII, complete cds /cds=(510,3941) /gb=D63998 /gi=974733 /ug=Hs.32965 /len=4101	39663_at
APOC4 (apolipoprotein C-IV)	U32576	Hs.110675	NM_001646	19q13.2	Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, complete cds /cds=(40,423) /gb=U32576 /gi=975892 /ug=Hs.110675 /len=613	34454_r_at
	AL096717				Cluster Incl. AL096717:Homo sapiens mRNA; cDNA DKFZp564P0662 (from clone DKFZp564P0662) /cds=UNKNOWN /gb=AL096717 /gi=5419852 /ug=Hs.24178 /len=2228	41328_s_at
C22orf4 (chromosome 22 open reading frame 4)	AL096779	Hs.20017		22q13.3	Cluster Incl. AL096779:Novel human gene mapping to chomosome 2213.3 similar to yeast ORF YOR070C, putative GTPase Activator (start missing) /cds=(51,917) /gb=AL096779 /gi=5420221 /ug=Hs.20017	33778_at

					/len=1416	
KIAA0257(RW1 protein)	D87446	Hs.75912		2	Cluster Incl. D87446:Human mRNA for KIAA0257 gene, partial cds /cds=(0,5418) /gb=D87446 /gi=1665780 /ug=Hs.75912 /len=6178	36971_at
KIAA0793(KIAA0793 gene product	AB018336	Hs.301283	NM_014808	2	Cluster Incl. AB018336:Homo sapiens mRNA for KIAA0793 protein, complete cds /cds=(117,3281) /gb=AB018336 /gi=3882306 /ug=Hs.26885 /len=3997	35188_at
IL24 (interleukin 24)	AA214546	Hs.315463	NM_006850	1q32	Cluster Incl. AA214546:zr92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516	41847_at
CSTF3 (cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD)	U15782	Hs.180034	NM_001326	11	Cluster Incl. U15782:Human cleavage stimulation factor 77kDa subunit mRNA, complete cds /cds=(131,2284) /gb=U15782 /gi=632497 /ug=Hs.180034	41183_at

						/len=2766	
	AB002448					Cluster Incl. AB002448:Homo sapiens mRNA from chromosome 5q21-22, clone-357Ex /cds=UNKNOWN /gb=AB002448 /gi=2943811 /ug=Hs.26968 /len=1270	36260_at
BICD1 (Bicaudal D (Drosophila) homolog 1)	U90028	Hs.164975	NM_001714	12p11.2-p11.1		Cluster Incl. U90028:Homo sapiens bicaudal-D (BICD) mRNA, complete cds /cds=(81,3008) /gb=U90028 /gi=2745975 /ug=Hs.164975 /len=3257	40548_at
GTT1(GTT1 protein)	AL041780	Hs.283722	NM_020151	2		Cluster Incl. AL041780:DKFZp434A0418_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434A0418 /clone_end=3 /gb=AL041780 /gi=5421127 /ug=Hs.239060 /len=723	41295_at

	AL03674				Cluster Incl. AL036744:DKFZp564I1663_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564I1663 /clone_end=5 /gb=AL036744 /gi=5927888 /ug=Hs.236327 /len=617	41288_at
SLC29A2 (solute carrier family 29 (nucleoside transporters), member 2)	AF034102	Hs.32951	NM_001532	11q13	Cluster Incl. AF034102:Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds /cds=(237,1607) /gb=AF034102 /gi=2811136 /ug=Hs.32951 /len=2522	39661_s_at
KIAA0769(KIAA0769 gene produc	AB018312	Hs.19056	NM_014824	11	Cluster Incl. AB018312:Homo sapiens mRNA for KIAA0769 protein, complete cds /cds=(239,2293) /gb=AB018312 /gi=3882258 /ug=Hs.19056 /len=4326	32224_at
KYNU (kynureninase (L-kynurenine hydrolase)	U57721	Hs.169139	NM_003937	2p14-q21.3	Cluster Incl. U57721:Human L-kynurenine hydrolase mRNA, complete cds /cds=(106,1503) /gb=U57721 /gi=1323714	40672_at

						/ug=Hs.81771 /len=1637	
GAPD (glyceraldehyde-3-phosphate dehydrogenase	M33197	Hs.169476	NM_002046	12p13		Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M
CTNNAL1 (catenin (cadherin-associated protein), alpha-like 1)	U97067	Hs.58488	NM_003798	9q31.2		Cluster Incl. U97067:Homo sapiens alpha-catenin-like protein mRNA, complete cds /cds=(43,2247) /gb=U97067 /gi=3342777 /ug=Hs.58488 /len=2446	35331_at
GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class	M63904	Hs.73797	NM_002068	19p13.3		Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	40365_at

KCNAB2 (potassium voltage-gated channel, shaker-related subfamily, beta member 2	AF044253	Hs.298184	NM_003636	1p36.3	Cluster Incl. AF044253:Homo sapiens potassium channel beta 2 subunit (HKvbeta2.2) mRNA, alternatively spliced, complete cds /cds=(0,1061) /gb=AF044253 /gi=2827465 /ug=Hs.154417 /len=1062	31901_at
TARS (threonyl-tRNA synthetase	M63180	Hs.84131	NM_003191	5p13-cen	Cluster Incl. M63180:Human threonyl-tRNA synthetase mRNA, complete cds /cds=(138,2276) /gb=M63180 /gi=339679 /ug=Hs.84131 /len=2644	38473_at
UQCRFS1 (ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1)	L32977	Hs.3712	NM_006003	19q12-q13.1	Cluster Incl. L32977:Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRFS1) gene /cds=(90,914) /gb=L32977 /gi=488298 /ug=Hs.3712 /len=1203	34401_at
ONECUT3 (one cut domain, family member 3)	AC004755			19	Cluster Incl. AC004755:Homo sapiens chromosome 19, fosmid 37502 /cds=(0,2726) /gb=AC004755 /gi=3165405	33685_at

					/ug=Hs.184922 /len=2727	
GAPD (glyceraldehyde-3-phosphate dehydrogenase	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M
MAX (MAX protein)	X60287	Hs.42712	NM_002382	14q23	X60287 /FEATURE=cds /DEFINITION=HSMAXM H.sapiens max mRNA	1981_s_at
SH3GL1 (SH3-domain GRB2-like 1	X99656	Hs.97616	NM_003025	19p13.3	Cluster Incl. X99656:H.sapiens mRNA for protein containing SH3 domain, SH3GL1 /cds=(15,1121) /gb=X99656 /gi=1869809 /ug=Hs.97616 /len=2349	39159_at
SFPQ (splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated))	W27050	Hs.180610	NM_005066	1pter-p32.3	Cluster Incl. W27050:19f7 Homo sapiens cDNA /gb=W27050 /gi=1306422 /ug=Hs.180610 /len=699	41199_s_at

PPP6C (protein phosphatase 6, catalytic subunit	X92972	Hs.80324	NM_002721	xq22.3	Cluster Incl. X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21,938) /gb=X92972 /gi=5701862 /ug=Hs.80324 /len=1292	37581_at
HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)	L24521	Hs.89525	NM_004494	xq25	Cluster Incl. L24521:Human transformation-related protein mRNA, 3 end /cds=(0,1108) /gb=L24521 /gi=403459 /ug=Hs.169225 /len=1240	36446_s_at
ACTG1 (actin, gamma 1	X04098	Hs.14376	NM_001614	17q25	Cluster Incl. X04098:Human mRNA for cytoskeletal gamma-actin /cds=(73,1200) /gb=X04098 /gi=28338 /ug=Hs.234733 /len=1918	34160_at
FBXO7 (F-box only protein 7)	AL050254	Hs.5912	NM_012179	22q11.2-qter	Cluster Incl. AL050254:Novel human gene mapping to chomosome 22 /cds=(205,1773) /gb=AL050254 /gi=4886422 /ug=Hs.5912 /len=2075	35337_at
SCML2 (sex comb on midleg (Drosophila)-like 2	Y18004	Hs.171558	NM_006089	xp22	Cluster Incl. Y18004:Homo sapiens mRNA for SCML2 protein /cds=(91,2193)	38518_at

						/gb=Y18004 /gi=4490941 /ug=Hs.171558 /len=4130	
UBE2L3 (ubiquitin-conjugating enzyme E2L	S81003	Hs.108104	NM_003347	22q11.21		S81003 /FEATURE= /DEFINITION=S81003 - L-UBC=ubiquitin conjugating enzyme [human, odontogenic keratocysts, mRNA Partial, 683 nt]	223_at
GNAQ (guanine nucleotide binding protein (G protein), q polypeptide	U40038	Hs.296261	NM_002072	9q21		Cluster Incl. U40038:Human GTP-binding protein alpha q subunit (GNAQ) mRNA, complete cds /cds=(42,1121) /gb=U40038 /gi=1181670 /ug=Hs.180950 /len=1450	38581_at
UGTREL7(UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter	D87449	Hs.82635	NM_015139	1		Cluster Incl. D87449:Human mRNA for KIAA0260 gene, partial cds /cds=(0,1153) /gb=D87449 /gi=1665786 /ug=Hs.82635 /len=5918	37888_at

Table 12:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
KIAA0101(KIAA0101 gene product)	D14657	Hs.81892	NM_014736	15	Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836	38116_at
IGFBP7 (insulin-like growth factor binding protein 7)	L19182	Hs.119206	NM_001553	4q12	L19182 /FEATURE= /DEFINITION=HUMMAC25X Human MAC25 mRNA, complete cds	2062_at
RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin))	X55988	Hs.728	NM_002934	14q24-q31	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	36766_at

SCYC2 (small inducible cytokine subfamily C, member 2)	D63789	Hs.174228	NM_003175	1q23-q25	Cluster Incl. D63789:Homo sapiens DNA for SCM-1beta precursor, complete cds /cds=(21,365) /gb=D63789 /gi=1754608 /ug=Hs.174228 /len=485	31495_at
DEFA1 (defensin, alpha 1, myeloid-related sequence)	AL036554	Hs.274463	NM_004084	8p23.2-p23.1	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	31793_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M
GSN (gelsolin (amyloidosis, Finnish type))	X04412	Hs.290070	NM_000177	9q33	Cluster Incl. X04412:Human mRNA for plasma gelsolin /cds=(14,2362) /gb=X04412 /gi=35447 /ug=Hs.80562	32612_at

					/len=2602	
GATA2 (GATA-binding protein 2)	M77810	Hs.334695	NM_002050	3q21	M77810 /FEATURE= /DEFINITION=HUMGATA2A Human transcription factor GATA-2 (GATA-2) mRNA, complete cds	1072_g_at
HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like))	L24521	Hs.89525	NM_004494	Xq25	Cluster Incl. L24521:Human transformation-related protein mRNA, 3 end /cds=(0,1108) /gb=L24521 /gi=403459 /ug=Hs.169225 /len=1240	36446_s_at
TUBG1 (tubulin, gamma 1)	M61764	Hs.21635	NM_001070	17q21	Cluster Incl. M61764:Human gamma-tubulin mRNA, complete cds /cds=(24,1379) /gb=M61764 /gi=183702 /ug=Hs.21635 /len=1568	33346_r_at
NUDEL(nuclear distribution gene E-like)	AF038203	Hs.3850	NM_030808	17	Cluster Incl. AF038203:Homo sapiens clone 23596 mRNA sequence /cds=UNKNOWN /gb=AF038203 /gi=2795924 /ug=Hs.3850 /len=1473	34413_at

TYMS (thymidylate synthetase)	D00596	Hs.82962	NM_001071	18p11.32	D00596 /FEATURE=cds /DEFINITION=HUMTS1 Homo sapiens gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 6, 7, complete cds	1505_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M
EZH2 (enhancer of zeste (Drosophila) homolog 2)	U61145	Hs.77256	NM_004456	7q35-q36	Cluster Incl. U61145:Human enhancer of zeste homolog 2 (EZH2) mRNA, complete cds /cds=(89,2329) /gb=U61145 /gi=1575348 /ug=Hs.77256 /len=2600	37305_at
STK12 (serine/threonine kinase 12)	AF015254	Hs.180655	NM_004217	17p13.1	Cluster Incl. AF015254:Homo sapiens serine/threonine kinase (STK-1) mRNA, complete cds /cds=(58,1101) /gb=AF015254 /gi=4090840	33266_at

						/ug=Hs.180655 /len=1234	
MPB1 (MYC promoter-binding protein 1)	M55914	Hs.284127	NM_005945	1pter-p35		M55914 /FEATURE= /DEFINITION=HUMCMYCQ Human c-myc binding protein (MBP-1) mRNA, complete cds	2035_s_at
PTTG1 (pituitary tumor-transforming 1)	AA203476	Hs.252587	NM_004219	5q35.1		Cluster Incl. AA203476:zx55e01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446424 /clone_end=5 /gb=AA203476 /gi=1799203 /ug=Hs.159626 /len=828	40412_at
ICA1 (islet cell autoantigen 1 (69kD))	U38260	Hs.167927	NM_004968	7p22		Cluster Incl. U38260:Human islet cell autoantigen ICAp69 mRNA, complete cds /cds=(169,942) /gb=U38260 /gi=1675205 /ug=Hs.167927 /len=1415	32634_s_at
PGD (phosphogluconate dehydrogenase)	U30255	Hs.75888	NM_002631	1p36.3-p36.13		Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324	36963_at

					/ug=Hs.75888 /len=1536	
FOXM1 (forkhead box M1)	U74612	Hs.239	NM_021953	12p13	Cluster Incl. U74612:Human hepatocyte nuclear factor-3/fork head homolog 11A (HFH-11A) mRNA complete cds /cds=(114,2519) /gb=U74612 /gi=1842252 /ug=Hs.239 /len=3474	34715_at
BPI (bactericidal/permeability-increasing protein)	J04739	Hs.89535	NM_001725	20q11.23-q12	Cluster Incl. J04739:Human bactericidal permeability increasing protein (BPI) mRNA, complete cds /cds=(30,1493) /gb=J04739 /gi=179528 /ug=Hs.89535 /len=1813	37054_at
H2AFY (H2A histone family, member Y)	AF054174	Hs.75258	NM_004893	5q31.3-q32	Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete cds /cds=(173,1288) /gb=AF054174 /gi=3341991 /ug=Hs.75258 /len=1881	36576_at
TKT (transketolase (Wernicke-Korsakoff syndrome))	L12711	Hs.89643	NM_001064	3p14.3	Cluster Incl. L12711:Homo sapiens transketolase (tk) mRNA, complete cds	38789_at

syndrome))					/cds=(98,1969) /gb=L12711 /gi=388890 /ug=Hs.89643 /len=2069	
GCDH (glutaryl-Coenzyme A dehydrogenase)	AD000092	Hs.184141	NM_000159	19p13.2	AD000092 /FEATURE=cds#4 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence	1749_at
RAD54L (RAD54 (S.cerevisiae)-like)	X97795	Hs.66718	NM_003579	1p32	X97795 /FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA homologous to S. cerevisiae RAD54	966_at
GNG5 (guanine nucleotide binding protein (G protein), gamma 5)	AI541042	Hs.5322	NM_005274	1p22	Cluster Incl. AI541042:pec1.2-1.D12.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI541042 /gi=4458415 /ug=Hs.5322 /len=688	35272_at
RAB32 (RAB32, member RAS oncogene family)	U59878	Hs.32217	NM_006834	6	Cluster Incl. U59878:Human low-Mr GTP-binding protein (RAB32) mRNA, partial cds	41523_at

						/cds=(0,632) /gb=U59878 /gi=1388196 /ug=Hs.32217 /len=980	
CD63 (CD63 antigen (melanoma 1 antigen))	X62654	Hs.76294	NM_001780		12q12-q13	Cluster Incl. X62654:H.sapiens gene for Me491/CD63 antigen /cds=(69,785) /gb=X62654 /gi=430755 /ug=Hs.76294 /len=873	37003_at
MPO (myeloperoxidase)	M19507	Hs.1817	NM_000250		17q23.1	Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	33284_at
TALDO1 (transaldolase 1)	AF010400	Hs.77290	NM_006755		11p15.5-p15.4	Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242	37311_at
CDKN3 (cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase))	L25876	Hs.84113	NM_005192		14q22	L25876 /FEATURE= /DEFINITION=HUMPTPB Homo sapiens protein tyrosine phosphatase (CIP2)mRNA, complete cds	1599_at

H2AV(histone H2A.F/Z variant)	AW007731	Hs.301005	NM_012412	7	Cluster Incl. AW007731:wf68d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512629 /clone_end=3 /gb=AW007731 /gi=5856509 /ug=Hs.9242 /len=659	39092_at
TXN (thioredoxin)	AI653621	Hs.76136	NM_003329	9q31	Cluster Incl. AI653621:tz21b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2289213 /clone_end=3 - /gb=AI653621 /gi=4737600 /ug=Hs.76136 /len=598	36992_at
ALAS1 (aminolevulinate, delta-, synthase 1)	Y00451	Hs.78712	NM_000688	3p21.1	Cluster Incl. Y00451:Human mRNA for 5-aminolevulinate synthase /cds=(83,2011) /gb=Y00451 /gi=36648 /ug=Hs.78712 /len=2156	37674_at
NUCB2 (nucleobindin 2)	X76732	Hs.3164	NM_005013	11p15.1-p14	Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /gb=X76732 /gi=2706486 /ug=Hs.3164 /len=1586	35643_at
BN51T (BN51 (BHK21) temperature sensitivity complementing)	M17754	Hs.1276	NM_001722	8q21	Cluster Incl. M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M17754	41694_at

complementing)					/gi=179512 /ug=Hs.1276 /len=1881	
CCR2 (chemokine (C-C motif) receptor 2)	U95626	Hs.395	NM_000647	3p21.1	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at
DEFA4 (defensin, alpha 4, corticostatin)	AI250799	Hs.2582	NM_001925	8p23	Cluster Incl. AI250799:qi36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1858620 /clone_end=3 /gb=AI250799 /gi=3847328 /ug=Hs.2582 /len=542	34546_at
HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like))	D16431	Hs.89525	NM_004494	xq25	Cluster Incl. D16431:Human mRNA for hepatoma-derived growth factor, complete cds /cds=(315,1037) /gb=D16431 /gi=598955 /ug=Hs.89525 /len=2376	38779_r_at
EPB72 (erythrocyte membrane protein band 7.2 (stomatin))	X85116	Hs.160483	NM_004099	9q34.1	Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035	40419_at

					/gi=1161561 /ug=Hs.160483 /len=3035	
DEFA3 (defensin, alpha 3, neutrophil-specific)	L12691	Hs.294176	NM_005217	8pter-p23.3	Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364 /ug=Hs.178741 /len=452	31506_s_at
ACTG1 (actin, gamma 1)	X04098	Hs.14376	NM_001614	17q25	Cluster Incl. X04098:Human mRNA for cytoskeletal gamma-actin /cds=(73,1200) /gb=X04098 /gi=28338 /ug=Hs.234733 /len=1918	34160_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M
KIAA0008(KIAA0008 gene product)	D13633	Hs.77695	NM_014750	14	Cluster Incl. D13633:Human mRNA for KIAA0008 gene, complete cds /cds=(121,2418) /gb=D13633 /gi=286012	37231_at

						/ug=Hs.77695 /len=2640	
LDHA (lactate dehydrogenase A)	X02152:	Hs.2795	NM_005566	11p15.4		Cluster Incl. X02152:Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) /cds=(97,1095) /gb=X02152 /gi=34312 /ug=Hs.2795 /len=1661	41485_at
ACTN1 (actinin, alpha 1)	M95178	Hs.119000	NM_001102	14q24		Cluster Incl. M95178:Human non-muscle alpha-actinin mRNA, complete cds /cds=(111,2789) /gb=M95178 /gi=178051 /ug=Hs.119000 /len=3081	39330_s_at
PRG2 (proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic	Z26248	Hs.99962	NM_002728	11q12		Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=940510 /ug=Hs.99962 /len=1637	39179_at
TCN1 (transcobalamin I (vitamin B12 binding protein, R binder family))	J05068	Hs.2012	NM_001062	11q11-q12		Cluster Incl. J05068:human transcobalamin I mRNA, complete cds /cds=(75,1376) /gb=J05068 /gi=307478 /ug=Hs.2012 /len=1537	35919_at

GGH (gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase))	U55206	Hs.78619	NM_003878	: 8p22-q21.13	Cluster Incl. U55206:Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds /cds=(59,1015) /gb=U55206 /gi=2957143 /ug=Hs.78619 /len=1265	37263_at
ACTB (actin, beta)	X00351	Hs.288061	NM_001101	7p15-p12	Homo sapiens /REF=X00351 /DEF=Human mRNA -for beta-actin /LEN=1761 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HSAC07/X003
LCN2 (lipocalin 2 (oncogene 24p3))	AI762213	Hs.204238	NM_005564	9q34	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at
AGPS (alkylglycerone phosphate synthase)	Y09443	Hs.22580	NM_003659	2q31	Cluster Incl. Y09443:H.sapiens mRNA for alkyl-dihydroxyacetonephosphate synthase precursor /cds=(15,1991) /gb=Y09443 /gi=1922284 /ug=Hs.22580	39225_at

					/len=2074	
H2AFZ (H2A histone family, member Z)	M37583	Hs.119192	NM_002106	4q24	Cluster Incl. M37583:Human histone (H2A.Z) mRNA, complete cds /cds=(106,492) /gb=M37583 /gi=184059 /ug=Hs.119192 /len=873	39337_at
MGC1780(hypothetical protein MGC1780)	AA926959	Hs.77550	NM_032636	1	Cluster Incl. AA926959:om68h08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1552383 /clone_end=3 /gb=AA926959 /gi=3075856 /ug=Hs.77550 /len=809	37347_at
CAT (catalase)	AL035079	Hs.76359	NM_001752	11p13	Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079 /gi=4775614 /ug=Hs.76359 /len=2287	37009_at
SLC6A7 (solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	S80071	Hs.241597	NM_014228	5q31-q32	Cluster Incl. S80071:hPROT=brain-specific L-proline transporter [human, hippocampus, mRNA Partial, 1911 nt] /cds=(0,1910) /gb=S80071 /gi=1839269 /ug=Hs.234765 /len=1911	34166_at

TYMS (thymidylate synthetase)	X02308	Hs.82962	NM_001071	18p11.32	Cluster Incl. X02308:Human mRNA for thymidylate synthase (EC 2.1.1.45) /cds=(105,1046) /gb=X02308 /gi=37478 /ug=Hs.82962 /len=1536	37899_at
C20orf1 (chromosome 20 open reading frame 1)	AB024704	Hs.9329	NM_012112	20q11.2	Cluster Incl. AB024704:Homo sapiens mRNA for fis353, complete cds /cds=(471,2714) /gb=AB024704 /gi=4589928 /ug=Hs.9329 /len=3403	39109_at
SERPINB1 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1)	M93056	Hs.183583	NM_030666	6p25	Cluster Incl. M93056:Human monocyte/neutrophil elastase inhibitor mRNA sequence /cds=UNKNOWN /gb=M93056 /gi=188621 /ug=Hs.183583 /len=1298	33305_at
DEEPEST(mitotic spindle coiled-coil related protein	AF063308	Hs.16244	NM_006461	17	Cluster Incl. AF063308:Homo sapiens coiled-coil related protein DEEPEST (DEEPEST) mRNA, complete cds /cds=(69,3431) /gb=AF063308 /gi=4106355 /ug=Hs.16244 /len=3770	32120_at

SLPI (secretory leukocyte protease inhibitor (antileukoproteinase))	X04470	Hs.251754	NM_003064	20pter-p12.3	Cluster Incl. X04470:Human mRNA for antileukoprotease (ALP) from cervix uterus /cds=(18,416) /gb=X04470 /gi=28638 /ug=Hs.169793 /len=594	32275_at
TTK (TTK protein kinase)	M86699	Hs.169840	NM_003318	6q13-q21	M86699 /FEATURE= /DEFINITION=HUMTTK Human kinase (TTK) mRNA, complete cds	572_at
ANXA1 (annexin A1)	X05908	Hs.78225	NM_000700	9q12-q21.2	Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X05908 /gi=34387 /ug=Hs.78225 /len=1399	37403_at
CTSG (cathepsin G)	M16117	Hs.100764	NM_001911	14q11.2	Cluster Incl. M16117:Human cathepsin G mRNA, complete cds /cds=(8,775) /gb=M16117 /gi=181181 /ug=Hs.100764 /len=857	37105_at
MS4A3 (membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific))	L35848	Hs.99960	NM_006138	11q12-q13.1	Cluster Incl. :Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds /cds=UNKNOWN /gb=L35848 /gi=561638 /ug=Hs.99960 /len=1646	32451_at

					/ug=Hs.99960 /len=1646	
MGST2 (microsomal glutathione S-transferase 2)	U77604	Hs.81874	NM_002413	4q28-q31	U77604 /FEATURE= /DEFINITION=HSU77604 Homo sapiens microsomal glutathione S-transferase 2 (MGST2) mRNA, complete cds	820_at
CLC (Charot-Leyden crystal protein)	L01664	Hs.132004	NM_013246	11q13.3	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	36809_at
FLJ10140(hypothetical protein FLJ10140)	AL031588	Hs.250671	NM_018006	22	Cluster Incl. AL031588:dJ1163J1.3 (novel protein similar to mouse B99) /cds=(0,2140) /gb=AL031588 /gi=4007108 /ug=Hs.122552 /len=2821	39872_at
GADD45A (growth arrest and DNA-damage-inducible, alpha)	M60974	Hs.80409	NM_001924	1p31.2-p31.1	M60974 /FEATURE= /DEFINITION=HUMGADD45 Human growth arrest and DNA-damage-inducible	1911_s_at

OAT (ornithine aminotransferase (gyrate atrophy))	M12267	Hs.75485	NM_000274	10q26	protein (gadd45) mRNA, complete cds Cluster Incl. M12267:Human ornithine aminotransferase mRNA, complete cds /cds=(54,1373) /gb=M12267 /gi=189328 /ug=Hs.75485 /len=2013	36636_at
CEACAM8 (carcinoembryonic antigen-related cell adhesion molecule 8)	M33326	Hs.41	NM_001816	19q13.2	Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	33530_at
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	AI126134	Hs.100000	NM_002964	1q21	Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at
U67369	U67369	Hs.73172	NM_005263	1p22	Cluster Incl. U67369:Human growth factor independence-1 (Gfi-1) mRNA, complete cds /cds=(267,1535) /gb=U67369 /gi=1698691 /ug=Hs.73172 /len=2799	33977_at

TFDP2 (transcription factor Dp-2 (E2F dimerization partner 2))	L40386	Hs.19131	NM_006286	3q23	L40386 /FEATURE=mRNA /DEFINITION=HUMDP2M Human DP-2 mRNA, complete cds	633_s_at
ELA2 (elastase 2, neutrophil)	M34379	Hs.99863	NM_001972	19p13.3	Cluster Incl. M34379:Human elastase/medullasin mRNA, complete cds /cds=(38,841) /gb=M34379 /gi=187116 /ug=Hs.99863 /len=920	37096_at
ITGAM (integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170),	J03925	Hs.172631	NM_000632	16p11.2	Cluster Incl. J03925:Human Mac-1 gene encoding complement receptor type 3, CD11b, complete cds /cds=(72,3533) /gb=J03925 /gi=187284 /ug=Hs.172631 /len=4699	38533_s_at
AZU1 (azurocidin 1 (cationic antimicrobial protein 37))	M96326	Hs.72885	NM_001700	19p13.3	Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771) /gb=M96326 /gi=179301 /ug=Hs.72885 /len=913	33963_at

PKM2 (pyruvate kinase, muscle)	M26252	Hs.198281	NM_002654	15q22	Cluster Incl. M26252:Human TCB gene encoding cytosolic thyroid hormone-binding protein, complete cds /cds=(89,1684) /gb=M26252 /gi=338826 /ug=Hs.198281 /len=2306	32378_at
S100A9 (S100 calcium-binding protein A9 (calgranulin B))	W72424	Hs.112405	NM_002965	1q21	Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	41471_at
CKS2 (CDC28 protein kinase 2)	X54942	Hs.83758	NM_001827	9q22	Cluster Incl. X54942:H.sapiens ckshs2 mRNA for Cks1 protein homologue /cds=(95,334) /gb=X54942 /gi=29978 /ug=Hs.83758 /len=612	40690_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	U34995	Hs.169476	NM_002046	12p13	Cluster Incl. U34995:Human normal keratinocyte substraction library mRNA, clone H22a, complete sequence /cds=UNKNOWN /gb=U34995 /gi=1497857 /ug=Hs.195188 /len=1626	35905_s_at

LOC95295(hypothetical gene supported by V00599; BC001938; BC007605; BC008791	V00599			6	V00599 /FEATURE=mRNA /DEFINITION=HSTUB2 Human mRNA fragment encoding beta-tubulin. (from clone D-beta-1)	151_s_at
ADAM15 (a disintegrin and metalloproteinase domain 15 (metargidin))	U41767	Hs.92208	NM_003815	1q21.3	Cluster Incl. U41767:Human metargidin precursor mRNA, complete cds /cds=(7,2451) /gb=U41767 /gi=1235673 /ug=Hs.92208 /len=2725	38282_at
LOC51304(DHHC1 protein)	AF052182	Hs.14896	NM_016598	3	Cluster Incl. AF052182:Homo sapiens clone 24590 mRNA sequence /cds=UNKNOWN /gb=AF052182 /gi=3360494 /ug=Hs.14896 /len=1298	39751_at
RAB13 (RAB13, member RAS oncogene family)	X75593	Hs.151536	NM_002870	12q13	Cluster Incl. X75593:H.sapiens mRNA for rab 13 /cds=(139,750) /gb=X75593 /gi=452319 /ug=Hs.151536 /len=1238	40210_at
BZRP (benzodiazapine receptor (peripheral))	M36035	Hs.202	NM_000714	22q13.31	Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035	32806_at

					/gi=184333 /ug=Hs.202 /len=811	
KNSL6 (kinesin-like 6 (mitotic centromere-associated kinesin))	U63743	Hs.69360	NM_006845	1	Cluster Incl. U63743:Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds /cds=(54,2231) /gb=U63743 /gi=1695881 /ug=Hs.69360 /len=2740	36837_at
MTX1 (metaxin 1)	U46920	Hs.247551	NM_002455	1q21	Cluster Incl. U46920:Human metaxin (MTX) gene, complete cds /cds=(0,953) /gb=U46920 /gi=1326107 /ug=Hs.181246 /len=1065	40890_at
DOK1 (docking protein 1, 62kD (downstream of tyrosine kinase 1)	U70987	Hs.103854	NM_001381	2p13	U70987 /FEATURE= /DEFINITION=HSU70987 Human GAP binding protein p62dok (DOK) mRNA, complete cds	816_g_at
E2-EPF(ubiquitin carrier protein)	M91670			17	M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds	893_at

NCF4 (neutrophil cytosolic factor 4 (40kD)	AL008637	Hs.196352	NM_000631	22q13.1	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136000 /ug=Hs.196352 /len=1744	38894_g_at
PGK1 (phosphoglycerate kinase 1)	V00572	Hs.78771	NM_000291	xq13	Cluster Incl. V00572:Human mRNA encoding phosphoglycerate kinase /cds=(79,1332) /gb=V00572 /gi=35434 /ug=Hs.78771 /len=1767	37677_at
S100P (S100 calcium-binding protein P)	AA131149	Hs.2962	NM_005980	4p16	Cluster Incl. AA131149:zo16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-587049 /clone_end=5 /gb=AA131149 /gi=1692640 /ug=Hs.2962 /len=464	34319_at

NKG7 (natural killer cell group 7 sequence)	S69115	Hs.10306	NM_005601	19q13.4	Cluster Incl. S69115:granulocyte colony-stimulating factor induced gene [human, CML patient, bone marrow mononuclear cells, mRNA, 833 nt] /cds=(180,677) /gb=S69115 /gi=545708 /ug=Hs.10306 /len=833	37121_at
ITGA5 (integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	X06256	Hs.149609	NM_002205	12q11-q13	Cluster Incl. X06256:Human mRNA for integrin alpha 5 subunit /cds=(23,3172) /gb=X06256 /gi=31437 /ug=Hs.149609 /len=4204	39753_at
PKMYT1(membrane-associated tyrosine-and threonine-specific cdc2-inhibitory kinase	U56816	Hs.77783	NM_004203	16	U56816 /FEATURE= /DEFINITION=HSU56816 Human kinase Myt1 (Myt1) mRNA, complete cds	480_at
CEACAM6 (carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross	M18728	Hs.73848	NM_002483	19q13.2	Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	36105_at

CREG (cellular repressor of E1A-stimulated genes)	AF084523	Hs.5710	NM_003851	1q24	Cluster Incl. AF084523:Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds /cds=(33,695) /gb=AF084523 /gi=3550342 /ug=Hs.5710 /len=1974	35311_at
KIAA0374(syntaphilin)	AB002372			20	Cluster Incl. AB002372:Human mRNA for KIAA0374 gene, complete cds /cds=(642,2258) /gb=AB002372 /gi=2224688 /ug=Hs.100837 /len=5530	41107_at
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at
CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at

TRB@ (T cell receptor beta locus)	M12886	Hs.303157		7q35	M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	1105_s_at
TAB2(TAK1-binding protein 2)	AB018276	Hs.109727	NM_015093		Cluster Incl. AB018276:Homo sapiens mRNA for KIAA0733 protein, partial cds /cds=(0,1586) /gb=AB018276 /gi=3882186 /ug=Hs.109727 /len=3479	38980_at
TNFRSF7 (tumor necrosis factor receptor superfamily, member 7)	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	38578_at
KIAA0275(KIAA0275 gene product)	D87465	Hs.74583	NM_014767		Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(316,1590) /gb=D87465 /gi=1665814 /ug=Hs.74583 /len=5316	36155_at
PTCH (patched (Drosophila) homolog)	U59464	Hs.159526	NM_000264	9q22.3	Cluster Incl. U59464:Human PATCHED protein (PTC) mRNA, complete cds	38214_at

					/cds=(0,4343) /gb=U59464 /gi=1381235 /ug=Hs.159526 /len=4344	
TRAM(translocating chain-associating membrane protein)	X63679	Hs.4147	NM_014294		Cluster Incl. X63679:H.sapiens mRNA for TRAMP protein /cds=(121,1245) /gb=X63679 /gi=37264 /ug=Hs.4147 /len=1267	34796_at
HLA-DMA (major histocompatibility complex, class II, DM alpha)	X62744	Hs.77522	NM_006120	6p21.3	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079	37344_at
HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)	X00457	Hs.914		6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	38833_at
KIAA1128(KIAA1128 protein)	U90912	Hs.81897			Cluster Incl. U90912:Human clone 23865 mRNA sequence /cds=UNKNOWN /gb=U90912 /gi=1913892 /ug=Hs.81897	37617_at

					/len=1633	
HLA-DRB1 (major histocompatibility complex, class II, DR beta 1)	M32578	Hs.180255	NM_002124	6p21.3	Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216	41723_s_at
MMD (monocyte to macrophage differentiation-associated)	X85750	Hs.79889	NM_012329	17q	Cluster Incl. X85750:H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation /cds=(81,797) /gb=X85750 /gi=1006664 /ug=Hs.79889 /len=2518	37565_at
HLA-DMB (major histocompatibility complex, class II, DM beta)	U15085	Hs.1162	NM_002118	6p21.3	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	41609_at
TGFBR3 (transforming growth factor, beta receptor III (betaglycan, 300kD))	L07594	Hs.79059	NM_003243	1p33-p32	L07594 /FEATURE= /DEFINITION=HUMTGFB3C Human transforming growth factor-beta type III	1897_at

					receptor (TGF-beta) mRNA, complete cds	
KRT10 (keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris))	X14487	Hs.99936	NM_000421	17q21-q23	Cluster Incl. X14487:Human gene for acidic (type I) cytokeratin 10 /cds=(25,1806) /gb=X14487 /gi=28316 /ug=Hs.99936 /len=2166	38610_s_at
MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))	AB023208	Hs.181002	NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
	AI700633				Cluster Incl. AI700633:we38g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2343412 /clone_end=3 /gb=AI700633 /gi=4988533 /ug=Hs.4815 /len=565	34840_at
CASP7 (caspase 7, apoptosis-related cysteine protease)	U67319	Hs.9216	NM_001227	10q25	Cluster Incl. U67319:Human Lice2 beta cysteine protease mRNA, complete cds /cds=(228,1238) /gb=U67319 /gi=1894912 /ug=Hs.9216 /len=2602	38281_at

SNRPN (small nuclear ribonucleoprotein polypeptide N)	U41303	Hs.48375	NM_003097	15q12	Cluster Incl. U41303:Human small nuclear ribonuleoprotein particle N (SNRPN) mRNA, complete cds /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326	34842_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38095_i_at
NCOA1 (nuclear receptor coactivator 1)	AJ000882	Hs.74002	NM_003743	2p23	Cluster Incl. AJ000882:Homo sapiens mRNA for steroid receptor coactivator 1e /cds=(201,4400) /gb=AJ000882 /gi=2924310 /ug=Hs.74002 /len=4709	36118_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814	38096_f_at

					/len=1501	
PSCD1 (pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1))	M85169	Hs.1050	NM_004762	17q25	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	38666_at
KIAA1041(KIAA1041 protein)	AB028964	Hs.26023	NM_014947		Cluster Incl. AB028964:Homo sapiens mRNA for KIAA1041 protein, complete cds /cds=(312,2180) /gb=AB028964 /gi=5689418 /ug=Hs.26023 /len=5341	35163_at
SLC7A6 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 6)	D87432	Hs.10315	NM_003983	16q22.1-q22.3	Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(261,1808) /gb=D87432 /gi=1665758 /ug=Hs.10315 /len=6296	39533_at
	AF038199				Cluster Incl. AF038199:Homo sapiens clone 23728 mRNA sequence /cds=UNKNOWN /gb=AF038199	38154_at

UCP2 (uncoupling protein 2 (mitochondrial, proton carrier))	U94592	Hs.80658	NM_003355	11q13		/gi=2795920 /ug=Hs.153106 /len=1112	
						Cluster Incl. U94592:Human uncoupling protein homolog (UCPH) mRNA, complete cds /cds=(314,1243) /gb=U94592 /gi=2052354 /ug=Hs.80658 /len=1888	37591_at
HLA-DQB1 (major histocompatibility complex, class II, DQ beta 1)	M81141	Hs.73931	NM_002123	6p21.3		Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171	36773_f_at
NCOA1 (nuclear receptor coactivator 1)	U59302	Hs.74002	NM_003743	2p23		U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	484_at
KIAA0542(KIAA0542 gene product)	AB011114	Hs.62209				Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, complete cds /cds=(393,3299) /gb=AB011114 /gi=3043607 /ug=Hs.62209 /len=5280	36545_s_at

JAK1 (Janus kinase 1 (a protein tyrosine kinase))	AL039831	Hs.50651	NM_002227	1p32.3-p31.3	Cluster Incl. AL039831:DKFZp434D1112_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5866713 /ug=Hs.50651 /len=579	34877_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
DKFZP434C171(DKFZP434C171 protein	AL080169	Hs.209100	NM_015621		Cluster Incl. AL080169:Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171) /cds=(0,544) /gb=AL080169 /gi=5262637 /ug=Hs.209100 /len=2595	34183_at
	X6730				Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407	41165_g_at

					/ug=Hs.179543 /len=1453	
TMSB10 (thymosin, beta 10)	M92383	Hs.76293	NM_021103	2	Cluster Incl. M92383:Homo sapiens thymosin beta-10 gene, 3end /cds=(0,149) /gb=M92383 /gi=339696 /ug=Hs.169250 /len=400	31481_s_at
AHNAK (AHNAK nucleoprotein (desmoyokin))	M80899	Hs.301417		11q12-q13	Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /cds=(0,3835) /gb=M80899 /gi=178282 /ug=Hs.76549 /len=4051	37027_at
KIAA1002(KIAA1002 protein)	AB023219	Hs.20340			Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete cds /cds=(800,3322) /gb=AB023219 /gi=4589647 /ug=Hs.102483 /len=4331	41366_at
HBOA(histone acetyltransferase)	AI951946	Hs.21907	NM_007067		Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523	41338_at

RNF6 (ring finger protein (C3H2C3 type) 6)	AJ010346	Hs.32597	NM_005977	13q12.2	Cluster Incl. AJ010346:Homo sapiens mRNA for RING-H2 protein RNF6, alternative exon 1a /cds=(360,2417) /gb=AJ010346 /gi=4583651 /ug=Hs.32597 /len=3503	35656_at
IGHM (immunoglobulin heavy constant mu)	X58529	Hs.302063		14q32.33	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325	41166_at
KIAA0660(ras-GTPase-activating protein (GAP<120>) SH3-domain-binding protein 2)	AB014560	Hs.6727	NM_012297		Cluster Incl. AB014560:Homo sapiens mRNA for KIAA0660 protein, complete cds /cds=(120,1568) /gb=AB014560 /gi=3327133 /ug=Hs.6727 /len=4210	35793_at
KIAA1093(KIAA1093 protein)	AB029016	Hs.117333			Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial cds /cds=(0,3613) /gb=AB029016 /gi=5689522 /ug=Hs.117333 /len=4159	37487_at

PRKRIR (protein-kinase, interferon-inducible double stranded RNA dependent inhibitor,	AL049970	Hs.177574	NM_004705	11q13.5	Cluster Incl. AL049970:Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102) /cds=(0,965) /gb=AL049970 /gi=4884219 /ug=Hs.177574 /len=2724	41141_at
SCAP1 (src family associated phosphoprotein 1)	Y11215	Hs.19126	NM_003726	17q21.3	Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524	38862_at
FLJ10140(hypothetical protein FLJ10140)	AL031588	Hs.250671	NM_018006		Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	41660_at
UBE2D2 (ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5))	AI310002	Hs.108332	NM_003339	5p14.2-q23.3	Cluster Incl. AI310002:qo77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1914548 /clone_end=3 /gb=AI310002	38705_at

					/gi=4004873 /ug=Hs.108332 /len=656	
KIAA0226(KIAA0226 gene product)	D86979	Hs.141296			Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(622,2877) /gb=D86979 /gi=1504031 /ug=Hs.141296 /len=5891	31802_at
SEP2(septin 6)	D50918	Hs.90998	Hs.90998		Cluster Incl. D50918:Human mRNA for KIAA0128 gene, partial cds /cds=(0,1276) /gb=D50918 /gi=1469178 /ug=Hs.90998 /len=4612	38826_at
UBE2N (ubiquitin-conjugating enzyme E2N (homologous to yeast UBC	D83004	Hs.75355	NM_003348	12	Cluster Incl. D83004:Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds /cds=(63,521) /gb=D83004 /gi=1181557 /ug=Hs.75355 /len=1203	36604_at
PKD2 (polycystic kidney disease 2 (autosomal dominant))	AL050147	Hs.91146	NM_016457	19q13.2	Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630)	38269_at

						/gb=AL050147 /gi=4884153 /ug=Hs.91146 /len=1837	
RUNX3 (runt-related transcription factor 3)	Z35278	Hs.170019	NM_004350	1p36		Z35278 /FEATURE=mRNA /DEFINITION=HSAML1RN H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA	106_at
RAGA(Ras-related GTP-binding protein)	U41654	Hs.57304	NM_006570			Cluster Incl. U41654:Human adenovirus protein E3-14.7k interacting protein 1 (FIP-1) mRNA, complete cds /cds=(243,1184) /gb=U41654 /gi=2058395 /ug=Hs.57304 /len=1610	35316_at
PPP1CC (protein phosphatase 1, catalytic subunit, gamma isoform)	X74008	Hs.79081	NM_002710	12q24.1-q24.2		Homo sapiens /REF=X74008 /DEF=Cluster Incl. :H.sapiens mRNA for protein phosphatase 1 gamma /cds=(154,1125) /gb= /gi=402777 /ug=Hs.79081 /len=2263 /LEN=2431	37725_at
H2BFL (H2B histone family, member L)	AI688098	Hs.239884	NM_003526	6p21.3		Cluster Incl. AI688098:wc92f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-	33458_r_at

BIN1 (bridging integrator 1)	U68485	Hs.193163	NM_004305	2q14	U68485 /DEFINITION=HSU68485 Homo sapiens bridging integrator protein-1 (BIN1) mRNA, complete cds	/FEATURE=	459_s_at
	AI749193				Cluster Incl. AI749193:at40e04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2374494 /clone_end=3 /gb=AI749193 /gi=5127457 /ug=Hs.17639 /len=544		40623_at
KIAA0911(calsyntenin 1)	AB020718	Hs.29665	NM_014944		Cluster Incl. AB020718:Homo sapiens mRNA for KIAA0911 protein, complete cds /cds=(793,3738) /gb=AB020718 /gi=4240310 /ug=Hs.29665 /len=5219		41498_at
	M13560				Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518		35016_at

					/ug=Hs.84298 /len=2080	
RERE (arginine-glutamic acid dipeptide (RE) repeats)	AB007927	Hs.194369	NM_012102	1p36.1-p36.2	Cluster incl. AB007927:Homo sapiens mRNA for KIAA0458 protein, complete cds /cds=(155,3961) /gb=AB007927 /gi=3413877 /ug=Hs.194369 /len=6642	32253_at
NIFU(nitrogen fixation cluster-like)	U47101	Hs.9908			Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819	39165_at
CD48 (CD48 antigen (B-cell membrane protein))	M37766	Hs.901	NM_001778	1q21.3-q22	Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds /cds=(20,751) /gb=M37766 /gi=187518 /ug=Hs.901 /len=1058	38006_at
BIN1 (bridging integrator 1)	AF001383	Hs.193163	NM_004305	2q14	Cluster Incl. AF001383:Homo sapiens amphiphysin II mRNA, complete cds /cds=(171,1619) /gb=AF001383 /gi=2199534 /ug=Hs.193163 /len=2115	32238_at

KIAA0239(KIAA0239 protein)	D87076	Hs.9729	NM_015288		Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,1716) /gb=D87076 /gi=1510152 /ug=Hs.9729 /len=5630	38342_at
CSK (c-src tyrosine kinase)	X59932	Hs.77793	NM_004383	15q23-q25	X59932 /FEATURE=mRNA /DEFINITION=HSCSRCKIN Human mRNA for C-SRC-kinase -	1768_s_at
RGS10 (regulator of G-protein signalling 10)	AF045229	Hs.82280	NM_002925	10q25	Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753	33121_g_at
RBL2 (retinoblastoma-like 2 (p130))	X76061	Hs.79362	NM_005611	16q12.2	Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835	32597_at
ZFR(zinc finger RNA binding protein)	AI743507	Hs.173518	NM_016107		Cluster Incl. AI743507:wf72a06.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-	40610_at

						2361106 /clone_end=3 /gb=AI743507 /gi=5111795 /ug=Hs.173518 /len=733	
SIT(SHP2 interacting transmembrane adaptor	AJ010059	Hs.88012	NM_014450			Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010059 /gi=4688891 /ug=Hs.88012 /len=1232	40723_at
PFTK1 (PFTAIRE protein kinase 1	AB020641	Hs.57856	NM_012395	7q21-q22		Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641 /gi=4240156 /ug=Hs.57856 /len=4957	36502_at
CDR2 (cerebellar degeneration-related protein (62kD))	M63256	Hs.75124		16p12.3		Cluster Incl. M63256:Human major Yo paraneoplastic antigen (CDR2) mRNA, 3 end /cds=(0,1529) /gb=M63256 /gi=180186 /ug=Hs.75124 /len=2570	36190_at
IFI16 (interferon, gamma-inducible protein 16)	M63838	Hs.155530	NM_005531	1q22		M63838 /FEATURE= /DEFINITION=HUMIFI16A Human interferon-gamma induced protein (IFI 16) gene, complete cds	1456_s_at

TCL1A (T-cell leukemia/lymphoma 1A)	X82240	Hs.2484	NM_021966	14q32.1	Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=(45,389) /gb=X82240 /gi=624960 /ug=Hs.2484 /len=1312	39318_at
NAF1(Nef-associated factor 1	AJ011896	Hs.109281	NM_006058		Cluster Incl. AJ011896:Homo sapiens mRNA for HIV-1, Nef-associated factor 1 beta (Naf1 beta) /cds=(110,2017) /gb=AJ011896 /gi=3758820 /ug=Hs.109281 /len=2710	38970_s_at
CD37 (CD37 antigen)	X14046	Hs.153053	NM_001774	19p13-q13.4	Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908) /gb=X14046 /gi=29793 /ug=Hs.153053 /len=1125	31870_at
PLCG1 (phospholipase C, gamma 1 (formerly subtype 148	AL022394	Hs.268177	NM_002660	20q12-q13.1	Cluster Incl. AL022394:dJ511B24.2 (1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 /cds=(68,3940) /gb=AL022394 /gi=3288442 /ug=Hs.317	34351_at

					/len=5151		
	AB018272				Cluster Incl. AB018272:Homo sapiens mRNA for KIAA0729 protein, partial cds /cds=(0,3591) /gb=AB018272 /gi=3882178 /ug=Hs.180948 /len=4143	41218_at
BLK (B lymphoid tyrosine kinase)	S76617	Hs.2243	NM_001715	8p23-p22	S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]	854_at
	H24861				Cluster Incl. H24861:yl42e11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-160940 /clone_end=5 /gb=H24861 /gi=893760 /ug=Hs.90145 /len=517	33168_at
NFATC1 (nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1)	U08015	Hs.96149	NM_006162	18q23	Cluster Incl. U08015:Human NF-ATc mRNA, complete cds /cds=(239,2389) /gb=U08015 /gi=500631 /ug=Hs.96149	39143_at

					/len=2743	
					Transcription Factor Oct-1a/1b, Alt. Splice 2, Oct-1b	1171_s_at
IFNAR2 (interferon (alpha, beta and omega) receptor 2)	L42243	Hs.86958	NM_000874	21q22.11	L42243 /FEATURE=cds#3 /DEFINITION=HUMIFNAM08 Homo sapiens (clone 51H8) alternatively spliced interferon receptor (IFNAR2) gene, exon 9 and complete cds s	1568_s_at
CD79A (CD79A antigen (immunoglobulin-associated alpha))	U05259	Hs.79630	NM_001783	19q13.2	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107	38017_at
XPA (xeroderma pigmentosum, complementation group A)	D14533	Hs.192803	NM_000380	9q22.3	D14533 /FEATURE= /DEFINITION=HUMXPAC Human mRNA for XPAC protein	1307_at
TLK1 (tousled-like kinase 1)	D50927	Hs.18895	NM_012290	8p22-p12	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927	32219_at

551

						/gi=1469196 /ug=Hs.18895 /len=4454	
SSH3BP1 (spectrin SH3 domain binding protein 1)	AF001628	Hs.24752	NM_005470	10p11.2		Cluster Incl. AF001628:Homo sapiens interactor protein AblBP4 (AblBP4) mRNA, complete cds /cds=(48,1403) /gb=AF001628 /gi=4100618 /ug=Hs.204036 /len=2175	38924_s_at
KIAA0494(KIAA0494 gene product)	AB007963	Hs.62515	NM_014774			Cluster Incl. AB007963:Homo sapiens mRNA for KIAA0494 protein, complete cds /cds=(977,2464) /gb=AB007963 /gi=3413937 /ug=Hs.62515 /len=5766	41830_at
KIAA0014(KIAA0014 gene product)	D25216	Hs.155650	NM_014665			Cluster Incl. D25216:Human mRNA for KIAA0014 gene, complete cds /cds=(146,1627) /gb=D25216 /gi=434774 /ug=Hs.155650 /len=5323	32062_at
	U92980					Cluster Incl. U92980:Homo sapiens clone DT1P1A10 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92980	33242_at

					/gi=2781398 /ug=Hs.178207 /len=1423	
CD19 (CD19 antigen)	M28170	Hs.96023	NM_001770	16p11.2	M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	1096_g_at
M17S2 (membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen	D30756	Hs.277721	NM_005899	17q21.1	Cluster Incl. D30756:Human mRNA for KIAA0049 gene, complete cds /cds=(140,3040) /gb=D30756 /gi=488500 /ug=Hs.233745 /len=4654	33444_at
LRMP (lymphoid-restricted membrane protein)	U10485	Hs.40202	NM_006152	12p12	Cluster Incl. U10485:Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds /cds=(574,2241) /gb=U10485 /gi=505685 /ug=Hs.40202 /len=2417	35974_at
FLJ20274(hypothetical protein FLJ20274)	AA442799	Hs.268371	NM_017736		Cluster Incl. AA442799:zv69b10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-758875 /clone_end=5 /gb=AA442799	40868_at

					/gi=2155474 /ug=Hs.173992 /len=512	
IL10RA (interleukin 10 receptor, alpha)	U00672	Hs.327	NM_001558	11q23	Cluster Incl. C:Human interleukin-10 receptor mRNA, complete cds /cds=(61,1797) /gb=U00672 /gi=482802 /ug=Hs.327 /len=3632	35659_at
RNF4 (ring finger protein 4)	AB000468	Hs.66394	NM_002938	4p16.3	Cluster Incl. AB000468:Homo sapiens mRNA for zinc finger protein, complete cds, clone-RES4-26 /cds=(297,869) /gb=AB000468 /gi=1843400 /ug=Hs.66394 /len=2903	35777_at
FCGR2B (Fc fragment of IgG, low affinity IIb, receptor for (CD32))	M28696	Hs.278443	NM_004001	1q23	Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-RII) mRNA, complete cds /cds=(41,916) /gb=M28696 /gi=184843 /ug=Hs.233450 /len=1416	34663_at
CLPTM1 (cleft lip and palate associated transmembrane protein	AF037339	Hs.106671	NM_001294	19q13.2-q13.3	Cluster Incl. AF037339:Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds	41413_at

					/cds=(15,2024) /gb=AF037339 /gi=4063032 /ug=Hs.106671 /len=2468	
SP140(nuclear body protein Sp140)	U36500	Hs.309943	NM_007237		Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173653 /ug=Hs.85283 /len=3252	40700_at

Table 13:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF001548	Hs.78344	NM_002474	16p13.13-p13.12	AF001548 /FEATURE=mRNA /DEFINITION=HUAF001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence	767_at
ARHGAP4 (Rho GTPase activating protein 4)	X78817	Hs.3109	NM_001666	xq28	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236	39649_at
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF013570	Hs.78344	NM_002474	16p13.13-p13.12	Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	37407_s_at

PBX3 (pre-B-cell leukemia transcription factor 3)	X59841	Hs.294101	NM_006195	9q33-q34	Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314 /ug=Hs.171680 /len=2581	32696_at
CTSW (cathepsin W (lymphopain))	AF013611	Hs.87450	NM_001335	11q13.1	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	40718_at
CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at
KIAA0906(KIAA0906 protein)	AB020713	Hs.56966		3	Cluster Incl. AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56966 /len=4217	41812_s_at
AOE372(thioredoxin peroxidase (antioxidant enzyme))	U25182	Hs.83383	NM_006406	11	Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380	38435_at

					/ug=Hs.83383 /len=921	
KIAA0246(KIAA0246 protein), Similar to Mouse notch 3	D87433	Hs.301989	NM_015136	3	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777	38487_at
HOXB2 (homeo box B2)	X16665	Hs.2733	NM_002145	17q21-q22	Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520	39610_at
PLXNB2 (plexin B2)	AB002313	Hs.3989		22q13.33	Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252	34780_at
SERPINB6 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6)	S69272	Hs.41072	NM_004568	6p25	Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072	34789_at

						/len=1465	
EIF4EL3 (eukaryotic translation initiation factor 4E-like 3)	AF038957	Hs.19122	NM_004846	2q37.1		Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961	32229_at
PLCB2 (phospholipase C, beta 2)	M95678	Hs.994	NM_004573	15q15		M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-2 mRNA, complete cds	210_at
SELL (selectin L (lymphocyte adhesion molecule 1))	M25280	Hs.82848	NM_000655	1q23-q25		M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds	245_at
NDUFC1 (NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI))	AA760866	Hs.84549	NM_002494	4q28.2-q31.1		Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549	38485_at

					/len=553	
PIG6(proline oxidase homolog)	AF010310	Hs.274550			Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888	34110_g_at
HLA-DRA (major histocompatibility complex, class II, DR alpha)	J00194	Hs.76807	NM_019111	6p21.3	Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199	37039_at
					Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080	35016_at
POU4F1 (POU domain, class 4, transcription factor 1)	L20433	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. L20433:Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588	35939_s_at

560

						/len=3824	
XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080		22q12.1	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802	39756_g_at
NDUFB5 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH))	AF047181	Hs.19236	NM_002492		3q25.1-q25.33	Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034	32232_at
						Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169	38972_at

					/gi=3360480 /ug=Hs.109438 /len=1385	
TIP30(Tat-interacting protein (30kD)	AF039103	Hs.90753	NM_006410	11	Cluster Incl. AF039103:Homo sapiens Tat-interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297	38824_at
HOXA9 (homeo box A9)	U41813	Hs.127428	NM_002142	7p15-p14	Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411	37809_at
VCL (vinculin)	M33308	Hs.75350	NM_003373	10q22.1-q23	Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102	36601_at
DUSP6 (dual specificity phosphatase 6)	AB013382	Hs.180383	NM_001946	12q22-q23	Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390	41193_at

PIG8(etoposide induced 2.4 mRNA)	AF010313	Hs.286027	NM_004879	11	Cluster Incl. AF010313:Homo sapiens Pig8 (PIG8) mRNA, complete cds /cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165	38097_at
SNRPN (small nuclear ribonucleoprotein polypeptide N)	U41303	Hs.48375	NM_003097	15q12	Cluster Incl. U41303:Human small nuclear ribonuleoprotein particle N (SNRPN) mRNA, complete cds - /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326	34842_at
TBC1D1 (TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1)	AB029031	Hs.278586		4	Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576	32506_at
STATI2(cytokine inducible SH2-containing protein 2)	AF037989	Hs.110776	NM_003877	12	Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913) /gb=AF037989 /gi=3265032 /ug=Hs.110776 /len=1937	38994_at

GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))	M63904	Hs.73797	NM_002068	19p13.3	Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	40365_at
BZRP (benzodiazapine receptor (peripheral))	M36035	Hs.202	NM_000714	22q13.31	Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035 /gi=184333 /ug=Hs.202 /len=811	32806_at
NPR3 (natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C))	M59305	Hs.123655	NM_000908	5p14-p13	Cluster Incl. M59305:Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, complete cds /cds=(362,1987) /gb=M59305 /gi=178651 /ug=Hs.123655 /len=2081	34519_at
AGRN (agrin)	AF016903	Hs.273330		1p36.3-p32	Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032	33454_at

EPB41L2 (erythrocyte membrane protein band 4.1-like 2)	AF027299	Hs.7857	NM_001431	6q23	Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /cds=(44,3061) /gb=AF027299 /gi=2739095 /ug=Hs.7857 /len=4316	32585_at
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	AI126134	Hs.100000	NM_002964	1q21	Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 - /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at
POU4F1 (POU domain, class 4, transcription factor 1)	X64624	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492	35940_at
LAK-4P(expressed in activated T/LAK lymphocytes)	AB002405	Hs.16165	NM_007267	17	Cluster Incl. AB002405:Homo sapiens mRNA for LAK-4p, complete cds /cds=(109,1149) /gb=AB002405 /gi=2760120 /ug=Hs.16165 /len=1376	32116_at

ITGB2 (integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophageantigen 1 (mac-1) beta subunit))	M15395	Hs.83968	NM_000211	21q22.3	Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA /cds=(72,2381) /gb=M15395 /gi=186933 /ug=Hs.83968 /len=2776	37918_at
NAGA (N-acetylgalactosaminidase, alpha-)	Z99716	Hs.75372	NM_000262	22q11	Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606	36607_at
KLF4 (Kruppel-like factor 4 (gut))	U70663	Hs.7934	NM_004235	9q31	Cluster Incl. U70663:Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds /cds=(503,1915) /gb=U70663 /gi=1857160 /ug=Hs.236377 /len=1953	36214_at
SIPA1 (signal-induced proliferation-associated gene 1)	AB005666	Hs.7019	NM_006747	11q13.3	Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein, complete cds /cds=(296,3424) /gb=AB005666 /gi=2389008 /ug=Hs.7019	36843_at

					/len=3885	
SPC18(signal peptidase complex (18kD))	AI357653	Hs.9534	NM_014300	15	Cluster Incl. AI357653:qy15c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2012084 /clone_end=3 /gb=AI357653 /gi=4109274 /ug=Hs.9534 /len=833	39139_at
KIAA0223(minor histocompatibility antigen HA-1)	D86976	Hs.196914		19	Cluster Incl. D86976:Human mRNA for KIAA0223 gene, partial cds /cds=(0,3498) /gb=D86976 /gi=1504025 /ug=Hs.196914 /len=4121	33748_at
CALR (calreticulin)	M84739	Hs.16488	NM_004343	19p13.3-p13.2	Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937	32543_at
MGC2747(hypothetical protein MGC2747	AL046940	Hs.250723	NM_024104	19	Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /clone_end=5	41273_at

						/gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695	
SDR1(retinal short-chain dehydrogenase/reductase 1)	AF061741	Hs.17144	NM_004753	1		Cluster Incl. AF061741:Homo sapiens retinal short-chain dehydrogenase/reductase retSDR1 mRNA, complete cds /cds=(54,962) /gb=AF061741 /gi=3450827 /ug=Hs.17144 /len=1401	40782_at
CBFA2T1 (core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related)	D43638	Hs.31551	NM_004349	8q22		Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	35638_at
CPA3 (carboxypeptidase A3 (mast cell))	M73720	Hs.646	NM_001870	3q21-q25		Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633	36749_at

XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080	22q12.1	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802	39755_at
DEK (DEK oncogene (DNA binding))	X64229	Hs.110713	NM_003472	6p23	Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502 /ug=Hs.110713 /len=2699	38992_at
PTGER2 (prostaglandin E receptor 2 (subtype EP2), 53kD)	U19487	Hs.2090	NM_000956	14q22	U19487 /FEATURE= /DEFINITION=HSU19487 Human prostaglandin E2 receptor mRNA, complete cds	828_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814	38095_i_at

						/len=1501	
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3		Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38096_f_at
MPO (myeloperoxidase)	M19507	Hs.1817	NM_000250	17q23.1		Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	33284_at
HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)	X00457	Hs.914		6p21.3		Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	38833_at
AHR (aryl hydrocarbon receptor)	L19872	Hs.170087	NM_001621	7p15		Cluster Incl. L19872:Human AH-receptor mRNA, complete cds /cds=(375,2921) /gb=L19872 /gi=416141 /ug=Hs.170087	40516_at

DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796	7	/len=5228 Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
HOXA7 (homeo box A7)	AC004080	Hs.70954	NM_006896	7p15-p14	Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170O19 from 7p15-p21 /cds=(0,1247) /gb=AC004080 /gi=2822164 /ug=Hs.110637 /len=1248	41448_at
					Cluster Incl. AL096717:Homo sapiens mRNA; cDNA DKFZp564P0662 (from clone DKFZp564P0662) /cds=UNKNOWN /gb=AL096717 /gi=5419852 /ug=Hs.24178 /len=2228	41328_s_at
S100A9 (S100 calcium-binding protein A9 (calgranulin B))	W72424	Hs.112405	NM_002965	1q21	Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	41471_at

CHD3 (chromodomain helicase DNA binding protein 3)	U91543	Hs.25601	NM_001272	17p13.1	Cluster Incl. U91543:Homo sapiens zinc-finger helicase (hZFH) mRNA, complete cds /cds=(150,6152) /gb=U91543 /gi=3298561 /ug=Hs.237761 /len=6771	34707_at
PPIB (peptidylprolyl isomerase B (cyclophilin B))	M63573	Hs.699	NM_000942	15q21-q22	Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671) /gb=M63573 /gi=337998 /ug=Hs.699 /len=893	35823_at
HLA-DMB (major histocompatibility complex, class II, DM beta)	U15085	Hs.1162	NM_002118	6p21.3	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	41609_at
TNFAIP3 (tumor necrosis factor, alpha-induced protein 3)	M59465	Hs.211600	NM_006290	6q23.1-q25.3	M59465 /FEATURE= /DEFINITION=HUMA20 Human tumor necrosis factor alpha inducible protein A20 mRNA, complete cds	595_at
LGALS9 (lectin, galactoside-binding, soluble, 9 (galectin 9))	AB006782	Hs.81337	NM_002308	17	AB006782 /FEATURE= /DEFINITION=AB006782 Homo sapiens	766_at

(galectin 9))					mRNA for galectin-9 isoform, complete cds	
RAD23A (RAD23 (S. cerevisiae) homolog A)	D21235	Hs.180455	NM_005053	19p13.2	Cluster Incl. D21235:Human mRNA for HHR23A protein, complete cds /cds=(36,1127) /gb=D21235 /gi=498145 /ug=Hs.180455 /len=1719	41197_at
SLC7A7 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 7)	AJ130718	Hs.194693	NM_003982	14q11.2	Cluster Incl. AJ130718:Homo sapiens mRNA for glycoprotein-associated amino acid transporter y+LAT1 /cds=(293,1828) /gb=AJ130718 /gi=3970724 /ug=Hs.194693 /len=2214	33731_at
BMI1 (murine leukemia viral (bmi-1) oncogene homolog)	L13689	Hs.431	NM_005180	10p13	Cluster Incl. L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cds=(479,1459) /gb=L13689 /gi=291872 /ug=Hs.431 /len=3203	41562_at
DDOST (dolichyl-diphosphooligosaccharide-protein glycosyltransferase)	D29643	Hs.34789	NM_005216	1p36.1	Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936	38791_at

					/ug=Hs.89674 /len=1668	
CEACAM6 (carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen))	M18728	Hs.73848	NM_002483	19q13.2	Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	36105_at
TPM4 (tropomyosin 4)	X05276	Hs.250641	NM_003290	19p13.1	Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049	33866_at
CD34 (CD34 antigen)	M81945	Hs.85289	NM_001773	1q32	Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616	38747_at
HLA-DRB1 (major histocompatibility complex, class II, DR beta 1)	M32578	Hs.180255	NM_002124	6p21.3	Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216	41723_s_at

SIAT4C (sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)	X74570	Hs.75268	NM_006278	11q23-q24	Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase /cds=(162,1151) /gb=X74570 /gi=414890 /ug=Hs.75268 /len=1741	36916_at
RGS10 (regulator of G-protein signalling 10)	AF045229	Hs.82280	NM_002925	10q25	Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753	33121_g_at
EBI2 (Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor))	L08177	Hs.784	NM_004951	13	L08177 /FEATURE= /DEFINITION=HUMGPCRB Human EBV induced G-protein coupled receptor (EBI2) mRNA, complete cds	931_at
NUCB1 (nucleobindin 1)	M96824	Hs.172609	NM_006184	19q13.2-q13.4	Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650	40817_at

PGRMC1 (progesterone receptor membrane component 1)	Y12711	Hs.90061	NM_006667	xq22-q24	Cluster Incl. Y12711:H.sapiens mRNA for putative progesterone binding protein /cds=(51,638) /gb=Y12711 /gi=2062021 /ug=Hs.90061 /len=1924	38802_at
CEACAM8 (carcinoembryonic antigen-related cell adhesion molecule 8)	M33326	Hs.41	NM_001816	19q13.2	Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	33530_at
HLA-DMA (major histocompatibility complex, class II, DM alpha)	X62744	Hs.77522	NM_006120	6p21.3	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079	37344_at
DKFZP586N1922(DKFZP586N1922 protein	N99340	Hs.7357		19	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110	36095_at

SLC9A3R1 (solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1)	AF015926	Hs.184276	NM_004252	17	Cluster Incl. AF015926:Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA, complete cds /cds=(212,1288) /gb=AF015926 /gi=3220018 /ug=Hs.184276 /len=1984	32174_at
MEL (mel transforming oncogene (derived from cell line NK14)- RAB8 homolog)	AI819948	Hs.5947	NM_005370	19p13.1	Cluster Incl. AI819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2409932 /clone_end=3 /gb=AI819948 /gi=5439027 /ug=Hs.5947 /len=569	35340_at
LYPLA1 (lysophospholipase I)	AF081281	Hs.12540	NM_006330	6pter-p25.1	Cluster Incl. AF081281:Homo sapiens lysophospholipase (LPL1) mRNA, complete cds /cds=(35,727) /gb=AF081281 /gi=3415122 /ug=Hs.12540 /len=2417	39396_at
PSCDBP (pleckstrin homology, Sec7 and coiled/coil domains, binding protein)	AF068836	Hs.270	NM_004288	2q11.2	Cluster Incl. AF068836:Homo sapiens cytohesin binding protein HE mRNA, complete cds /cds=(33,1112) /gb=AF068836 /gi=3192908 /ug=Hs.270	39604_at

						/len=1771	
						Cluster Incl. M22806:Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene /cds=(66,1592) /gb=M22806 /gi=487831 /ug=Hs.75655 /len=2438	36666_at
CXX1 (CAAX box 1)	Y13374	Hs.250708	NM_003928	xq26		Cluster Incl. Y13374:Homo sapiens mRNA for putatively prenylated protein /cds=(343,972) /gb=Y13374 /gi=2370152 /ug=Hs.239533 /len=1186	33856_at
SERPING1 (serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary))	X54486	Hs.151242	NM_000062	11q12-q13.1		Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827	39775_at
KIAA0088(KIAA0088 protein)	D42041	Hs.76847	NM_014610	11		Cluster Incl. D42041:Human mRNA for KIAA0088 gene, partial cds /cds=(0,2832) /gb=D42041 /gi=577294 /ug=Hs.76847	37040_at

					/len=3820	
MTCP1 (mature T-cell proliferation 1)	Z24459	Hs.3548	NM_014221	xq28	Cluster Incl. Z24459:H.sapiens MTCP1 gene, exons 2A to 7 (and joined mRNA) /cds=(1419,1625) /gb=Z24459 /gi=2252491 /ug=Hs.3548 /len=1847	35688_g_at
NFKBIA (nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha)	M69043	Hs.81328	NM_020529	14q13	M69043 /FEATURE= /DEFINITION=HUMMAD3A Homo sapiens MAD-3 mRNA encoding IkB-like activity, complete cds	1461_at
MST1 (macrophage stimulating 1 (hepatocyte growth factor-like))	U37055	Hs.278657	NM_020998	3p21	U37055 /FEATURE=mRNA /DEFINITION=HSU37055 Human hepatocyte growth factor-like protein gene, complete cds	1047_s_at
ABR (active BCR-related gene)	U01147	Hs.118021	NM_001092	17p13.3	Cluster Incl. U01147:Human guanine nucleotide regulatory protein (ABR) mRNA, complete cds /cds=(110,2689) /gb=U01147 /gi=393094 /ug=Hs.118021	39058_at

					/len=5242	
TRA1 (tumor rejection antigen (gp96) 1)	X15187	Hs.82689	NM_003299	12q24.2-q24.3	X15187 . /FEATURE=cds /DEFINITION=HSTRA1 Human tra1 mRNA for human homologue of murine tumor rejection antigen gp96	442_at
CEBPD (CCAAT/enhancer binding protein (C/EBP), delta)	M83667	Hs.76722	NM_005195	8p11.2-p11.1	M83667 /FEATURE=mRNA /DEFINITION=HUMNFIL6BA Human NF-IL6-beta protein mRNA, complete cds	1052_s_at

Table 14:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
CAMP (cathelicidin antimicrobial peptide)	Z38026	Hs.51120	NM_004345	3p21.3	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	36710_at
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF001548	Hs.78344	NM_002474	16p13.13-p13.12	AF001548 /FEATURE=mRNA /DEFINITION=HUAF001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence	767_at
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF013570	Hs.78344	NM_002474	16p13.13-p13.12	Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944	37407_s_at

						/ug=Hs.78344 /len=2580	
SYNE-1B(synaptic nuclear envelope 1)	AB018339					Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
	K03000	Hs.76392	NM_000689		9q21	Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560	37015_at
ARHGAP4 (Rho GTPase activating protein 4)	X78817	Hs.3109	NM_001666		xq28	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236	39649_at
LIG1 (ligase I, DNA, ATP-dependent)	AL039458	Hs.4193			3p14	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N0910 /clone_end=3 /gb=AL039458 /gi=5408506 /ug=Hs.4193	34800_at

					/len=849	
CTSW (cathepsin W (lymphopain))	AF013611	Hs.87450	NM_001335	11q13.1	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	40718_at
LCN2 (lipocalin 2 (oncogene 24p3))	AI762213	Hs.204238	NM_005564	9q34	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at
CCR2 (chemokine (C-C motif) receptor 2)	U95626			3p21	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at
PBX3 (pre-B-cell leukemia transcription factor 3)	X59841	Hs.294101	NM_006195	9q33-q34	Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314	32696_at

CBX7 (chromobox homolog 7)	AL031846	Hs.395	NM_000647	22q13.1	/ug=Hs.171680 /len=2581 Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
SGP28(specific granule protein (28 kDa); cysteine-rich secretory protein-3)	X94323	Hs.54431	NM_006061		Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	36464_at
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	41796_at
KIAA0246(KIAA0246 protein)	D87433	Hs.301989	NM_015136		Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777	38487_at

PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39209_r_at
KIAA0906(KIAA0906 p	AB020713	Hs.56966			Cluster Incl. AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56966 /len=4217	41812_s_at
KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2)	AF052728	Hs.188021	NM_000238	7q35-q36	Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively spliced, partial cds /cds=(0,284) /gb=AF052728 /gi=3549258 /ug=Hs.165664 /len=767	38225_at
CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at

PLSCR1 (phospholipid scramblase 1)	AB006746	Hs.198282	NM_021105	3q23	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077	32775_r_at
PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39208_i_at
PLXNB2 (plexin B2)	AB002313	Hs.3989		22q13.33	Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252	34780_at
TRB@ (T cell receptor beta locus)	M12886	Hs.303157		Hs.303157	M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	1105_s_at
NS1-BP(NS1-binding protein)	AB020657	Hs.197298	NM_006469		Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete cds	33752_at

						/cds=(630,2558) /gb=AB020657 /gi=4240188 /ug=Hs.197298 /len=3682	
XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080	22q12.1		Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802	39756_g_at
SYNE-2(synaptic nuclei expressed gene 2)	AL080133	Hs.57749	NM_015180			Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	41815_at
HLA-F (major histocompatibility complex, class I, F)	AL022723	Hs.110309	NM_018950	6p21.3		Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, class I, F (CDA12)) /cds=(97,1185) /gb=AL022723	37420_i_at

					/gi=5002624 /ug=Hs.110309 /len=1303	
AOE372(thioredoxin peroxidase (antioxidant enzyme))	U25182	Hs.83383	NM_006406		Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921	38435_at
SELL (selectin L (lymphocyte adhesion molecule 1))	M25280	Hs.82848	NM_000655	1q23-q25	M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds	245_at
PF4 (platelet factor 4)	M25897	Hs.81564	NM_002619	4q12-q21	M25897 /FEATURE=mRNA /DEFINITION=HUMPF4A Human platelet factor 4 (PF4) mRNA, complete cds	1115_at
SERPINB6 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6)	S69272	Hs.41072	NM_004568	6p25	Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072	34789_at

HOXB2 (homeo box B2)	X16665	Hs.2733	NM_002145	17q21-q22	/len=1465 Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520	39610_at
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	AI126134	Hs.100000	NM_002964	1q21	Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at
CD59 (CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32	M84349	Hs.119663	NM_000611	11p13	Cluster Incl. M84349:Human transmembrane protein (CD59) gene /cds=(18,404) /gb=M84349 /gi=180150 /ug=Hs.119663 /len=1840	39351_at
GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))	M63904	Hs.73797	NM_002068	19p13.3	Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891	40365_at

						/ug=Hs.73797 /len=2060	
PIG6(proline oxidase homolog)	AF010310	Hs.274550				Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888	34110_g_at
	AF052169					Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169 /gi=3360480 /ug=Hs.109438 /len=1385	38972_at
EIF4EL3 (eukaryotic translation initiation factor 4E-like 3)	AF038957	Hs.19122	NM_004846	2q37.1		Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961	32229_at
DDOST (dolichyl-diphosphooligosaccharide-protein glycosyltransferase)	D29643	Hs.34789	NM_005216	1p36.1		Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936	38791_at

					/ug=Hs.89674 /len=1668	
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase))	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at
CALR (calreticulin	M84739	Hs.16488	NM_004343	19p13.3-p13.2	Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937	32543_at
DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796		Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080	22q12.1	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815)	39755_at

						/gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802	
VCL (vinculin)	M33308	Hs.75350	NM_003373	10q22.1-q23		Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102	36601_at
POU4F1 (POU domain, class 4, transcription factor 1)	L20433	Hs.211588	NM_006237	13q21.1-q22		Cluster Incl. L20433:Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588 /len=3824	35939_s_at
MIC2 (antigen identified by monoclonal antibodies 12E7, F21 and O13)	M16279	Hs.177543	NM_002414	xp22.32; yp11.3		Cluster Incl. M16279:Human MIC2 mRNA, complete cds /cds=(177,734) /gb=M16279 /gi=188542 /ug=Hs.177543 /len=1238	41138_at
DEFA4 (defensin, alpha 4, corticostatin)	AI250799	Hs.2582	NM_001925	8p23		Cluster Incl. AI250799:qi36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-	34546_at

					1858620 /clone_end=3 /gb=AI250799 /gi=3847328 /ug=Hs.2582 /len=542	
NDUFC1 (NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI))	AA760866	Hs.84549	NM_002494	4q28.2-q31.1	Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549 /len=553	38485_at
SPTA1 (spectrin, alpha, erythrocytic 1 (elliptocytosis 2))	M61877	Hs.1985	NM_003126	1q21	Cluster Incl. M61877:Human erythroid alpha-spectrin (SPTA1) mRNA, complete cds /cds=(186,7475) /gb=M61877 /gi=338437 /ug=Hs.1985 /len=8001	38906_at
EPB72 (erythrocyte membrane protein band 7.2 (stomatin))	X85116	Hs.160483	NM_004099	9q34.1	Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035	40419_at
CD24 (CD24 antigen (small cell lung carcinoma cluster 4 antigen))	L33930	Hs.286124	NM_013230	6q21	L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3 region	266_s_at

HOXA9 (homeo box A9)	U41813	Hs.127428	NM_002142	7p15-p14	Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411	37809_at
HLA-DRA (major histocompatibility complex, class II, DR alpha)	J00194	Hs.76807	NM_019111	6p21.3	Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199	37039_at
OLR1 (oxidised low density lipoprotein (lectin-like) receptor 1)	AF079167	Hs.77729	NM_002543	12p13.2-p12.3	Cluster Incl. AF079167:untitled /cds=(61,882) /gb=AF079167 /gi=4050003 /ug=Hs.77729 /len=2468	37233_at
	M1872				Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	36105_at
DEK (DEK oncogene (DNA binding))	X64229	Hs.110713	NM_003472	6p23	Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502	38992_at

					/ug=Hs.110713 /len=2699	
AGRN (agrin)	AF016903	Hs.273330		1p36.3-p32	Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032	33454_at
PIR121(p53 inducible protein)	L47738	Hs.258503			Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881	37579_at
ITGB2 (integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage	M15395	Hs.83968	NM_000211	21q22.3	Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA /cds=(72,2381) /gb=M15395 /gi=186933 /ug=Hs.83968 /len=2776	37918_at
STATI2(cytokine inducible SH2-containing protein 2)	AF037989	Hs.110776	NM_003877		Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913) /gb=AF037989 /gi=3265032	38994_at

					/ug=Hs.110776 /len=1937	
TBC1D1 (TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1)	AB029031	Hs.278586		4	Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576	32506_at
DEFA1 (defensin, alpha 1, myeloid-related sequence)	AL036554	Hs.274463	NM_004084	8p23.2-p23.1	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	31793_at
MGC2747(hypothetical protein MGC2747)	AL046940	Hs.250723	NM_024104		Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /clone_end=5 /gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695	41273_at

LILRB2 (leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains),	AF004231	Hs.22405	NM_005874	19q13.4	Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds /cds=(208,2001) /gb=AF004231 /gi=2343110 /ug=Hs.22405 /len=2863	39221_at
CPA3 (carboxypeptidase A3 (mast cell))	M73720	Hs.646	NM_001870	3q21-q25	Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633	36749_at
	M13560				Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080	35016_at
	M3332				Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	33530_at

DEFA3 (defensin, alpha 3, neutrophil-specific)	L12691	Hs.294176	NM_005217	8pter-p23.3	Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364 /ug=Hs.178741 /len=452	31506_s_at
PLXNC1 (plexin C1)	AF030339	Hs.286229	NM_005761	12	Cluster Incl. AF030339:Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds /cds=(249,4955) /gb=AF030339 /gi=3176761 /ug=Hs.184697 /len=5121	32193_at
	U7066				Cluster Incl. U70663:Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds /cds=(503,1915) /gb=U70663 /gi=1857160 /ug=Hs.236377 /len=1953	36214_at
	AF035315				Cluster Incl. AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence /cds=UNKNOWN /gb=AF035315 /gi=2661077 /ug=Hs.180737 /len=1331	33267_at

CTSE (cathepsin E)	J05036	Hs.1355	NM_001910	1q31	J05036 /FEATURE=mRNA /DEFINITION=HUMCTSE Human cathepsin E mRNA, complete cds	271_s_at
NDUFB5 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH))	AF047181	Hs.19236	NM_002492	3q25.1-q25.33	Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034	32232_at
S100A9 (S100 calcium-binding protein A9 (calgranulin B))	W72424	Hs.112405	NM_002965	1q21	Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	41471_at
SNRPN (small nuclear ribonucleoprotein polypeptide N)	U41303	Hs.48375	NM_003097	15q12	Cluster Incl. U41303:Human small nuclear ribonuleoprotein particle N (SNRPN) mRNA, complete cds /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326	34842_at

SLU7(step II splicing factor SLU7)	AI660656	Hs.76325	NM_006425		Cluster Incl. AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2351436 /clone_end=3 /gb=AI660656 /gi=4764239 /ug=Hs.76325 /len=522	37006_at
ADD2 (adducin 2 (beta))	U43959	Hs.247423	NM_001617	2p14-p13	Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145 /ug=Hs.4852 /len=1284	36052_at
DF (D component of complement (adipsin))	M84526	Hs.155597	NM_001928	19	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	40282_s_at
PLCB2 (phospholipase C, beta 2)	M95678	Hs.994	NM_004573	15q15	M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-2 mRNA, complete cds	210_at
POU4F1 (POU domain, class 4, transcription factor 1)	X64624	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein	35940_at

factor 1)					/cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492	
PPIB (peptidylprolyl isomerase B (cyclophilin B))	M63573	Hs.699	NM_000942	15q21-q22	Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671) /gb=M63573 /gi=337998 /ug=Hs.699 /len=893	35823_at
KIAA0088(KIAA0088 protein)	D42041	Hs.76847	NM_014610		Cluster Incl. D42041:Human mRNA for KIAA0088 gene, partial cds /cds=(0,2832) /gb=D42041 /gi=577294 /ug=Hs.76847 /len=3820	37040_at
LAK-4P(expressed in activated T/LAK lymphocytes)	AB002405	Hs.16165	NM_007267		Cluster Incl. AB002405:Homo sapiens mRNA for LAK-4p, complete cds /cds=(109,1149) /gb=AB002405 /gi=2760120 /ug=Hs.16165 /len=1376	32116_at
TFDP1 (transcription factor Dp-1)	L23959	Hs.79353	NM_007111	13q34	Cluster Incl. L23959:Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds /cds=(37,1269) /gb=L23959	37757_at

					/gi=414316 /ug=Hs.79353 /len=1440	
CPO (coproporphyrinogen oxidase (coproporphyria, harderoporphyria))	D16611	Hs.89866	NM_000097	3q12	Cluster Incl. D16611:Human mRNA for coproporphyrinogen oxidase, complete cds /cds=(93,1157) /gb=D16611 /gi=469488 /ug=Hs.89866 /len=2333	37999_at
MMP8 (matrix metalloproteinase 8 (neutrophil collagenase))	J05556	Hs.73862	NM_002424	11q22.3	J05556 /FEATURE=mRNA /DEFINITION=HUMCLGNA Homo sapiens collagenase mRNA, complete cds	681_at
DUSP6 (dual specificity phosphatase 6)	AB013382	Hs.180383	NM_001946	12q22-q23	Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390	41193_at
NPR3 (natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C))	M59305	Hs.123655	NM_000908	5p14-p13	Cluster Incl. M59305:Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, complete cds /cds=(362,1987) /gb=M59305 /gi=178651 /ug=Hs.123655 /len=2081	34519_at

MPO (myeloperoxidase)	M19507	Hs.1817	NM_000250	17q23.1	Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	33284_at
MINPP1 (multiple inositol polyphosphate histidine phosphatase, 1)	AL050356	Hs.95907	NM_004897	10q23	Cluster Incl. AL050356:Homo sapiens mRNA; cDNA DKFZp564L2016 (from clone DKFZp564L2016) /cds=UNKNOWN /gb=AL050356 /gi=4914568 /ug=Hs.95907 /len=2396	38325_at
	S67247				Cluster Incl. S67247:smooth muscle myosin heavy chain isoform SMemb [human, umbilical cord, fetal aorta, mRNA Partial, 971 nt] /cds=(0,681) /gb=S67247 /gi=452986 /ug=Hs.2094 /len=971	32838_at
TPM4 (tropomyosin 4)	X05276	Hs.250641	NM_003290	19p13.1	Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pI) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049	33866_at

CBFA2T1 (core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related)	D43638	Hs.31551	NM_004349	8q22	Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	35638_at
LEF1 (lymphoid enhancer-binding factor 1)	AL049409	Hs.44865	NM_016269	4q23-q25	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	36021_at
AHR (aryl hydrocarbon receptor)	L19872	Hs.170087	NM_001621	7p15	Cluster Incl. L19872:Human AH-receptor mRNA, complete cds /cds=(375,2921) /gb=L19872 /gi=416141 /ug=Hs.170087 /len=5228	40516_at
SERPING1 (serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1,	X54486	Hs.151242	NM_000062	11q12-q13.1	Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827	39775_at
PIG8(etoposide induced 2.4 mRNA)	AF010313	Hs.286027	NM_004879		Cluster Incl. AF010313:Homo sapiens Pig8 (PIG8) mRNA, complete cds	38097_at

						/cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165	
SEPT3 (septin 3)	Z99716	Hs.8073	NM_019106	22q13.2		Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606	36607_at
TPM1 (tropomyosin 1 (alpha))	M19267	Hs.77899	NM_000366	15q22.1		Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	36791_g_at
AMPD3 (adenosine monophosphate deaminase (isoform E))	U29926	Hs.83918	NM_000480	11p15		Cluster Incl. U29926:Human AMP deaminase (AMPD3) gene, promoter 1a region /cds=(453,2777) /gb=U29926 /gi=1002661 /ug=Hs.83918 /len=4018	38463_s_at

HELO1(homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	AL034374	Hs.250175	NM_021814		Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL	33821_at
PRKWNK1 (protein kinase, lysine deficient 1)	U00946	Hs.184592	NM_018979	12p13.3	Cluster Incl. U00946:Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA /cds=UNKNOWN /gb=U00946 /gi=405048 /ug=Hs.184592 /len=1971	32185_at
EPB41L2 (erythrocyte membrane protein band 4.1-like 2)	AF027299	Hs.7857	NM_001431	6q23	Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /cds=(44,3061) /gb=AF027299 /gi=2739095 /ug=Hs.7857 /len=4316	32585_at
CD48 (CD48 antigen (B-cell membrane protein))	M37766	Hs.901	NM_001778	1q21.3-q22	Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds	38006_at

					/cds=(20,751) /gb=M37766 /gi=187518 /ug=Hs.901 /len=1058	
PRDX2 (peroxiredoxin 2)	L19185	Hs.146354	NM_005809	13q12	Cluster Incl. L19185:Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds /cds=(124,720) /gb=L19185 /gi=440307 /ug=Hs.146354 /len=980	39729_at
TIP30(Tat-interacting protein (30kD)	AF039103	Hs.90753	NM_006410		Cluster Incl. AF039103:Homo sapiens Tat-interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297	38824_at
ARG1 (arginase, liver)	M14502	Hs.289057	NM_000045	6q23	M14502 /FEATURE=mRNA /DEFINITION=HUMARGL Human liver arginase mRNA, complete cds	1962_at
TRA1 (tumor rejection antigen (gp96) 1)	X15187	Hs.82689	NM_003299	12q24.2-q24.3	X15187 /FEATURE=cds /DEFINITION=HSTRA1 Human tra1 mRNA for human homologue of murine tumor rejection antigen gp96	442_at

HOXA7 (homeo box A7)	AC004080	Hs.70954	NM_006896	7p15-p14	Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170O19 from 7p15-p21 /cds=(0,1247) /gb=AC004080 /gi=2822164 /ug=Hs.110637 /len=1248	41448_at
CD34 (CD34 antigen)	M81945	Hs.85289	NM_001773	1q32	Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616	38747_at
SNL (singed (Drosophila)-like (sea urchin fascin homolog like))	U03057	Hs.118400	NM_003088	7p22	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	39070_at
BZRP (benzodiazapine receptor (peripheral))	M36035	Hs.202	NM_000714	22q13.31	Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035 /gi=184333 /ug=Hs.202 /len=811	32806_at

SIAT4C (sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase))	X74570	Hs.75268	NM_006278	11q23-q24	Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase /cds=(162,1151) /gb=X74570 /gi=414890 /ug=Hs.75268 /len=1741	36916_at
TCF7 (transcription factor 7 (T-cell specific, HMG-box))	X59871	Hs.169294	NM_003202	5q31.1	Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form C) /cds=(79,885) /gb=X59871 /gi=36789 /ug=Hs.169294 /len=2910	32649_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38095_i_at
BMI1 (murine leukemia viral (bmi-1) oncogene homolog)	L13689	Hs.431	NM_005180	10p13	Cluster Incl. L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cds=(479,1459) /gb=L13689 /gi=291872 /ug=Hs.431 /len=3203	41562_at

RBM9 (RNA binding motif protein 9)	AL009266	Hs.5011	NM_014309	22q13.1	Cluster Incl. AL009266:H. sapiens cDNA similar to C. elegans RNA binding protein U14946, Q10572, complete cds /cds=(170,1273) /gb=AL009266 /gi=2664428 /ug=Hs.155156 /len=1876	40260_g_at
NUCB1 (nucleobindin 1)	M96824	Hs.172609	NM_006184	19q13.2-q13.4	Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650	40817_at
IGF2R (insulin-like growth factor 2 receptor)	Y00285	Hs.76473	NM_000876	6q26	Y00285 /FEATURE=cds /DEFINITION=HSIGFIIR Human mRNA for insuline-like growth factor II receptor /NOTE=replacement of probe set 972_s_at	160027_s_at
FCN1 (ficolin (collagen/fibrinogen domain-containing) 1)	S80990	Hs.252136	NM_002003	9q34	Cluster Incl. S80990:ficolin [human, uterus, mRNA, 1736 nt] /cds=(532,1512) /gb=S80990 /gi=1911529 /ug=Hs.169237 /len=1723	36447_at

HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)	X00457	Hs.914		6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	38833_at
	M22806				Cluster Incl. M22806:Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene /cds=(66,1592) /gb=M22806 /gi=487831 /ug=Hs.75655 /len=2438	36666_at
					Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete cds /cds=(631,1866) /gb=AB011085 /gi=3043549 /ug=Hs.85053 /len=7758	38735_at
MGEA5 (meningioma expressed antigen 5 (hyaluronidase))	AB014579	Hs.5734	NM_012215	10q24.1-q24.3	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303	35317_at

Table 15:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
TNFRSF7 (tumor necrosis factor receptor superfamily, member 7)	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	38578_at
DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796	7	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
PFTK1 (PFTAIRE protein kinase 1)	AB020641	Hs.57856	NM_012395	7q21-q22	Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641 /gi=4240156 /ug=Hs.57856 /len=4957	36502_at

CBX7 (chromobox homolog 7)	AL031846			22q13.1	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
IGHM (immunoglobulin heavy constant mu)	X58529	Hs.302063		14q32.33	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325	41166_at
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	41796_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41165_g_at

IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
					Cluster Incl. X62822:H.sapiens gene encoding beta-galactoside alpha-2,6-sialyltransferase /cds=(310,1530) /gb=X62822 /gi=29433 /ug=Hs.2554 /len=2699	41352_at
HLA-DOB (major histocompatibility complex, class II, DO beta)	X03066	Hs.1802	NM_002120	6p21.3	Cluster Incl. X03066:Human mRNA for HLA-D class II antigen DO beta chain /cds=(56,877) /gb=X03066 /gi=32271 /ug=Hs.1802 /len=1322	38570_at
	W30677				Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614	34871_at

IL24 (interleukin 24)	AA214546	Hs.315463	NM_006850	1q32	Cluster Incl. AA214546:zr92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516	41847_at
CELSR1 (cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog)	AL031588	Hs.252387	NM_014246	22q13.3	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	41660_at
LOC54103(hypothetical protein)	AL079277	Hs.12969		7	Cluster Incl. AL079277:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605 /cds=(0,806) /gb=AL079277 /gi=5102581 /ug=Hs.12969 /len=1414	41710_at
NIFU(nitrogen fixation cluster-like)	U47101	Hs.9908		12	Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101	39165_at

					/ug=Hs.9908 /len=819	
CD79A (CD79A antigen (immunoglobulin-associated alpha))	U05259	Hs.79630	NM_001783	19q13.2	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107	38017_at
SETBP1 (SET binding protein 1)	AB022660	Hs.151717	NM_015559	18q21.1	Cluster Incl. AB022660:Homo sapiens mRNA for SET-binding protein (SEB), complete cds /cds=(5,4633) /gb=AB022660 /gi=5478317 /ug=Hs.151717 /len=5744	34990_at
NCOA3 (nuclear receptor coactivator 3)	AF012108	Hs.225977	NM_006534	20q12	Cluster Incl. AF012108:Homo sapiens Amplified in Breast Cancer (AIB1) mRNA, complete cds /cds=(200,4462) /gb=AF012108 /gi=2331249 /ug=Hs.225977 /len=6818	33381_at
POU2AF1 (POU domain, class 2, associating factor 1)	Z49194	Hs.2407	NM_006235	11q23.1	Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407	36239_at

					/len=3301	
SYNE-2(synaptic nuclei expressed gene 2)	AL080133	Hs.57749	NM_015180	22	Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	41815_at
SP140(nuclear body protein Sp140)	U36500	Hs.309943	NM_007237	2	Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173653 /ug=Hs.85283 /len=3252	40700_at
CAMP (cathelicidin antimicrobial peptide)	Z38026	Hs.51120	NM_004345	3p21.3	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	36710_at
TOSO(regulator of Fas-induced apoptosis)	AF057557	Hs.58831	NM_005449	1	Cluster Incl. AF057557:Homo sapiens anti-Fas-induced apoptosis (TOSO) mRNA, complete cds /cds=(19,1191)	32967_at

						/gb=AF057557 /gi=3169292 /ug=Hs.238857 /len=1339	
TC21(oncogene TC21)	AI365215	Hs.206097	NM_012250		11	Cluster Incl. AI365215:qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2029426 /clone_end=3 /gb=AI365215 /gi=4124904 /ug=Hs.206097 /len=918	32827_at
	AI434146					Cluster Incl. AI434146:ti36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2132604 /clone_end=3 /gb=AI434146 /gi=4294137 /ug=Hs.164284 /len=299	36403_s_at
DGKA (diacylglycerol kinase, alpha (80kD))	X62535	Hs.172690	NM_001345		12q13.3	Cluster Incl. X62535:H.sapiens mRNA for diacylglycerol kinase /cds=(103,2310) /gb=X62535 /gi=30822 /ug=Hs.172690 /len=2564	32716_at
SAC2(cDNA sequence, clone 3-26)	AB023183	Hs.52463	NM_014937		10	Cluster Incl. AB023183:Homo sapiens mRNA for KIAA0966 protein, complete cds /cds=(166,3564) /gb=AB023183	36089_at

					/gi=4589575 /ug=Hs.52463 /len=4924	
SYNE-1B(synaptic nuclear envelope 1)	AB018339	Hs.8182		6	Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
MSF (MLL septin-like fusion)	AB023208	Hs.181002	NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
BCL2 (B-cell CLL/lymphoma 2)	M14745	Hs.79241	NM_000633	18q21.3	M14745 /FEATURE= /DEFINITION=HUMBCL2C Human bcl-2 mRNA	1909_at
E2F5 (E2F transcription factor 5, p130-binding)	U31556	Hs.2331	NM_001951	8p22-q21.3	Cluster Incl. U31556:Human transcription factor E2F-5 mRNA, complete cds /cds=(38,1075) /gb=U31556 /gi=939728 /ug=Hs.2331 /len=1728	41275_at

E2F5 (E2F transcription factor 5, p130-binding)	U31556	Hs.2331	NM_001951	8p22-q21.3	U31556 /FEATURE= /DEFINITION=HSU31556 Human transcription factor E2F-5 mRNA, complete cds	1044_s_at
IL4R (interleukin 4 receptor)	X52425	Hs.75545	NM_000418	16p11.2-12.1	X52425 /FEATURE=mRNA /DEFINITION=HSIL4R Human IL-4-R mRNA for the interleukin 4 receptor	404_at
TLK1 (tousled-like kinase 1)	D50927	Hs.18895	NM_012290	8p22-p12	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927 /gi=1469196 /ug=Hs.18895 /len=4454	32219_at
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase))	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at
SH3BP5 (SH3-domain binding protein 5 (BTK-associated))	AB005047	Hs.109150	NM_004844	1q43	Cluster Incl. AB005047:Homo sapiens mRNA for SH3 binding protein, complete cds /cds=(63,1340) /gb=AB005047	38968_at

GGA2(Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2	AB029003	Hs.155546	NM_015044	16		/gi=3116213 /ug=Hs.109150 /len=2570	
						Cluster Incl. AB029003:Homo sapiens mRNA for KIAA1080 protein, partial cds /cds=(0,1554) /gb=AB029003 /gi=5689496 /ug=Hs.155546 /len=4791	40278_at
SGP28(specific granule protein (28 kDa); cysteine-rich secretory protein-3)	X94323	Hs.54431	NM_006061	6		Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	36464_at
KIAA0430(KIAA0430 gene product)	AB007890			16		Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=(0,3172) /gb=AB007890 /gi=2887438 /ug=Hs.166163 /len=6011	31936_s_at
	U92981					Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429	38577_at

E2F5 (E2F transcription factor 5, p130-binding)	U15642	Hs.2331	NM_001951	8p22-q21.3	U15642 /FEATURE= /DEFINITION=HSU15642 Human transcription factor E2F-5 mRNA, complete cds	1639_s_at
ABCA6 (ATP-binding cassette, sub-family A (ABC1), member 6)	AI651024	Hs.15780		17q21	Cluster Incl. AI651024:wa96h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2304059 /clone_end=3 /gb=AI651024 /gi=4735003 /ug=Hs.15780 /len=657	35390_at
EZH1 (enhancer of zeste (Drosophila) homolog 1)	AB002386	Hs.194669	NM_001991	17q21.1-q21.3	Cluster Incl. AB002386:Human mRNA for KIAA0388 gene, complete cds /cds=(100,2343) /gb=AB002386 /gi=2224716 /ug=Hs.194669 /len=4606	32259_at
CD19 (CD19 antigen)	M28170	Hs.96023	NM_001770	16p11.2	M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	1096_g_at
PRDM2 (PR domain containing 2, with ZNF domain)	D45132	Hs.26719	NM_012231	1p36	D45132 /FEATURE= /DEFINITION=HUMHOXY1 Homo sapiens	316_g_at

domain)						mRNA for zinc-finger DNA-binding protein, complete cds	
PSCD1 (pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1))	M85169	Hs.1050	NM_004762		17q25	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, - complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	38666_at
KIAA0136(DNA segment, Chr 16, Johns Hopkins University 32, expressed)	D50926	Hs.70359			21q22.13	Cluster Incl. D50926:Human mRNA for KIAA0136 gene, partial cds /cds=(0,2854) /gb=D50926 /gi=1469194 /ug=Hs.70359 /len=4197	36845_at
TGFBR3 (transforming growth factor, beta receptor III (betaglycan, 300kD))	L07594	Hs.79059	NM_003243		1p33-p32	L07594 /FEATURE= /DEFINITION=HUMTGFB3C Human transforming growth factor-beta type III receptor (TGF-beta) mRNA, complete cds	1897_at
DKFZP586F2423(hypothetical protein DKFZp586F2423)	AL080209	Hs.13659			7	Cluster Incl. AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN /gb=AL080209 /gi=5262698 /ug=Hs.13659	39692_at

					/len=4241	
AIM2 (absent in melanoma 2)	AF024714	Hs.105115	NM_004833	1q22	Cluster Incl. AF024714:Homo sapiens interferon-inducible protein (AIM2) mRNA, complete cds /cds=(245,1276) /gb=AF024714 /gi=2558941 /ug=Hs.105115 /len=1485	34439_at
LCN2 (lipocalin 2 (oncogene 24p3))	AI762213	Hs.204238	NM_005564	9q34	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at
KIAA0922(KIAA0922 protein)	AB023139	Hs.37892	NM_015196	4	Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505	39929_at
KIAA0769(KIAA0769 gene product)	AB018312	Hs.19056	NM_014824	11	Cluster Incl. AB018312:Homo sapiens mRNA for KIAA0769 protein, complete cds /cds=(239,2293) /gb=AB018312	32224_at

KIAA0746(KIAA0746 protein)	AB018289	Hs.49500		4	/gi=3882258 /ug=Hs.19056 /len=4326 Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein, partial cds /cds=(0,3091) /gb=AB018289 /gi=3882212 /ug=Hs.49500 /len=4086	41585_at
FCER2 (Fc fragment of IgE, low affinity II, receptor for (CD23A))	M15059	Hs.1416	NM_002002	19p13.3	Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds (H107 epitope) /cds=(213,1178) /gb=M15059 /gi=182447 /ug=Hs.1416 /len=1530	34960_g_at
AKAP11 (A kinase (PRKA) anchor protein 11)	AB014529	Hs.232076	NM_016248	13q12.2-13q14.3	Cluster Incl. AB014529:Homo sapiens mRNA for KIAA0629 protein, partial cds /cds=(0,1840) /gb=AB014529 /gi=3327071 /ug=Hs.232076 /len=5883	34657_at
KIAA0543(KIAA0543 protein)	AB011115	Hs.98507		7	Cluster Incl. AB011115:Homo sapiens mRNA for KIAA0543 protein, partial cds /cds=(0,3336) /gb=AB011115 /gi=3043609	41077_at

					/ug=Hs.98507 /len=6443	
PIR121(p53 inducible protein)	L47738	Hs.258503		5	Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881	37579_at
MAP3K5 (mitogen-activated protein kinase kinase kinase 5)	U67156	Hs.151988	NM_005923	6q22.33	U67156 /FEATURE= /DEFINITION=HSU67156 Human mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds	1327_s_at
FLJ22531(hypothetical protein FLJ22531)	W80358	Hs.55613	NM_024650	11	Cluster Incl. W80358:zh49a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-415380 /clone_end=3 /gb=W80358 /gi=1391395 /ug=Hs.55613 /len=547	41804_at
MGEA5 (meningioma expressed antigen 5 (hyaluronidase))	AB014579	Hs.5734	NM_012215	10q24.1-q24.3	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303	35317_at

MDS019(phorbolin-like protein MDS019)	AL078641	Hs.250619	NM_021822	22	Cluster Incl. AL078641:Human DNA sequence from clone 494G10 on chromosome 22 Contains part of a gene similar to phorbolin 2, ESTs and a GSS /cds=(0,419) /gb=AL078641 /gi=5162948 /ug=Hs.112449 /len=751	41472_at
KIAA0240(KIAA0240 protein)	D87077	Hs.196275		6	Cluster Incl. D87077:Human mRNA for KIAA0240 gene, partial cds /cds=(0,2953) /gb=D87077 /gi=1510154 /ug=Hs.196275 /len=6060	38892_at
PRKCB1 (protein kinase C, beta 1)	X07109	Hs.77202	NM_002738	16p11.2	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II /NOTE=replacement of probe set 1216_at	160029_at
CCR7 (chemokine (C-C motif) receptor 7)	L31584	Hs.1652	NM_001838	17q12-q21.2	L31584 /FEATURE=exon /DEFINITION=HUMEBI103 Human G protein-coupled receptor (EBI 1) gene exon 3, complete cds	1097_s_at

CDC25B (cell division cycle 25B)	S78187	Hs.153752	NM_004358	20p13	S78187 /FEATURE= /DEFINITION=S78187 CDC25Hu2=cdc25+ homolog [human, mRNA, 3118 nt]	1347_at
CCR2 (chemokine (C-C motif) receptor 2)	U95626	Hs.395	NM_000647	3p21	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at
	AL049701				Cluster Incl. AL049701:Human gene from PAC 433G19, chromosome 1 /cds=(0,370) /gb=AL049701 /gi=4678835 /ug=Hs.107325 /len=648	34446_at
P2Y10(putative purinergic receptor)	AF000545	Hs.296433	NM_014499	X	AF000545 /FEATURE=cds /DEFINITION=HSAF000545 Homo sapiens putative purinergic receptor P2Y10 gene, complete cds	358_at

MGC12335(hypothetical protein MGC12335)	AL022724	Hs.97411	NM_032744	6	Cluster Incl. AL022724:Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs /cds=(94,861) /gb=AL022724 /gi=4468306 /ug=Hs.97411 /len=1037	34043_at
P2Y10(putative purinergic receptor)	Z82200	Hs.296433	NM_014499	X	Cluster Incl. Z82200:Human DNA sequence from clone 333E23 on chromosome Xq21.1 Contains putative purinergic receptor P2Y10 /cds=(0,1019) /gb=Z82200 /gi=2370075 /ug=Hs.166137 /len=1020	36413_at
IFI41 (interferon-induced protein 41, 30kD)	L22342	Hs.241510	NM_004509		Cluster Incl. L22342:Human nuclear phosphoprotein mRNA, complete cds /cds=(0,746) /gb=L22342 /gi=402204 /ug=Hs.38125 /len=835	35718_at
ARHH (ras homolog gene family, member H)	Z35227	Hs.109918	NM_004310	4p13	Cluster Incl. Z35227:H.sapiens TTF mRNA for small G protein /cds=(579,1154)	37416_at

						/gb=Z35227 /gi=609016 /ug=Hs.109918 /len=1427	
PRKCB1 (protein kinase C, beta 1)	X07109	Hs.77202	NM_002738	16p11.2		X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II	1217_g_at
	AL049471					Cluster Incl. AL049471:Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012) /cds=UNKNOWN /gb=AL049471 /gi=4500266 /ug=Hs.12702 /len=2905	41690_at
KCNN4 (potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4)	AF022797	Hs.10082	NM_002250	19q13.2		Cluster Incl. AF022797:Homo sapiens intermediate conductance calcium-activated potassium channel (hKCa4) mRNA, complete cds /cds=(396,1679) /gb=AF022797 /gi=2674355 /ug=Hs.10082 /len=2238	41106_at

USF2 (upstream transcription factor 2, c-fos interacting)	AD000684	Hs.93649	NM_003367	19q13	Cluster Incl. AD000684:Homo sapiens DNA from chromosome 19-cosmid R30879 containing USF2, genomic sequence /cds=(0,1290) /gb=AD000684 /gi=1905917 /ug=Hs.95697 /len=1291	38324_at
KIAA0471(KIAA0471 gene product)	AB007940			1	Cluster Incl. AB007940:Homo sapiens mRNA for KIAA0471 protein, complete cds /cds=(412,1524) /gb=AB007940 /gi=3413903 /ug=Hs.107325 /len=6834	34445_at
SLC23A1 (solute carrier family 23 (nucleobase transporters), member 1)	D87075	Hs.82042	NM_005116	20p13	Cluster Incl. D87075:Human mRNA for KIAA0238 gene, partial cds /cds=(0,992) /gb=D87075 /gi=1510150 /ug=Hs.82042 /len=5608	38122_at
KIAA0441(KIAA0441 gene product)	AB007901				Cluster Incl. AB007901:Homo sapiens KIAA0441 mRNA, complete cds /cds=(168,2261) /gb=AB007901 /gi=2662162 /ug=Hs.32511 /len=5597	39658_at

				6	Cluster Incl. X07203:Human mRNA for CD20 receptor (S7) /cds=(90,983) /gb=X07203 /gi=29775 /ug=Hs.89751 /len=1597	40749_at
LEF1 (lymphoid enhancer-binding factor 1)	AL049409	Hs.44865	NM_016269	4q23-q25	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	36021_at
TCL1A (T-cell leukemia/lymphoma 1A)	X82240	Hs.2484	NM_021966	14q32.1	Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=(45,389) /gb=X82240 /gi=624960 /ug=Hs.2484 /len=1312	39318_at
SCAP1 (src family associated phosphoprotein 1)	Y11215	Hs.19126	NM_003726	17q21.3	Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524	38862_at

NCOA1 (nuclear receptor coactivator 1)	U59302	Hs.74002	NM_003743	2p23	U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	484_at
TRAF1 (TNF receptor-associated factor 1)	U19261	Hs.2134	NM_005658	9q33-q34	U19261 /FEATURE= /DEFINITION=HSU19261 Homo sapiens Epstein-Barr virus-induced protein mRNA, complete cds	849_g_at
KIAA0239(KIAA0239 protein)	D87076	Hs.9729	NM_015288	5	Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,1716) /gb=D87076 /gi=1510152 /ug=Hs.9729 /len=5630	38342_at
CASK (calcium/calmodulin-dependent serine protein kinase (MAGUK family))	AF035582	Hs.151469	NM_003688	xp11.4	Cluster Incl. AF035582:Homo sapiens CASK mRNA, complete cds /cds=(15,2708) /gb=AF035582 /gi=2661105 /ug=Hs.151469 /len=3919	31854_at
KIAA0053(KIAA0053 gene product)	D29642	Hs.1528	NM_014882	2	Cluster Incl. D29642:Human mRNA for KIAA0053 gene, complete cds	38149_at

					/cds=(193,2109) /gb=D29642 /gi=473934 /ug=Hs.1528 /len=2739	
APOC4 (apolipoprotein C-IV)	U32576	Hs.110675	NM_001646	19q13.2	Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, complete cds /cds=(40,423) /gb=U32576 /gi=975892 /ug=Hs.110675 /len=613	34454_r_at
SP100 (nuclear antigen Sp100)	M60618	Hs.77617	NM_003113	2q37.1	Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complete cds /cds=(31,1473) /gb=M60618 /gi=178688 /ug=Hs.77617 /len=1879	37352_at
KIAA1010(KIAA1010 protein)	AB023227	Hs.23860		10	Cluster Incl. AB023227:Homo sapiens mRNA for KIAA1010 protein, partial cds /cds=(0,3949) /gb=AB023227 /gi=4589669 /ug=Hs.23860 /len=5524	34712_at
SP100 (nuclear antigen Sp100)	M60618	Hs.77617	NM_003113	2q37.1	Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complete cds /cds=(31,1473) /gb=M60618	37353_g_at

					/gi=178688 /ug=Hs.77617 /len=1879	
JAK1 (Janus kinase 1 (a protein tyrosine kinase))	AL039831	Hs.50651	NM_002227	1p32.3-p31.3	Cluster Incl. AL039831:DKFZp434D1112_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5866713 /ug=Hs.50651 /len=579	34877_at
PPP3CC (protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma))	S46622	Hs.75206	NM_005605	8	Cluster Incl. S46622:calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] /cds=(286,1794) /gb=S46622 /gi=258000 /ug=Hs.75206 /len=2134	32541_at
MTMR1 (myotubularin related protein 1)	AJ224979	Hs.23200		xq28	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200 /len=2582	34654_at
HLA-F (major histocompatibility complex, class I, F)	AL022723	Hs.110309	NM_018950	6p21.3	Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, class I, F (CDA12)) /cds=(97,1185) /gb=AL022723	37420_i_at

						/gi=5002624 /ug=Hs.110309 /len=1303	
PRKCB1 (protein kinase C, beta 1)	X06318	Hs.77202	NM_002738	16p11.2		X06318 /FEATURE=cds /DEFINITION=HSPKCB1A Human mRNA for protein kinase C (PKC) type beta I	1336_s_at
GTSE1 (G-2 and S-phase expressed 1)	AL031588	Hs.122552	NM_016426	22q13.2-q13.3		Cluster Incl. AL031588:dJ1163J1.3 (novel protein similar to mouse B99) /cds=(0,2140) /gb=AL031588 /gi=4007108 /ug=Hs.122552 /len=2821	39872_at
SLC7A6 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 6)	D87432	Hs.10315	NM_003983	16q22.1-q22.3		Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(261,1808) /gb=D87432 /gi=1665758 /ug=Hs.10315 /len=6296	39533_at

Table 16: Major Types (BM, CLL, CML, ALL, AML)

HAUPTGRUPPEN

COMPARISON		Description					
CLL - CML		M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	HG_U95_Target: 1105_s_at_HG-U95Av2	1105_s_at	T cell receptor beta locus	TRB	7q35
AML - CML		Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.13793 /len=517	HG_U95_Target: 31793_at_HG-U95Av2	31793_at	defensin, alpha 3, neutrophil-specific	DEFA3	8pter-p23.3
AML - BM	ALL - BM	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077	HG_U95_Target: 32775_r_at_HG-U95Av2	32775_r_at	phospholipid scramblase 1	PLSCR1	3q23

AML - CML	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	HG_U95_Target: 32821_at_HG-U95Av2	32821_at	lipocalin 2 (oncogene 24p3)	LCN2	9q34
ALL - BM	Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150	HG_U95_Target: 33860_at_HG-U95Av2	33860_at	KIAA0462 protein	KIAA0462*	1p36.13
ALL - AML	Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.64797 /len=3727	HG_U95_Target: 33944_at_HG-U95Av2	33944_at	amyloid beta (A4) precursor-like protein 2	APLP2.	11q24
ALL - AML	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	HG_U95_Target: 36021_at_HG-U95Av2	36021_at	lymphoid enhancer-binding factor 1	LEF1	4q23-q25
AML - CLL	Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407 /len=3301	HG_U95_Target: 36239_at_HG-U95Av2	36239_at	POU domain, class 2, associating factor 1	POU2AF1	11q23.1
AML - CML	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	HG_U95_Target: 36464_at_HG-	36464_at	specific granule protein (28 kDa)	SGP28*	6p12.3

		U95Av2				
AML - BM	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	HG_U95_Target: 36710_at_HG-U95Av2	36710_at	cathelicidin antimicrobial peptide	CAMP	3p21.3
ALL - CML	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	HG_U95_Target: 36809_at_HG-U95Av2	36809_at	Charot-Leyden crystal protein	CLC	19q13.1
ALL - AML	Cluster Incl. U41635:Human OS-9 precurosor mRNA, complete cds /cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736	HG_U95_Target: 36996_at_HG-U95Av2	36996_at	amplified in osteosarcoma	OS-9*	12q13
ALL - CML	Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242	HG_U95_Target: 37311_at_HG-U95Av2	37311_at	transaldolase 1	TALDO1	11p15.5-p15.4
BM - CML	Cluster Incl. U52682:Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds /cds=(125,1477) /gb=U52682 /gi=1378108 /ug=Hs.82132 /len=5320	HG_U95_Target: 37625_at_HG-U95Av2	37625_at	interferon regulatory factor 4	IRF4	6p25-p23

BM - CLL	Cluster Incl. AB023169:Homo sapiens mRNA for KIAA0952 protein, complete cds /cds=(359,1927) /gb=AB023169 /gi=4589547 /ug=Hs.7935 /len=4856	HG_U95_Target: 37755_at_HG-U95Av2	37755_at	KIAA0952 protein	KIAA0952	20p12.1
ALL - CLL	Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429	HG_U95_Target: 38577_at_HG-U95Av2	38577_at	unknown	Unknown*	unknown -
AML - CLL	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	HG_U95_Target: 38578_at_HG-U95Av2	38578_at	tumor necrosis factor receptor superfamily, member 7	TNFRSF7	12p13
ALL - BM	Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) mRNA, complete cds /cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.188021 /len=4070	HG_U95_Target: 38858_at_HG-U95Av2	38858_at	potassium voltage-gated channel, subfamily H (eag-related), member 2	KCNH2	7q35-q36
ALL - AML	Cluster Incl. AL008726:dJ337O18.2 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C)) /cds=(133,1575) /gb=AL008726 /gi=3183870 /ug=Hs.118126 /len=1946	HG_U95_Target: 39062_at_HG-U95Av2	39062_at	protective protein for beta-galactosidase (galactosialidosis)	PPGB	20q13.1
BM - CLL	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	HG_U95_Target: 39070_at_HG-	39070_at	singed (Drosophila)-like (sea urchin fascin homolog like)	SNL	7p22

		U95Av2				
ALL - AML	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	HG_U95_Target: 41220_at_HG-U95Av2	41220_at	MLL septin-like fusion	MSF	17q25
CLL - CML	BM - CML	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	HG_U95_Target: 41609_at_HG-U95Av2	41609_at	major histocompatibility complex, class II, DM beta	HLA-DMB	6p21.3
ALL - CLL		U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	HG_U95_Target: 484_at_HG-U95Av2	484_at	nuclear receptor coactivator 1	NCOA1	2p23
		description	HG-U95 Target	Probe Set ID	Title	Gene Symbol	Map Location

Table 17. AML_WHO [other, t(11q23)/MLL, t(8;21), inv(16), t(15;17)]

INV16-	INV16-OTHER	INV16-T821		Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	HG_U95_Target:37407_s_at_HG-U95Av2	37407_s_at	myosin, heavy polypeptide 11, smooth muscle	MYH11	16p13.13-p13.12
INV16-				AF001548 /FEATURE=mRNA /DEFINITION=HUAF001548 Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence	HG_U95_Target:767_at_HG-U95Av2	767_at	myosin, heavy polypeptide 11, smooth muscle	MYH11	16p13.13-p13.12
INV16-OTHER				Cluster Incl. U68186:Human extracellular matrix protein 1 mRNA, complete cds /cds=(103,1725) /gb=U68186 /gi=2660683 /ug=Hs.81071 /len=1819	HG_U95_Target:37600_at_HG-U95Av2	37600_at	extracellular matrix protein 1	ECM1	1q21

INV16-T1517			M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds	HG_U95_Target:245_a_HG-U95Av2	245_at	selectin L (lymphocyte adhesion molecule 1)	SELL	1q23-q25
INV16-T1517			Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	HG_U95_Target:38833_at_HG-U95Av2	38833_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	6p21.3
INV16-T821			Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor protein (doc-1) mRNA, complete cds /cds=(522,863) /gb=AF006484 /gi=2738496 /ug=Hs.3436 /len=1608	HG_U95_Target:41535_at_HG-U95Av2	41535_at	CDK2-associated protein 1	CDK2AP1	12q24.31
MLL-			Cluster Incl. AB007888:Homo sapiens KIAA0428 mRNA, complete cds /cds=(1414,2526) /gb=AB007888 /gi=2887430 /ug=Hs.28578 /len=5940	HG_U95_Target:34306_at_HG-U95Av2	34306_at	muscleblind (Drosophila)-like	MBNL	3q25
MLL-	MLL-T821		Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein beta subunit /cds=(27,794) /gb=X71129 /gi=297901	HG_U95_Target:36881_at_HG-U95Av2	36881_at	electron-transfer-flavoprotein, beta polypeptide	ETFB	19q13.3

			/ug=Hs.74047 /len=835						
MLL-INV16			Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913) /gb=AF037989 /gi=3265032 /ug=Hs.110776 /len=1937	HG_U95_Target:38994_at_HG-U95Av2	38994_at	STAT induced STAT inhibitor-2	STATI2*	12q	
MLL-INV16			Cluster Incl. M33680:Human 26-kDa cell surface protein TAPA-1 mRNA, complete cds /cds=(238,948) /gb=M33680 /gi=338677 /ug=Hs.54457 /len=1480	HG_U95_Target:35282_r_at_HG-U95Av2	35282_r_at	CD81 antigen (target of antiproliferative antibody 1)	CD81	11p15	
MLL-INV16			Cluster Incl. X79683:H.sapiens LAMB2 mRNA for beta2 laminin /cds=(165,5561) /gb=X79683 /gi=663206 /ug=Hs.90291 /len=5673	HG_U95_Target:38812_at_HG-U95Av2	38812_at	laminin, beta 2 (laminin S)	LAMB2	3p21	
MLL-OTHER			Y08200 /FEATURE= /DEFINITION=HSRABGTRA Homo sapiens mRNA for rab geranylgeranyl transferase, alpha-subunit	HG_U95_Target:100_g_at_HG-U95Av2	100_g_at	Rab geranylgeranyltransferase, alpha subunit	RABGGTA	14q11.2	

MLL-OTHER			Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,1096) /gb=U03105 /gi=476094 /ug=Hs.75969 /len=2061	HG_U95_Target:36980 _at_HG-U95Av2	36980_at	proline-rich protein with nuclear targeting signal	B4-2*	6q16.1
MLL-OTHER			Cluster Incl. AF001461:Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA, complete cds /cds=(30,881) /gb=AF001461 /gi=3378030 /ug=Hs.76526 /len=1354	HG_U95_Target:37026 _at_HG-U95Av2	37026_at	core promoter element binding protein	COPEB	10p15
MLL-OTHER			Cluster Incl. M36542:Human lymphoid specific transcription factor mRNA, complete cds /cds=(54,1445) /gb=M36542 /gi=339495 /ug=Hs.1101 /len=2048	HG_U95_Target:37417 _at_HG-U95Av2	37417_at	POU domain, class 2, transcription factor 2	POU2F2	19q13.31
MLL-T1517			Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921	HG_U95_Target:38435 _at_HG-U95Av2	38435_at	peroxiredoxin 4	PRDX4	Xp22.13
MLL-T1517	OTHER-T1517	T1517-T1821	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817	HG_U95_Target:39649 _at_HG-U95Av2	39649_at	Rho GTPase activating protein 4	ARHGAP4	Xq28

			/gi=840785 /ug=Hs.3109 /len=3236							
MLL-T821	OTHER-T821		Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cds=(8,736) /gb=M63582 /gi=190297 /ug=Hs.182231 /len=1457	HG_U95_Target:32323_at HG-U95Av2	32323_at	thyrotropin-releasing hormone	TRH	3q13.3-q21		
OTHER-T1517	T1517-T821		Cluster Incl. M92299:Human homeobox 2.1 protein (HOX2A) mRNA, complete cds /cds=(275,1084) /gb=M92299 /gi=184292 /ug=Hs.22554 /len=2037	HG_U95_Target:34251_at HG-U95Av2	34251_at	homeo box B5	HOXB5	17q21-q22		
			Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	HG_U95_Target:40718_at HG-U95Av2	40718_at	cathepsin W (lymphopain)	CTSW	11q13.1		
OTHER-T821	T821-T1517		Cluster Incl. AF042792:Homo sapiens alpha 2 delta calcium channel subunit isoform mRNA, complete cds /cds=(161,3598) /gb=AF042792 /gi=2781438 /ug=Hs.127436 /len=5463	HG_U95_Target:37811_at HG-U95Av2	37811_at	calcium channel, voltage-dependent, alpha 2/delta subunit 2	CACNA2D2	3p21.3		

T1517-			Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777	HG_U95_Target:38487_at_HG-U95Av2	38487_at	hypothetical protein FLJ12442, KIAA0246	STAB1* 3p21.31
T821-			Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753	HG_U95_Target:33121_g_at_HG-U95Av2	33121_g_at	regulator of G-protein signalling - 10	RGS10 10q25
T821-			Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	HG_U95_Target:35638_at_HG-U95Av2	35638_at	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related	CBFA2T1 8q22
T821-			Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492	HG_U95_Target:35940_at_HG-U95Av2	35940_at	POU domain, class 4, transcription factor 1	POU4F1 13q21.1-q22
used in comparison			Description	HG-U95 Target	Probe Set ID	Title	Gene Symbol Map Location

Table 17. Hierachical clustering of 55 AML samples (rows) versus 25 informative genes (columns). In total, 15 comparisons within the 5 groups were performed (pairwise and one-versus-all). Genes were selected for maximal accuracy and confidence based on a modified signal-to-noise (S2N) algorithm [see (Ref)]. The scaled gene expression levels are coded by intensity and shown on a scale from black (no gene expression) to bright red (highest expression). The AML subgroups 'other' (n=10), t(11q23)/MLL (n=10), inv(16) (n=10), t(8;21) (n=9), and t(15;17) (n=16) are colored according to their chromosomal aberrations. The minimal set of informative genes is given by approved symbols by the HGNC (not yet approved genes are marked by asterisks).

Table 18. ALL_detail [t(11q23)/MLL, t(9;22), t(8;14), T-ALL]

ALLPH-ALLT		M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	HG_U95_Target:1105_s_at_HG-U95Av2	**1105_s_at**	T cell receptor beta locus	**TRB**	7q35
ALLPH-		J03779 /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblastic leukemia antigen (CALLA) mRNA, complete cds	HG_U95_Target:1389_at_HG-U95Av2	**1389_at**	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	**MME**	3q25.1-q25.2
ALL814-		M16038 /FEATURE= /DEFINITION=HUMLYN Human lyn mRNA encoding a tyrosine kinase	HG_U95_Target:1402_at_HG-U95Av2	**1402_at**	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	**LYN**	8q13
ALL814-ALLMLL		U22376 /FEATURE=cds#3 /DEFINITION=HSU22376 Human (c-myb) gene, complete primary cds, and five complete alternatively spliced cds	HG_U95_Target:1474_s_at_HG-U95Av2	**1474_s_at**	v-myb myeloblastosis viral oncogene homolog (avian)	**MYB**	6q22-q23
ALL814-ALLMLL		M15024 /FEATURE= /DEFINITION=HUMCMYBLA Human c-myb mRNA, complete cds	HG_U95_Target:2042_s_at_HG-U95Av2	**2042_s_at**	v-myb avian myeloblastosis viral oncogene homolog	**MYB**	6q22-q23

ALLMLL-ALLT	L23805 /FEATURE= /DEFINITION=HUMCATENIN Human alpha1(E)-catenin mRNA, complete cds	HG_U95_Target:2069 s_at_HG-U95Av2	2069_s_at	catenin (cadherin-associated protein), alpha 1 (102kD)	CTNNA1	5q31
ALLT-	Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL034374 /gi=4455565 /ug=Hs.234555 /len=2432	HG_U95_Target:3382 1_at_HG-U95Av2	33821_at	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	HELO1	6
ALL814-ALLPH	Cluster Incl. AB020674:Homo sapiens mRNA for KIAA0867 protein, complete cds /cds=(152,1732) /gb=AB020674 /gi=4240222 /ug=Hs.52081 /len=4339	HG_U95_Target:3526 0_at_HG-U95Av2	35260_at	KIAA0867 protein	MONDOA*	12q21.31
ALL814-ALLT	Cluster Incl. D90144:Homo sapiens gene for LD78 alpha precursor, complete cds /cds=(86,364) /gb=D90144 /gi=219905 /ug=Hs.73817 /len=781	HG_U95_Target:3610 3_at_HG-U95Av2	36103_at	small inducible cytokine A3 (homologous to mouse Mip-1a)	SCYA3	17q11-q21
ALLMLL-	Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312	HG_U95_Target:3663 8_at_HG-U95Av2	36638_at	connective tissue growth factor	CTGF	6q23.1

ALLMLL-ALLPH	Cluster Incl. D16532:Human gene for very low density lipoprotein receptor, 5flanking and /cds=(615,3236) /gb=D16532 /gi=407220 /ug=Hs.73729 /len=3853	HG_U95_Target:3687 3_at_HG-U95Av2	36873_at	very low density lipoprotein receptor	VLDLR	9p24
ALL814-ALLPH	Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U05770 /gi=2182176 /ug=Hs.79274 /len=1597	HG_U95_Target:3774 7_at_HG-U95Av2	37747_at	annexin A5	ANXA5	4q28-q32
ALLPH-ALLT	Cluster Incl. AA919102:ol84h02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gi=3058992 /ug=Hs.95327 /len=622	HG_U95_Target:3831 9_at_HG-U95Av2	38319_at	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D	11q23
ALLMLL-ALLPH	Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010059 /gi=4688891 /ug=Hs.88012 /len=1232	HG_U95_Target:4072 3_at_HG-U95Av2	40723_at	SHP2 interacting transmembrane adaptor	SIT*	9p13-p12
ALLMLL-ALLT	Cluster Incl. AF102803:unitled /cds=(2,2722) /gb=AF102803 /gi=4092760 /ug=Hs.178452 /len=3868	HG_U95_Target:4115 3_f_at_HG-U95Av2	41153_f_at	catenin (cadherin-associated protein), alpha 1 (102kD	CTNNA1	5q31
ALL814-ALLPH	Cluster Incl. AW024285:wt69d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512715 /clone_end=3 /gb=AW024285 /gi=5877815 /ug=Hs.179882 /len=550	HG_U95_Target:4117 7_at_HG-U95Av2	41177_at	hypothetical protein FLJ12443	FLJ12443*	5p15.33

ALL814-ALLT		Cluster Incl. X02994:Human mRNA for adenosine deaminase (adenosine aminohydrolase, EC 3.5.4.4) /cds=(95,1186) /gb=X02994 /gi=28379 /ug=Hs.12174 /len=1498	HG_U95_Target:4165 4_at_HG-U95Av2	41654_at	adenosine deaminase	ADA	20q12-q13.11
ALLPH-		Cluster Incl. AB020677:Homo sapiens mRNA for KIAA0870 protein, complete cds /cds=(436,1998) /gb=AB020677 /gi=4240228 /ug=Hs.18166 /len=4484	HG_U95_Target:4173 4_at_HG-U95Av2	41734_at	KIAA0870 protein	KIAA0870*	8q24.3
ALLMLL-ALLPH		Glucocorticoid Receptor, Beta	HG_U95_Target:706_at_HG-U95Av2	706_at	Glucocorticoid Receptor, Beta		
used in comparison		Decsvription_Affymetrix	HG-U95 Target	Probe Set ID	Title	Gene Symbol	Map Location

Table 18. Hierachical clustering of 17 ALL samples (rows) versus 19 informative genes (columns). In total, 10 pairwise or OVA comparisons within the 4 groups were performed. Genes were selected for maximal accuracy and confidence based on a modified

S2N algorithm [see (Ref)]. The scaled gene expression levels are coded by intensity and shown on a scale from black (no gene expression) to bright red (highest expression). The ALL subgroups t(11q23)/MLL (n=4), t(9;22) (n=7), t(8;14) (n=3), and T-ALL (n=3) are colored according to their chromosomal aberrations. The minimal set of informative genes is given by approved symbols by the HGNC (asterisks mark not yet approved genes).

Table 19 - Additional Comparisons

ALLPHNEG - ALLPHPOS						
38336_at	Cluster Incl. AB023230:Homo sapiens mRNA for KIAA1013 protein, partial cds /cds=(0,3188) /gb=AB023230 /gi=4589675 /ug=Hs.96427 /len=4783	HG_U95_Target:38336_at_HG-U95Av2	38336_at	KIAA1013 protein	KIAA1013	3
33134_at	Cluster Incl. AB011083:Homo sapiens mRNA for KIAA0511 protein, partial cds /cds=(0,2802) /gb=AB011083 /gi=3043545 /ug=Hs.8402 /len=3563	HG_U95_Target:33134_at_HG-U95Av2	33134_at	adenylate cyclase 3	ADCY3	2p24-p22

ALLB - ALLT						
38319_at	Cluster Incl. AA919102:ol84h02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gi=3058992 /ug=Hs.95327 /len=622	HG_U95_Target:38319_at_HG-U95Av2	38319_at	CD3D antigen, delta polypeptide (TIT3 complex)	CD3D	11q23

1105_s_at	M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA complete cds	HG_U95_Target:1105_s_at_HG-U95Av2	1105_s_at	T cell receptor beta locus	TRB	7q35

ALLPH - CML			-	-		
38894_g_at	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136	HG_U95_Target:38894_g_at_HG-U95Av2	38894_g_at	Cluster	AL008637	unknown
35016_at	Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080	HG_U95_Target:35016_at_HG-U95Av2	35016_at	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)	CD74	5q32
39301_at	Cluster Incl. X85030:H.sapiens mRNA for skeletal muscle-specific calpain /cds=(0,2465) /gb=X85030 /gi=791039 /ug=Hs.239689 /len=2466	HG_U95_Target:39301_at_HG-U95Av2	39301_at	calpain 3, (p94)	CAPN3	15q15.1-q21.1

ALLMLL - AMLMLL						
266_s_at	L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3 region	HG_U95_Target:266_s_at HG-U95Av2	266_s_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21
36638_at	Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312	HG_U95_Target:36638_at HG-U95Av2	36638_at	connective tissue growth factor	CTGF	6q23.1

Table 20

1. Analyse: major leukemia types versus normal bone marrow

	ALL - AML	samples: 18 / 59	pValue	**selected**
	accuracy	*0.974025974025974*		
	confidence	*0.949191799863432*		
1	41220_at	1.43161207339479	0	*
2	36996_at	-1.41523985920205	0	*
3	33944_at	-1.36856428236618	0	*
4	41809_at	1.34726978852919	0	
5	39062_at	-1.32477468024042	0	*
6	36021_at	1.29482788383042	0	*
7	40282_s_at	-1.25276275727203	0	
8	39801_at	-1.18216117554755	0	
9	41808_at	1.16535104461878	0	
10	38791_at	-1.16212420300011	0	

11	38705_at	1.10578452683281	0	
12	38017_at	1.09519463190211	0	
13	38233_at	-1.08734958364712	0	
14	40081_at	-1.06895950257537	0	
15	33414_at	-1.06893939139052	0	
16	36644_at	-1.06866972901421	0	
17	1497_at	-1.05371604908866	0	
18	34670_at	-1.0471297974693	0	
19	39689_at	-1.02349800799274	0	
20	36553_at	0.461827371901751	0	
	ALL - BM	samples: 18 / 8		
	accuracy	*1*		
	confidence	*0.973577941615687*		
1	32775_r_at	-1.99123472883631	0	*
2	38858_at	-1.89835994048167	0	*
3	33860_at	-1.8349786493313	0	*
4	33944_at	-1.79527299060519	0	

5	32800_at	-1.78206927960542	0
6	35204_at	-1.77698316964481	0
7	38112_g_at	-1.75527325798005	0
8	38735_at	-1.75431905717345	0
9	137_at	-1.75261998994426	0
10	1495_at	-1.73006006400362	0
11	36661_s_at	-1.70636382014738	0
12	38225_at	-1.66016477586249	0
13	39860_at	1.65854625573936	0
14	32166_at	-1.65691236756089	0
15	32530_at	1.64232673980553	0
16	35355_at	1.62316234982832	0
17	1529_at	-1.60938224689727	0
18	36790_at	-1.6093508135706	0
19	2045_s_at	-1.59880026139776	0
20	36553_at	0.997704664996536	0

ALL - CLL samples: 18 / 8

	accuracy	*1*	
	confidence	*1*	
1	484_at	-2.96991037890552	0
2	38577_at	-2.76720679743789	0
3	2019_s_at	-2.66997144118244	0
4	33812_at	-2.65004620998946	0
5	34663_at	-2.56576070575816	0
6	36894_at	-2.56382539311197	0
7	39670_at	-2.48013356223836	0
8	41660_at	-2.4799018378336	0
9	39165_at	-2.3871739157192	0
10	31870_at	-2.36838597731039	0
11	34871_at	-2.36033294682702	0
12	34830_at	-2.33471776306134	0
13	31936_s_at	-2.25951360532653	0
14	1062_g_at	-2.25550068155602	0
15	41847_at	-2.23298915825072	0
16	1217_g_at	-2.21920314115838	0

17	1529_at	-2.17991363072808	0	
18	41796_at	-2.17392867117507	0	
19	32597_at	-2.13552223797253	0	
20	33266_at	1.44232706973843	0	
	ALL - CML	samples: 18 / 10		
	accuracy	*1*		
	confidence	*1*		
1	36809_at	-2.79788870256583	0	*
2	37311_at	-2.20009414203519	0	*
3	36766_at	-2.15356495523503	0	
4	38894_g_at	-2.11314073543331	0	
5	39179_at	-2.08890598787237	0	
6	38893_at	-2.05723533682216	0	
7	37897_s_at	-2.05026870146261	0	
8	41809_at	1.98458593845403	0	
9	36963_at	-1.95232400595449	0	
10	39301_at	-1.91549367394028	0	

11	40610_at	1.91246286924336	0	
12	38879_at	-1.87541355348469	0	
13	41338_at	1.86506063801814	0	
14	39968_at	-1.81415292791782	0	
15	33371_s_at	-1.81111388769192	0	
16	37149_s_at	-1.77170759525375	0	
17	38895_i_at	-1.77027078711718	0	
18	41220_at	1.75387842844952	0	
19	37099_at	-1.74839569592051	0	
20	40159_r_at	-1.35163593608562	0	

	AML - BM	samples: 59 / 8		
	accuracy	*1*		
	confidence	*0.995997161972555*		
1	36710_at	-2.29217042550277	0	*
2	32775_r_at	-2.24397275344625	0	*
3	32821_at	-1.98392215005915	0	
4	37149_s_at	-1.94686927462724	0	

5	37015_at	-1.89128914250756	0
6	36894_at	-1.80507021485339	0
7	38735_at	-1.78884482794867	0
8	33752_at	-1.77319451495748	0
9	34654_at	-1.67560279229506	0
10	1115_at	-1.62050106692579	0
11	31859_at	-1.52416410078922	0
12	1980_s_at	1.51765867172316	0
13	36464_at	-1.49540428238676	0
14	38858_at	-1.48511074361835	0
15	38225_at	-1.4790110074487	0
16	39170_at	-1.45392862675606	0
17	39929_at	-1.44420537588163	0
18	36021_at	-1.42322337311917	0
19	32259_at	-1.41395952112425	0
20	41138_at	1.25347154740786	0

AML - CLL samples: 59 / 8

	accuracy	*1*		
	confidence	*1*		
1	36239_at	-3.31028543322741	0	*
2	41220_at	-3.2480863078754	0	
3	1096_g_at	-3.1269759462136	0	
4	36155_at	-3.08191178811872	0	
5	38578_at	-3.06174627261543	0	*
6	34871_at	-3.02230826662657	0	
7	38006_at	-2.88939117591885	0	
8	41165_g_at	-2.87065891259428	0	
9	1105_s_at	-2.81674515012354	0	
10	41166_at	-2.75359060509193	0	
11	31936_s_at	-2.75277577570011	0	
12	33812_at	-2.74332185979714	0	
13	41796_at	-2.71763998725163	0	
14	36894_at	-2.64049311405919	0	
15	38577_at	-2.63072228466709	0	
16	38666_at	-2.61485585331331	0	

17	32597_at	-2.61456952032068	0	
18	41847_at	-2.59409998700552	0	
19	34830_at	-2.5698161906968	0	
20	33266_at	1.336807541194	0	
	AML - CML	samples: 59 / 10		
	accuracy	*1*		
	confidence	*0.956293899622379*		
1	36464_at	-2.85754269919935	0	*
2	32821_at	-2.55228282645443	0	*
3	31859_at	-2.27761090295808	0	
4	37149_s_at	-2.11494842606363	0	
5	36710_at	-1.94749857224656	0	
6	34546_at	-1.85596431666606	0	
7	33530_at	-1.82614283985583	0	
8	35919_at	-1.74217437339032	0	
9	37099_at	-1.7184463713752	0	
10	36165_at	1.7091639497163	0	

11	37054_at	-1.69705232668157	0	
12	31381_at	-1.6873086898061	0	
13	37579_at	-1.68217107035442	0	
14	33371_s_at	-1.67508882502583	0	
15	1117_at	-1.67009743506797	0	
16	38894_g_at	-1.66951302748224	0	
17	31793_at	-1.63477764661912	0	*
18	40419_at	-1.62639286532631	0	
19	37926_at	-1.59510369191926	0	
20	40159_r_at	-0.830070056055723	0	

	BM - CLL	samples: 8 / 8		
	accuracy	*1*		
	confidence	*1*		
1	39070_at	6.29661458968093	0	*
2	37755_at	4.71476584328837	0	*
3	33963_at	4.63206684324173	0	
4	38415_at	-4.49254544394577	0	

5	36123_at	4.12198883271914	0
6	37615_at	3.82297014835908	0
7	38116_at	3.70165567234484	0
8	38414_at	3.60409203763551	0
9	41220_at	-3.59882846329979	0
10	34871_at	-3.59319336097498	0
11	35643_at	3.56571508955085	0
12	1096_g_at	-3.51858708122275	0
13	33386_at	3.50471765190995	0
14	1884_s_at	3.48564292772594	0
15	37149_s_at	3.4769522926405	0
16	820_at	3.37687376127416	0
17	38269_at	-3.31356010895055	0
18	35995_at	3.26267624054277	0
19	33358_at	3.25001188548107	0
20	33284_at	3.23482135945872	0

BM - CML samples: 8 / 10

	accuracy	*1*		
	confidence	*1*		
1	37625_at	2.87622426554922	0	*
2	41609_at	2.52321020501761	0	*
3	36661_s_at	2.51057654386246	0	
4	1911_s_at	-2.42145340446397	0	
5	854_at	2.37696256335487	0	
6	36773_f_at	2.32488494287137	0	
7	35016_at	2.24094140253387	0	
8	33274_f_at	2.21051775352204	0	
9	38112_g_at	2.13305817504128	0	
10	38194_s_at	2.09822821859324	0	
11	41165_g_at	2.09291822272078	0	
12	33273_f_at	2.0687446585274	0	
13	39179_at	-2.04974106118371	0	
14	432_s_at	2.01424464352775	0	
15	36588_at	1.99886555057795	0	
16	39968_at	-1.98085064661371	0	

17	1385_at	1.98022588084225	0	
18	36629_at	-1.9763991250365	0	
19	38728_at	1.95859957483225	0	
20	38472_at	1.95627106051459	0	
	CLL - CML	samples: 8 / 10		
	accuracy	*1*		
	confidence	*1*		
1	1105_s_at	6.65345823459692	0	*
2	41609_at	5.09272743129851	0	*
3	1096_g_at	4.79791769602114	0	
4	34210_at	4.5885400157468	0	
5	36155_at	4.51821220572632	0	
6	36766_at	-4.38087516961473	0	
7	41220_at	4.30356291392085	0	
8	41165_g_at	4.29933289075313	0	
9	37625_at	4.27214024229386	0	
10	37027_at	4.17726581707744	0	

11	34871_at	4.11725674890371	0
12	38095_i_at	4.01294758950756	0
13	38578_at	3.96024474623017	0
14	38116_at	-3.93637939332745	0
15	35643_at	-3.90694033464584	0
16	38833_at	3.90073371467641	0
17	41164_at	3.89237729890143	0
18	37344_at	3.8687581898534	0
19	39670_at	3.86448376068684	0
20	35016_at	3.74007150430317	0

2. Analyse: analysis of AML subtypes according to the WHO nomenclature

	AMLMLL -	samples: 10 / 45		
	accuracy	*1*		
	confidence	*0.92125170098711*		
1	34306_at	1.36682833853864	0	*
2	36881_at	1.25743716610113	0	*

3	38994_at	1.25633105431216	0	*
4	38485_at	1.20820491820515	0	
5	32696_at	1.20289326580336	0	
6	1983_at	-1.20116171703008	0	
7	37026_at	-1.18461413291823	0	
8	138_at	1.18310205413783	0	
9	38812_at	-1.17846157492535	0	
10	33284_at	-1.16681898560395	0	
11	32232_at	1.14845507137154	0	
12	39921_at	1.13232410733091	0	
13	34679_at	-1.12714040987389	0	
14	37992_s_at	1.11986637618528	0	
15	37029_at	1.06646924971963	0	
16	40775_at	-1.06615341562387	0	
17	36709_at	1.04614233632581	0	
18	37809_at	1.03749230715704	0	
19	38097_at	1.03525254247508	0	
20	36608_at	0.747544727295107	0	

	AMLMLL - INV16	samples: 10 / 10		
	accuracy	*1*		
	confidence	*1*		
1	38812_at	-3.34686451971904	0	*
2	37407_s_at	-3.22294767554078	0	
3	35282_r_at	2.34298696520172	0	*
4	37026_at	-2.25660818336648	0	
5	33856_at	2.25212063750729	0	
6	32174_at	-2.16867472363265	0	
7	33284_at	-2.14901777919516	0	
8	38653_at	-2.09296931036988	0	
9	1983_at	-2.06674088426528	0	
10	32696_at	2.03331671439074	0	
11	767_at	-1.99007511677258	0	
12	35329_at	1.92663715318122	0	
13	36881_at	1.88821561232545	0	
14	40767_at	-1.84600140068058	0	

15	36095_at	-1.77023425026019	0	
16	538_at	-1.75720288873792	0	
17	33319_at	1.6982626829354	0	
18	38485_at	1.69464482881744	0	
19	38747_at	-1.69240449076905	0	
20	38994_at	1.50803351291881	0	

	AMLMLL - OTHER	samples: 10 / 10		
	accuracy	*1*		
	confidence	*0.972144217378764*		
1	36980_at	-1.34035598763443	0	*
2	100_g_at	1.32781895440119	0	*
3	38994_at	1.27848227020726	0	
4	37029_at	1.27656800999718	0	
5	37026_at	-1.24955259337174	0	*
6	37417_at	1.19110502379759	0	*
7	39993_at	-1.18099046398082	0	
8	39118_at	-1.1584453284446	0	

9	36881_at	1.12737149627183	0	
10	34251_at	-1.12590878042921	0	
11	35813_at	1.10960381779872	0	
12	138_at	1.09814796011793	0	
13	36945_at	1.09593061163621	0	
14	40281_at	1.083400522626	0	
15	35941_f_at	1.0833686449051	0	
16	36952_at	1.069544205786	0	
17	37403_at	-1.06943971961994	0	
18	33689_s_at	1.06337639894231	0	
19	35372_r_at	-1.05302441823616	0	
20	32072_at	1.02664886940357	0	

	AMLMLL - T1517	samples: 10 / 16		
	accuracy	*1*		
	confidence	*1*		
1	39649_at	3.23957503042803	0	*
2	38435_at	2.60733219271303	0	*

3	38097_at	2.52025252941371	0
4	32229_at	2.40682119042641	0
5	38487_at	-2.31348932548076	0
6	32696_at	2.21878031159682	0
7	38485_at	2.10692284528305	0
8	33284_at	-2.09299435714406	0
9	38824_at	2.08124417022995	0
10	41138_at	-2.03312026813146	0
11	37967_at	1.92254422115649	0
12	33866_at	-1.91543446589406	0
13	32543_at	-1.87715920226866	0
14	1983_at	-1.87444715294745	0
15	35823_at	-1.86189545486519	0
16	36749_at	-1.81025193870165	0
17	38063_at	-1.7878938995328	0
18	39814_s_at	-1.75490742013487	0
19	36843_at	1.74046122003025	0
20	38992_at	1.71753799928796	0

	AMLMLL - T821	samples: 10 / 9		
	accuracy	*1*		
	confidence	*1*		
1	36881_at	2.29294544811647	0	*
2	32323_at	-1.98347658852059	0	*
3	37811_at	-1.98247325351143	0	
4	38391_at	1.94083259845207	0	
5	33412_at	1.92827460657744	0	
6	33284_at	-1.8385557317965	0	
7	33856_at	1.77909423724864	0	
8	38097_at	1.75444250975416	0	
9	34679_at	-1.72476579402037	0	
10	37399_at	-1.70947276971912	0	
11	36571_at	1.65482279043264	0	
12	35638_at	-1.65089605723885	0	
13	32696_at	1.63638794888669	0	
14	32184_at	1.62897781786406	0	

15	1911_s_at	-1.61083786198679	0	
16	34306_at	1.59626133274337	0	
17	138_at	1.59241136884495	0	
18	41694_at	-1.55909099909815	0	
19	32232_at	1.54494819348846	0	
20	36608_at	1.1358211663482	0	

	INV16 -	samples: 10 / 45		
	accuracy	*1*		
	confidence	*1*		
1	37407_s_at	3.02509409963287	0	*
2	767_at	1.85632628490303	0	*
3	245_at	1.70794453836984	0	
4	35282_r_at	-1.55233894025198	0	
5	38465_at	1.52686366669143	0	
6	36095_at	1.40576248502182	0	
7	32174_at	1.39467340729953	0	
8	1385_at	1.35491176363704	0	

9	41609_at	1.33680396130546	0	
10	36607_at	1.31728883029627	0	
11	34210_at	1.25533053163606	0	
12	33731_at	1.18379724417068	0	
13	2019_s_at	1.1724338503802	0	
14	40456_at	-1.17211851173852	0	
15	277_at	1.16888798816433	0	
16	931_at	1.16565119574672	0	
17	37762_at	1.14260401763247	0	
18	35230_at	1.13832458283537	0	
19	34780_at	1.12142169279465	0	
20	41200_at	1.10294533672324	0	
	INV16 - OTHER	samples: 10 / 10		
	accuracy	*1*		
	confidence	*1*		
1	37407_s_at	3.18736190788495	0	*
2	37600_at	2.62690062253569	0	*

3	767_at	2.03572561609575	0
4	41609_at	1.96219869102861	0
5	32174_at	1.91764639873215	0
6	41723_s_at	1.8341348306376	0
7	38833_at	1.8197922525705	0
8	38465_at	1.80863491318623	0
9	38095_i_at	1.80209304301982	0
10	1230_g_at	1.64339686952341	0
11	1252_at	1.59751061992943	0
12	32434_at	-1.5885630305188	0
13	40856_at	1.50737403239702	0
14	37762_at	1.49715599199852	0
15	37344_at	1.46932515754743	0
16	35016_at	1.44723563131209	0
17	35078_at	1.44013020473382	0
18	37001_at	1.43580114615375	0
19	33920_at	1.39389220008214	0
20	245_at	1.37591797605968	0

	INV16 - T1517	samples: 10 / 16		
	accuracy	*1*		
	confidence	*1*		
1	245_at	4.57658935261639	0	*
2	38833_at	4.25223366871621	0	*
3	38095_i_at	3.57578878481709	0	
4	39649_at	3.23025693895729	0	
5	38096_f_at	3.14225313100266	0	
6	35016_at	3.0787769409051	0	
7	38435_at	3.03350943051849	0	
8	37039_at	2.97439961013438	0	
9	38465_at	2.96526060073085	0	
10	37407_s_at	2.87881711895892	0	
11	34210_at	2.84796613729927	0	
12	41723_s_at	2.82100515486823	0	
13	41471_at	2.80737102015788	0	
14	34789_at	2.75455608102168	0	

15	1052_s_at	2.6975735697327	0	
16	36601_at	2.67187833778929	0	
17	41096_at	2.59449996104956	0	
18	41609_at	2.57402348086536	0	
19	37344_at	2.56147220347162	0	
20	40698_at	2.54689030859799	0	

	INV16 - T821	samples: 10 / 9		
	accuracy	*1*		
	confidence	*1*		
1	37407_s_at	3.01984756968935	0	*
2	2019_s_at	2.27319677276044	0	
3	36607_at	2.26121735205867	0	
4	41535_at	2.20248916475367	0	*
5	40198_at	1.86811562002606	0	
6	35264_at	1.84583120098715	0	
7	36661_s_at	1.8131267115673	0	
8	36095_at	1.79878279442616	0	

9	32747_at	1.78653441127702	0
10	40718_at	1.77233756136773	0
11	37326_at	1.76038682206377	0
12	34780_at	1.74785276488982	0
13	39610_at	1.74122046729845	0
14	33390_at	1.73740374189728	0
15	767_at	1.72097134093781	0
16	32080_at	-1.70225469167763	0
17	39358_at	1.695944330956	0
18	37747_at	1.67498682162383	0
19	245_at	1.65171897393137	0
20	33731_at	1.62582771838167	0

	OTHER -	samples: 10 / 45	
	accuracy	*0.981818181818182*	
	confidence	*0.981818181818182*	
1	34251_at	1.12590878042921	0 *
2	37018_at	1.10268143578403	0

3	33920_at	-0.956076703831482	0
4	35941_f_at	-0.90383440767488	0
5	256_s_at	-0.858111816204111	0.01
6	37333_at	0.8275447098375	0
7	32434_at	0.805850409739795	0
8	1959_at	0.796925434525945	0
9	37147_at	-0.773953141034502	0
10	33284_at	-0.771438360960095	0
11	40864_at	-0.770641950715737	0
12	35154_at	-0.764874807980337	0
13	2047_s_at	-0.748787188622726	0
14	41763_g_at	0.748545954599463	0
15	36900_at	-0.74265889729539	0
16	33351_at	0.742532920653334	0
17	36936_at	0.733922207115175	0
18	37263_at	0.729044492680672	0
19	38695_at	-0.71970619250199	0
20	40509_at	0.712799214281053	0

	OTHER - T1517	samples: 10 / 16	
	accuracy	*1*	
	confidence	*1*	
1	39649_at	3.30712305398492 0	*
2	40718_at	-2.52673625599382 0	*
3	39775_at	-1.97869028082043 0	
4	34789_at	1.95413968158198 0	
5	32543_at	-1.91464724323262 0	
6	34110_g_at	-1.77793772892734 0	
7	38487_at	-1.76846306892822 0	
8	40493_at	-1.6739728895294 0	
9	40698_at	1.65346991374979 0	
10	41273_at	-1.61494643368443 0	
11	33284_at	-1.59460520214407 0	
12	32434_at	1.57854380538056 0	
13	39755_at	-1.57527382190822 0	
14	40817_at	-1.54437681308404 0	

15	37408_at	-1.53683716438534	0	
16	33102_at	1.53530070976794	0	
17	1752_at	-1.52886252404363	0	
18	37954_at	-1.5109989255419	0	
19	38791_at	-1.48386160940786	0	
20	34210_at	1.44938674947878	0	

	OTHER - T821	samples: 10 / 9		
	accuracy	*1*		
	confidence	*0.994837795579117*		
1	32323_at	-1.94417836607133	0	*
2	37811_at	-1.61775423684388	0	*
3	34512_at	-1.39224768490919	0	
4	37809_at	1.31872220085798	0	
5	40585_at	1.31087716877391	0	
6	33284_at	-1.29020750912798	0	
7	38096_f_at	-1.25756828218199	0	
8	36973_at	1.23300907353238	0	

9	35940_at	-1.20559489876876	0	
10	38808_at	-1.18153953430958	0	
11	37333_at	1.17979557242332	0	
12	2047_s_at	-1.17934561734238	0	
13	AFFX-HUMRGE/M10098_M_at	-1.15756874447998	0	
14	958_s_at	1.1376378956	0	
15	34251_at	1.12590878042921	0	
16	38963_i_at	-1.12200244261352	0	
17	35638_at	-1.12014975713644	0	
18	38095_i_at	-1.10572791785236	0	
19	37657_at	-1.08109523793911	0	
20	40718_at	0.918288266614732	0	

	T1517 -	samples: 16 / 39		
	accuracy	*1*		
	confidence	*0.99537936517205*		
1	39649_at	-3.29831494694965	0	*
2	40718_at	2.08511115510612	0	*

3	38487_at	2.00096141225403	0	*
4	34110_g_at	1.76946763277471	0	
5	34789_at	-1.70643590139573	0	
6	38435_at	-1.66171359352607	0	
7	32543_at	1.59263172662039	0	
8	41273_at	1.54397178886438	0	
9	40493_at	1.48615605789895	0	
10	38096_f_at	-1.44819099507958	0	
11	41471_at	-1.41828217671556	0	
12	37954_at	1.41406051783378	0	
13	33454_at	1.39832642238269	0	
14	38791_at	1.38083401177366	0	
15	41096_at	-1.36447605743032	0	
16	1752_at	1.36363148385769	0	
17	38833_at	-1.34891815086687	0	
18	210_at	-1.34320613976446	0	
19	35016_at	-1.33685666840696	0	
20	37669_s_at	0.806171390298286	0	

	T1517 - T821	samples: 16 / 9		
	accuracy	*1*		
	confidence	*1*		
1	40718_at	3.23930438679201	0	*
2	39649_at	-3.19787649222746	0	*
3	40698_at	-3.08468795621776	0	
4	38096_f_at	-2.65789275034265	0	
5	39775_at	2.36672318019601	0	
6	38487_at	2.29609697942891	0	
7	33121_g_at	-2.21859945215003	0	
8	35016_at	-1.96619441751917	0	
9	38095_i_at	-1.91141006266887	0	
10	32506_at	-1.88419268611225	0	
11	38833_at	-1.85079137548356	0	
12	34110_g_at	1.85075648886345	0	
13	41096_at	-1.8279606340398	0	
14	38391_at	1.81966548635468	0	

15	35766_at	1.75448820173577	0	
16	34789_at	-1.71046499814806	0	
17	41609_at	-1.710217028597	0	
18	41273_at	1.70663861548637	0	
19	37344_at	-1.69281730857466	0	
20	35340_at	1.69006593600413	0	

	T821 -	samples: 9 / 46		
	accuracy	*1*		
	confidence	*0.920027437519393*		
1	37811_at	1.59605072597366	0	*
2	38391_at	-1.3878317468135	0	
3	35638_at	1.38266687057184	0	*
4	32323_at	1.35561326937612	0	
5	35940_at	1.20094762805468	0	*
6	36973_at	-1.17706120019907	0	
7	35264_at	-1.10943417036523	0	
8	361_at	1.07264489085601	0	

9	36802_at	-1.02457173409803	0	
10	34512_at	1.0204248889286	0	
11	35939_s_at	0.955125481450532	0	
12	39061_at	-0.947115729172708	0	
13	37326_at	-0.935233446940231	0	
14	32747_at	-0.930843404980031	0	
15	1096_g_at	0.927398573506987	0	
16	33121_g_at	0.923255276498333	0	*
17	41535_at	-0.916652918883009	0	
18	37023_at	-0.915934376270622	0	
19	38780_at	-0.915816135921152	0	

3. Analyse: analysis of ALL subtypes

	ALL814 -	samples: 3 / 14		
	accuracy	*1*		
	confidence	*1*		
1	1402_at	2.08175003568258	0.01	*
2	37747_at	2.03525291878921	0	*

3	37701_at	1.72252048284758	0.01
4	2042_s_at	-1.63373519277864	0
5	35260_at	-1.63074548017429	0
6	1476_s_at	-1.58695680100552	0
7	32616_at	1.57366205688451	0
8	932_i_at	-1.57233356229385	0
9	36139_at	-1.5665197341194	0
10	39730_at	-1.5464188647031	0.01
11	2024_s_at	1.48918618192137	0.01
12	38730_at	-1.45475301578891	0.01
13	37021_at	1.45440716568168	0
14	933_f_at	-1.42175300666003	0
15	41396_at	-1.38553827410353	0
16	33856_at	1.37781449850137	0
17	33905_at	1.3359321134002	0.01

ALL814 - ALLMLL samples: 3 / 4

accuracy *1*

		confidence	1	
1	2042_s_at	-8.02342094912714	0.05	*
2	36638_at	-4.58127332202829	0.02	
3	1474_s_at	-4.09073883260025	0.03	*
4	706_at	-3.85465872728703	0.02	
5	38994_at	-3.74888987537358	0.02	
6	34785_at	-3.3713121522884	0.03	
7	36798_g_at	-3.35179120581516	0	
8	41191_at	-3.25108066126486	0.01	
9	39827_at	-3.14944671750591	0.02	
10	585_at	-3.09495658747361	0.04	
11	2069_s_at	-3.01980201927276	0.02	
12	529_at	2.93352551602605	0.01	
13	307_at	2.92372091093276	0.03	
14	32842_at	-2.85788132874268	0.01	
15	36873_at	-2.84199424616029	0.05	
16	41747_s_at	-2.76420890085279	0.01	

	ALL814 - ALLPH	samples: 3 / 7		
	accuracy	*1*		
	confidence	*1*		
1	35260_at	-2.82900147590099	0.01	*
2	41177_at	2.74938757132087	0	*
3	36638_at	-2.41641563333395	0.01	
4	38767_at	-2.40416010568405	0.01	
5	37747_at	2.39180707441687	0	
6	39327_at	-2.27856651600595	0	
7	1476_s_at	-2.09613072968554	0.02	
8	1636_g_at	-2.00644064085741	0.01	
9	37159_at	-1.98769010758559	0	
10	932_i_at	-1.95869341917388	0	
11	38994_at	-1.94783634512686	0.02	
12	1402_at	1.91294884399227	0	
13	32319_at	-1.89265256004687	0.01	
14	2047_s_at	-1.89118154910995	0	
15	40936_at	-1.84560154590494	0	

16	39730_at	-1.84157870686046	0.03	
17	39089_at	-1.83344549691856	0	
18	41734_at	-1.82721322918029	0.01	
19	39755_at	-1.80690655801942	0.03	

	ALL814 - ALLT	samples: 3 / 3		
	accuracy	*1*		
	confidence	*1*		
1	36103_at	3.43807291883285	0.01	*
2	35350_at	3.3144051465682	0.04	
3	41654_at	-3.10101195313041	0.04	*

	ALLMLL -	samples: 4 / 13		
	accuracy	*1*		
	confidence	*1*		
1	36873_at	2.83046978285357	0	*
2	36638_at	2.81082924166381	0	*
3	33358_at	2.41284542345819	0	

4	34785_at	2.01800062696643	0
5	36667_at	2.00264026114972	0
6	41503_at	1.98278140811591	0
7	36690_at	1.97928285044649	0.01
8	706_at	1.96737076450007	0
9	32842_at	1.88883935305863	0
10	41747_s_at	1.87619134543011	0
11	32145_at	1.87136682311337	0
12	36798_g_at	1.76515008934463	0.01
13	41191_at	1.7369773616741	0
14	40763_at	1.69441997605083	0
15	585_at	1.66246850330104	0
16	41470_at	1.53671027688439	0
17	40786_at	1.52293758990032	0
18	38037_at	1.50762328192198	0.01
19	34583_at	1.46227478562542	0
20	1140_at	1.46133065433595	0

	ALLMLL - ALLPH	samples: 4 / 7		
	accuracy	*1*		
	confidence	*1*		
1	40723_at	3.55841873411154	0	*
2	706_at	3.32668949661753	0	*
3	41191_at	2.96542484991746	0	
4	36638_at	2.84067512400178	0	
5	36873_at	2.8258041781711	0	
6	36690_at	2.54358082956883	0	
7	33358_at	2.34079500414888	0	
8	36798_g_at	2.21311555975342	0.01	
9	36667_at	2.20932580996057	0.01	
10	41177_at	2.1413450003396	0	
11	40865_at	2.11221046250059	0	
12	37967_at	-2.08412772392346	0	
13	34892_at	-2.08369333371306	0	
14	40396_at	1.96552338894503	0	
15	1140_at	1.96261636340905	0	

16	33134_at	-1.95145751139773	0	
17	32842_at	1.84503319654406	0	
18	41503_at	1.8284794750916	0	
19	32145_at	1.82248695271075	0	
20	40763_at	1.78804175908387	0.01	

	ALLMLL - ALLT	samples: 4 / 3		
	accuracy	*1*		
	confidence	*1*		
1	2069_s_at	13.292701923441	0	*
2	41153_f_at	10.2582391724747	0	*
3	41156_g_at	5.75960819662385	0.01	
4	33352_at	4.58870845894255	0	
5	36638_at	4.58127332202829	0.03	
6	1185_at	4.45457229345442	0.01	
7	37775_at	-4.11123301947466	0.02	
8	1105_s_at	-4.04867441577307	0.03	
9	41155_at	3.98831214950398	0.01	

10	38994_at	3.88924207710779	0.02
11	34785_at	3.83690018368942	0.01
12	32819_at	3.567056723698	0.03
13	38319_at	-3.55471475398643	0.01
14	2045_s_at	3.54943843148795	0.02
15	40159_r_at	3.40746200289675	0.03
16	39136_at	-3.36701895470486	0.02
17	1110_at	-3.33969464270628	0.01
18	38017_at	3.32515685260135	0.01
19	605_at	-3.28310118648462	0.02

4. Analyse: other analyses

	ALLPH -	samples: 7 / 10		
	accuracy	*1*		
	confidence	*1*		
1	1389_at	1.58617196971584	0	*
2	41734_at	1.55949651759221	0	*
3	38336_at	1.52692526781459	0	

4	33134_at	1.449713769608	0
5	36878_f_at	1.36077477960263	0
6	39755_at	1.27483851783738	0
7	38833_at	1.2244093710462	0
8	33924_at	1.22263315100349	0
9	34362_at	1.1962046547055	0
10	36536_at	1.19336569573264	0
11	37344_at	1.18918159634593	0
12	38095_i_at	1.16331309702494	0
13	35260_at	1.12932649576543	0
14	41177_at	-1.07976913600882	0
15	38096_f_at	1.05014739949744	0.01
16	36773_f_at	1.0492226005037	0
17	39824_at	1.03626825828771	0
18	31898_at	1.02765158070601	0
19	1636_g_at	1.0227576964995	0
20	41609_at	0.997013086295946	0

	ALLPH - ALLT	samples: 7 / 3		
	accuracy	*1*		
	confidence	*1*		
1	1105_s_at	-4.05162267253209	0	*
2	38319_at	-3.66580320533053	0.03	*
3	38096_f_at	2.88234070062166	0.02	
4	37039_at	2.80755189593111	0	
5	35016_at	2.77774834690928	0.01	
6	38833_at	2.75560710134977	0.01	
7	39262_at	-2.59234132448068	0	
8	32649_at	-2.55542908459441	0	
9	33821_at	-2.5421725262322	0.01	
10	41609_at	2.5109183575568	0	
11	38147_at	-2.50135496035854	0	
12	38095_i_at	2.48939716688646	0.02	
13	37739_at	-2.44732228148107	0	
14	38894_g_at	2.42422840620003	0.01	
15	36638_at	2.41641563333395	0	

16	38361_g_at	2.38116082851993	0.01	
17	2059_s_at	-2.37547551809124	0.01	
18	33425_at	-2.36441631934975	0	
19	38949_at	-2.27455845085004	0	
20	39755_at	2.26518913381284	0	
	ALLT -	samples: 3 / 14		
	accuracy	*1*		
	confidence	*1*		
1	38319_at	3.50494628126444	0	*
2	33821_at	2.86458211053638	0	*
3	1105_s_at	2.7919896009269	0	
4	38147_at	2.2999876938771	0	
5	38949_at	2.275851563485	0	
6	33425_at	2.24691287113975	0	
7	40407_at	2.23626457040595	0	
8	1110_at	2.23213485898084	0	
9	39136_at	2.21536950680885	0	

10	41535_at	2.20104335983474	0	
11	2059_s_at	2.17544015063967	0	
12	39262_at	2.14503507257872	0	
13	34367_at	2.14251924457163	0	
14	35016_at	-2.12822205034103	0	
15	38096_f_at	-2.0151362322022	0	
16	37775_at	2.0098435918241	0.01	
17	38917_at	2.00844440766432	0	
18	33238_at	2.00529430466423	0	
19	1498_at	1.98727437856937	0	
20	41163_at	1.90540704553591	0	

	ALLPHNEG - ALLPHPOS	samples: 11 / 7		
	accuracy	*1*		
	confidence	*0.946908445764721*		
1	38336_at	-1.5382379030083	0	*
2	33134_at	-1.30650437502273	0	*
3	39755_at	-1.28612797222091	0	

4	1636_g_at	-1.04852861613762	0
5	38833_at	-1.04767357167583	0
6	41177_at	1.04154428480732	0
7	34168_at	-1.00022056220148	0
8	38096_f_at	-0.991139993364388	0
9	38095_i_at	-0.969632957696579	0
10	33924_at	-0.965257886268051	0
11	39756_g_at	-0.964856826724863	0
12	38312_at	-0.964240310753493	0
13	36878_f_at	-0.961827994429321	0
14	41193_at	-0.957818027300299	0
15	37384_at	-0.934644823332001	0
16	32706_at	0.916645445316056	0
17	33441_at	-0.910220742840358	0
18	41547_at	0.895837845645142	0
19	36773_f_at	-0.884139970624711	0
20	32649_at	0.833759113455451	0

Table 21

Affymetrix_ID	Description_microarray	Symbol	Description_NetAffx	Chromosome
100_g_at	Y08200 /FEATURE= /DEFINITION=HSRABGTRA Homo sapiens mRNA for rab geranylgeranyl transferase, alpha-subunit	RABGGTA	Rab geranylgeranyltransferase, alpha subunit	14q11.2
1052_s_at	M83667 /FEATURE=mRNA /DEFINITION=HUMNFIL6BA Human NF-IL6-beta protein mRNA, complete cds	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	8p11.2-p11.1
1062_g_at	U00672 /FEATURE= /DEFINITION=U00672 Human interleukin-10 receptor mRNA, complete cds	IL10RA	interleukin 10 receptor, alpha	11q23
1096_g_at	M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	CD19	CD19 antigen	16p11.2
1105_s_at	M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	TRB	T cell receptor beta locus	7q35
1110_a	M21624 /FEATURE=mRNA /DEFINITION=HUMTCRGC Human T-	TRD	T cell receptor delta locus	14q11.2

t	cell receptor delta chain mRNA (VJC-region), complete cds		delta locus	2
1115_at	M25897 /FEATURE=mRNA /DEFINITION=HUMPF4A Human platelet factor 4 (PF4) mRNA, complete cds	PF4	platelet factor 4	4q12-q21
1117_at	L27943 /FEATURE=mRNA /DEFINITION=HUMCYDE Homo sapiens cytidine deaminase (CDA) mRNA, complete cds	CDA	cytidine deaminase	1p36.2-p35
1140_at	L25851 /FEATURE= /DEFINITION=HUMINAE Homo sapiens integrin alpha E precursor, mRNA, complete cds	ITGAE	"integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)"	17p13
1185_at	D49410 /FEATURE=expanded_cds /DEFINITION=HUMIL3RA12 Human gene for interleukin 3 receptor alpha subunit, exon 12 and partial cds			
1217_g_at	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II	PRKCB1	protein kinase C, beta 1	16p11.2
1230_g_at	U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete	CRA	cisplatin resistance associated	1q12-q21

	cds			
1252_at	M73547 /FEATURE= /DEFINITION=HUMPOLLA Human polyposis locus (DP1 gene) mRNA, complete cds	D5S346	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis	5q22-q23
137_at	U65404 /FEATURE= /DEFINITION=HSU65404 Human erythroid-specific transcription factor EKLF mRNA, complete cds	KLF1	Kruppel-like factor 1 (erythroid)	19p13.13-p13.12
1385_at	M77349 /FEATURE= /DEFINITION=HUMTGFBIG Human transforming growth factor-beta induced gene product (BIGH3) mRNA, complete cds	TGFBI	transforming growth factor, beta-induced, 68kD	5q31
1389_at	J03779 /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblastic leukemia antigen (CALLA) mRNA, complete cds	MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	3q25.1-q25.2
138_at	U66464 /FEATURE= /DEFINITION=HSU66464 Human hematopoietic progenitor kinase (HPK1) mRNA, complete cds	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	19q13.1-q13.4
1402_at	M16038 /FEATURE= /DEFINITION=HUMLYN Human lyn mRNA encoding a tyrosine kinase	LYN	v-yes-1 Yamaguchi sarcoma viral	8q13

t	mRNA encoding a tyrosine kinase		related oncogene homolog	
1474_s_at	U22376 /FEATURE=cds#3 /DEFINITION=HSU22376 Human (c-myb) gene, complete primary cds, and five complete alternatively spliced cds			
1476_s_at	U22376 /FEATURE=cds#5 /DEFINITION=HSU22376 Human (c-myb) gene, complete primary cds, and five complete alternatively spliced cds			
1495_at	M34057 /FEATURE= /DEFINITION=HUMTGFB1B Human transforming growth factor-beta 1 binding protein mRNA, complete cds	LTBP1	latent transforming growth factor beta binding protein 1	2p22-p21
1497_at	L04270 /FEATURE= /DEFINITION=HUMTNFRRP Homo sapiens (clone CD18) tumor necrosis factor receptor 2 related protein mRNA, complete cds	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	12p13
1498_at	L05148 /FEATURE= /DEFINITION=HUMTYRKIN Human protein tyrosine kinase related mRNA sequence			
1529_at	U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence CG003			

1636_g_at	U07563 /FEATURE=Poly_A_Site#1 /DEFINITION=HSABLGR3 Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds			
1752_at	AD000092 /FEATURE=cds#6 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence			
1884_s_at	M15796 /FEATURE= /DEFINITION=HUMCYL Human cyclin protein gene, complete cds	PCNA	proliferating cell nuclear antigen	20pter-p12
1911_s_at	M60974 /FEATURE= /DEFINITION=HUMGADD45 Human growth arrest and DNA-damage-inducible protein (gadd45) mRNA, complete cds	GADD 45A	growth arrest and DNA-damage-inducible, alpha	1p31.2-p31.1
1959_at	D88674 /FEATURE= /DEFINITION=D88674 Homo sapiens mRNA for antizyme inhibitor, complete cds	OAZIN	ornithine decarboxylase antizyme inhibitor	8q22.3
1980_s_at	X58965 /FEATURE= /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2 gene	NME2	non-metastatic cells 2, protein (NM23B) expressed in	17q21.3
1983_a	X68452 /FEATURE=cds /DEFINITION=HSCYCD2 H.sapiens	CCND 2	cyclin D2	12p13

t	mRNA for cyclin D2	2		
2019_s_at	M68892 /FEATURE= /DEFINITION=HUMINTB7 Human integrin beta-7 subunit mRNA, complete cds	ITGB7	integrin, beta 7	12q13.13
2024_s_at	M79321 /FEATURE= /DEFINITION=HUMLYNTK Human Lyn B protein mRNA, complete cds	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	8q13
2042_s_at	M15024 /FEATURE= /DEFINITION=HUMCMYBLA Human c-myb mRNA, complete cds	MYB	v-myb avian myeloblastosis viral oncogene homolog	6q22-q23
2045_s_at	M16592 /FEATURE=mRNA /DEFINITION=HUMHCKB Human hemopoietic cell protein-tyrosine kinase (HCK) gene, complete cds, clone HK24	HCK	hemopoietic cell kinase	20q11-q12
2047_s_at	M23410 /FEATURE= /DEFINITION=HUMPLAKO Human plakoglobin (PLAK) mRNA, complete cds	JUP	junction plakoglobin	17q21
2059_s_at	M36881 /FEATURE=mRNA /DEFINITION=HUMLCKAA Human lymphocyte-specific protein tyrosine kinase (lck) mRNA, complete cds	LCK	lymphocyte-specific protein tyrosine kinase	1p35-p34.3

2069_s_at	L23805 /FEATURE= /DEFINITION=HUMCATENIN Human alpha1(E)-catenin mRNA, complete cds	CTNNA1	catenin (cadherin-associated protein), alpha 1 (102kD)	5q31
210_at	M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-2 mRNA, complete cds	PLCB2	phospholipase C, beta 2	15q15
245_at	M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds	SELL	selectin L (lymphocyte adhesion molecule 1)	1q23-q25
256_s_at	M14199 /FEATURE= /DEFINITION=HUMLAMR Human laminin receptor (2H5 epitope) mRNA, 5 end	LAMR1	laminin receptor 1 (67kD, ribosomal protein SA)	3p21.3
277_at	L08246 /FEATURE= /DEFINITION=HUMMCL1X Human myeloid cell differentiation protein (MCL1) mRNA			
307_at	J03600 /FEATURE= /DEFINITION=HUMLOX5 Human lipoxygenase mRNA, complete cds	ALOX5	arachidonate 5-lipoxygenase	10q11.2
31381_at	Cluster Incl. AF076483:Homo sapiens peptidoglycan recognition protein precursor (PGRP) mRNA, complete cds /cds=(44,634) /gb=AF076483 /gi=3342532 /ug=Hs.137583 /len=690	PGLYRP	peptidoglycan recognition protein	19q13.2-q13.3

31793_at	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	DEFA3	defensin, alpha 3, neutrophil-specific	8pter-p23.3
31859_at	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	20q11.2-q13.1
31870_at	Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908) /gb=X14046 /gi=29793 /ug=Hs.153053 /len=1125	CD37	CD37 antigen	19p13-q13.4
31898_at	Cluster Incl. D86967:Human mRNA for KIAA0212 gene, complete cds /cds=(58,2031) /gb=D86967 /gi=1504007 /ug=Hs.154332 /len=6072	KIAA0212	KIAA0212 gene product	3p25.3
31936_s_at	Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=(0,3172) /gb=AB007890 /gi=2887438 /ug=Hs.166163 /len=6011	KIAA0430	KIAA0430 gene product	16p13.12
32072_at	Cluster Incl. U40434:Human mesothelin or CAK1 antigen precursor mRNA, complete cds /cds=(99,1985) /gb=U40434 /gi=1145723 /ug=Hs.155981 /len=2114	MSLN	mesothelin	16p13.3

32080_at	Cluster Incl. L11669:Human tetracycline transporter-like protein mRNA, complete cds /cds=(120,1487) /gb=L11669 /gi=307501 /ug=Hs.157145 /len=1758	TETRAN	tetracycline transporter-like protein	4p16.3
32145_at	Cluster Incl. X58141:Human mRNA for erythrocyte adducin alpha subunit /cds=(154,2367) /gb=X58141 /gi=28381 /ug=Hs.183706 /len=3905			
32166_at	Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027 protein, partial cds /cds=(0,5088) /gb=AB028950 /gi=5689390 /ug=Hs.18420 /len=5542	TLN1	talin 1	9p13
32174_at	Cluster Incl. AF015926:Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA, complete cds /cds=(212,1288) /gb=AF015926 /gi=3220018 /ug=Hs.184276 /len=1984	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1	17q25.2
32184_at	Cluster Incl. X61118:Human TTG-2 mRNA for a cysteine rich protein with LIM motif /cds=UNKNOWN /gb=X61118 /gi=663012 /ug=Hs.184585 /len=2292	LMO2	LIM domain only 2 (rhombotin-like 1)	11p13
32229_at	Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961	EIF4EL3	eukaryotic translation initiation factor 4E-like 3	2q37.1

32232_at	Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subunit Cl-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH)	3q27.1
32259_at	Cluster Incl. AB002386:Human mRNA for KIAA0388 gene, complete cds /cds=(100,2343) /gb=AB002386 /gi=2224716 /ug=Hs.194669 /len=4606	EZH1	enhancer of zeste (Drosophila) homolog 1	17q21.1-q21.3
32319_at	Cluster Incl. AL022310:dJ395P12.2 (tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L)) /cds=(137,688) /gb=AL022310 /gi=3646083 /ug=Hs.181097 /len=3470			
32323_at	Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cds=(8,736) /gb=M63582 /gi=190297 /ug=Hs.182231 /len=1457			
32434_at	Cluster Incl. D10522:Homo sapiens mRNA for 80K-L protein, complete cds /cds=(369,1367) /gb=D10522 /gi=219893 /ug=Hs.75607 /len=2589	MACS	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)	6q22.2
32506_at	Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	4

			1	
32530_at	Cluster Incl. X56468:Human mRNA for 14.3.3 protein, a protein kinase regulator /cds=(125,862) /gb=X56468 /gi=23221 /ug=Hs.74405 /len=1862	YWHAQ	tyrosine 3-monooxygenase /tryptophan 5-monooxygenase activation protein, theta polypeptide	22q12-qter
32543_at	Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937	CALR	calreticulin	19p13.3-p13.2
32597_at	Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835	RBL2	retinoblastoma-like 2 (p130)	16q12.2
32616_at	Cluster Incl. M16038:Human lyn mRNA encoding a tyrosine kinase /cds=(297,1835) /gb=M16038 /gi=187268 /ug=Hs.80887 /len=2298	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	8q13
32649_at	Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form C) /cds=(79,885) /gb=X59871 /gi=36789 /ug=Hs.169294 /len=2910	TCF7	transcription factor 7 (T-cell specific, HMG-box)	5q31.1
32696_at	Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314 /ug=Hs.171680 /len=2581	PBX3	pre-B-cell leukemia transcription	9q33-q34

at	/gi=35314 /ug=Hs.171680 /len=2581		factor 3	
32706_at	Cluster Incl. X89887:Homo sapiens mRNA for WD repeat protein (HIRA) /cds=(220,3273) /gb=X89887 /gi=3928218 /ug=Hs.172350 /len=4018	HIRA	HIR (histone cell cycle regulation defective) homolog A (S. cerevisiae)	22q11.21
32747_at	Cluster Incl. X05409:Human RNA for mitochondrial aldehyde dehydrogenase I ALDH I (EC 1.2.1.3) /cds=(36,1586) /gb=X05409 /gi=28605 /ug=Hs.195432 /len=1989	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	12q24.2
32775_r_at	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077	PLSCR1	phospholipid scramblase 1	3q23
32800_at	Cluster Incl. U66306:Human retinoid X receptor alpha mRNA, 3 UTR, partial sequence /cds=UNKNOWN /gb=U66306 /gi=3411007 /ug=Hs.20084 /len=3772			
32819_at	Cluster Incl. AJ223352:Homo sapiens mRNA for for histone H2B, clone pjG4-5-14 /cds=(16,396) /gb=AJ223352 /gi=3255996 /ug=Hs.20418 /len=793	H2BFA	H2B histone family, member A	6p21.3
32821_at	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	LCN2	lipocalin 2 (oncogene 24p3)	9q34

32842_at	Cluster Incl. X89984:H.sapiens mRNA for BCL7A protein /cds=(953,1648) /gb=X89984 /gi=929614 /ug=Hs.211563 /len=4522	BCL7A	B-cell CLL/lymphoma 7A	12q24.13
33102_at	Cluster Incl. D67031:Homo sapiens ADDL mRNA for adducin-like protein, complete cds /cds=(183,2207) /gb=D67031 /gi=2696053 /ug=Hs.8110 /len=2920	ADD3	adducin 3 (gamma)	10q24.2-q24.3
33121_g_at	Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753	RGS10	regulator of G-protein signalling 10	10q25
33134_at	Cluster Incl. AB011083:Homo sapiens mRNA for KIAA0511 protein, partial cds /cds=(0,2802) /gb=AB011083 /gi=3043545 /ug=Hs.8402 /len=3563	ADCY3	adenylate cyclase 3	2p24-p22
33238_at	Cluster Incl. U23852:Human T-lymphocyte specific protein tyrosine kinase p56lck (lck) abberant mRNA, complete cds /cds=(59,1150) /gb=U23852 /gi=775207 /ug=Hs.1765 /len=2129			
33266_at	Cluster Incl. AF015254:Homo sapiens serine/threonine kinase (STK-1) mRNA, complete cds /cds=(58,1101) /gb=AF015254 /gi=4090840 /ug=Hs.180655 /len=1234	STK12	serine/threonine kinase 12	17p13.1

33273_f_at	Cluster Incl. X57809:Human rearranged immunoglobulin lambda light chain mRNA /cds=(114,815) /gb=X57809 /gi=33714 /ug=Hs.181125 /len=915	IGL	immunoglobulin lambda locus	22q11.1-q11.2
33274_f_at	Cluster Incl. M18645:Human Ig rearranged lambda-chain mRNA VJC-region subgroup lambda-IV from heterohybridoma H6-3C4 /cds=(30,731) /gb=M18645 /gi=186103 /ug=Hs.181125 /len=872	IGL	immunoglobulin lambda locus	22q11.1-q11.2
33284_at	Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	MPO	myeloperoxidase	17q23.1
33319_at	Cluster Incl. AF009674:Homo sapiens axin (AXIN) mRNA, partial cds /cds=(0,2703) /gb=AF009674 /gi=2252819 /ug=Hs.184434 /len=3385	AXIN1	axin	16p13.3
33351_at	Cluster Incl. AF064607:Homo sapiens GC20 protein mRNA, complete cds /cds=(70,411) /gb=AF064607 /gi=3152667 /ug=Hs.21756 /len=812	GC20	translation factor sui1 homolog	3p21.33
33352_at	Cluster Incl. X57985:H.sapiens genes for histones H2B.1 and H2A /cds=(42,422) /gb=X57985 /gi=510989 /ug=Hs.2178 /len=2223			
33358_at	Cluster Incl. W29087:56b8 Homo sapiens cDNA /gb=W29087 /gi=1309053 /ug=Hs.21894 /len=877	KIAA1157	KIAA1157 protein	12q13.3-q14.1

at	/gi=1309053 /ug=Hs.21894 /len=877			q14.1
33371_s_at	Cluster Incl. U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds /cds=(60,644) /gb=U59877 /gi=1388194 /ug=Hs.223025 /len=907	RAB31	RAB31, member RAS oncogene family	18p11.3
33386_at	Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome 22q12-13 Contains H1F0(H1 histone family, member 0) gene, 2-amino-3-ketobutyrate -CoA ligase(nuclear gene encoding mitochondrial protein), GALR3 (galanin receptor) gene, ESTs, GSSs an			
33390_at	Cluster Incl. AA203487:zx53d03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446213 /clone_end=5 /gb=AA203487 /gi=1799460 /ug=Hs.226237 /len=863		ESTs	
33412_at	Cluster Incl. AI535946:vicpro2.D07.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI535946 /gi=4450081 /ug=Hs.227751 /len=647	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	22q13.1
33414_at	Cluster Incl. X57398:Human mRNA for pM5 protein /cds=(0,3572) /gb=X57398 /gi=35526 /ug=Hs.227823 /len=4086	PM5	pM5 protein	16p13.11
33425_at	Cluster Incl. X97548:H.sapiens mRNA for TIF1beta zinc finger protein /cds=(361,2868) /gb=X97548 /gi=1524108 /ug=Hs.228059 /len=3035	TRIM28	tripartite motif-containing 28	5

	/gi=1524108 /ug=Hs.228059 /len=3035			
33441_at	"Cluster Incl. L41143:Homo sapiens expressed pseudo TCTA mRNA at t(1;3) translocation site, complete cds /cds=(221,532) /gb=L41143 /gi=736684 /ug=Hs.232069 /len=2146"			
33454_at	Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032	AGRN	agrin	1p36.3-p32
33530_at	Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	19q13.2
33689_s_at	Cluster Incl. AF012434:untitled /cds=(38,394) /gb=AF012434 /gi=2352914 /ug=Hs.186570 /len=573			
33731_at	Cluster Incl. AJ130718:Homo sapiens mRNA for glycoprotein-associated amino acid transporter y+LAT1 /cds=(293,1828) /gb=AJ130718 /gi=3970724 /ug=Hs.194693 /len=2214	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	14q11.2
33752_at	Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete cds /cds=(630,2558) /gb=AB020657 /gi=4240188 /ug=Hs.197298 /len=3682	NS1-BP	NS1-binding protein	1q25.1-q31.1

33812_at	"Cluster Incl. AL049415:Homo sapiens mRNA; cDNA DKFZp586N2119 (from clone DKFZp586N2119) /cds=UNKNOWN /gb=AL049415 /gi=4500196 /ug=Hs.204290 /len=1232"			
33821_at	Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL			
33856_at	Cluster Incl. Y13374:Homo sapiens mRNA for putatively prenylated protein /cds=(343,972) /gb=Y13374 /gi=2370152 /ug=Hs.239533 /len=1186	CXX1	CAAX box 1	Xq26
33860_at	Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150	KIAA0462	KIAA0462 protein	1p36.13
33866_at	Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049	TPM4	tropomyosin 4	19p13.1
33905_at	Cluster Incl. AF072242:Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds /cds=(229,1464) /gb=AF072242	MBD2	methyl-CpG binding domain protein 2	18q21

	/gi=3800792 /ug=Hs.25674 /len=1948			
33920_at	Cluster Incl. AF051782:Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds /cds=(0,3746) /gb=AF051782 /gi=2947237 /ug=Hs.26584 /len=5635	DIAPH1	diaphanous (Drosophila, homolog) 1	5q31
33924_at	Cluster Incl. AB029014:Homo sapiens mRNA for KIAA1091 protein, partial cds /cds=(0,4080) /gb=AB029014 /gi=5689518 /ug=Hs.26797 /len=4248	KIAA1091	KIAA1091 protein	11
33944_at	Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.64797 /len=3727	APLP2	amyloid beta (A4) precursor-like protein 2	11q24
33963_at	Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771) /gb=M96326 /gi=179301 /ug=Hs.72885 /len=913			
34110_g_at	Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888	PIG6	proline oxidase homolog	
34168_at	Cluster Incl. M11722:Human terminal transferase mRNA, complete cds /cds=(328,1854) /gb=M11722 /gi=339436 /ug=Hs.234772 /len=2068	DNTT	deoxynucleotidyltransferase, terminal	10q23-q24
34210_	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end	CDW52	CDW52 antigen (CAMPATH-1	1p36

at	/clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	2	antigen)	
34251_at	Cluster Incl. M92299:Human homeobox 2.1 protein (HOX2A) mRNA, complete cds /cds=(275,1084) /gb=M92299 /gi=184292 /ug=Hs.22554 /len=2037	HOXB5	homeo box B5	17q21-q22
34306_at	Cluster Incl. AB007888:Homo sapiens KIAA0428 mRNA, complete cds /cds=(1414,2526) /gb=AB007888 /gi=2887430 /ug=Hs.28578 /len=5940	MBNL	muscleblind (Drosophila)-like	3q25
34362_at	Cluster Incl. M55531:Human glucose transport-like 5 (GLUT5) mRNA, complete cds /cds=(75,1580) /gb=M55531 /gi=183297 /ug=Hs.33084 /len=2218	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	1p36.2
34367_at	Cluster Incl. AF006043:Homo sapiens 3-phosphoglycerate dehydrogenase mRNA, complete cds /cds=(692,2293) /gb=AF006043 /gi=2674061 /ug=Hs.3343 /len=2467	PHGDH	phosphoglycerate dehydrogenase	1p12
34512_at	Cluster Incl. J03853:Human kidney alpha-2-adrenergic receptor mRNA, complete cds /cds=(38,1423) /gb=J03853 /gi=178193 /ug=Hs.123022 /len=1491	ADRA2C	adrenergic, alpha-2C-, receptor	4p16
34546_	Cluster Incl. AI250799:qi36g07.x1 Homo sapiens cDNA, 3 end	DEFA4	defensin, alpha 4, corticostatin	8p23

at	/clone=IMAGE-1858620 /clone_end=3 /gb=AI250799 /gi=3847328 /ug=Hs.2582 /len=542		4, corticostatin	
34583_at	Cluster Incl. U02687:Human growth factor receptor tyrosine kinase (STK-1) mRNA, complete cds /cds=(57,3038) /gb=U02687 /gi=409572 /ug=Hs.385 /len=3475	FLT3	fms-related tyrosine kinase 3	13q12
34654_at	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200 /len=2582	MTMR1	myotubularin related protein 1	Xq28
34663_at	Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-RII) mRNA, complete cds /cds=(41,916) /gb=M28696 /gi=184843 /ug=Hs.233450 /len=1416	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor for (CD32)	1q23
34670_at	Cluster Incl. U60899:Human lysosomal alpha-mannosidase (manB) gene /cds=(309,3341) /gb=U60899 /gi=2209014 /ug=Hs.234070 /len=3443			
34679_at	Cluster Incl. X02596:Human mRNA for bcr (breakpoint cluster region) gene in Philadelphia chromosome /cds=(488,4303) /gb=X02596 /gi=29420 /ug=Hs.234799 /len=4739	BCR	breakpoint cluster region	22q11.23
34780_at	Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252	PLXNB2	plexin B2	22q13.33

	/gi=2280475 /ug=Hs.3989 /len=6252			
34785_at	Cluster Incl. AB028948:Homo sapiens mRNA for KIAA1025 protein, partial cds /cds=(0,3441) /gb=AB028948 /gi=5689386 /ug=Hs.4084 /len=6131	KIAA1025	KIAA1025 protein	12q24.22
34789_at	Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072 /len=1465	SERPINB6	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	6p25
34830_at	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	DKFZP564K0822	hypothetical protein DKFZp564K0822	6
34871_at	Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614		Homo sapiens cDNA FLJ11714 fis, clone HEMBA1005219, weakly similar to NUCLEAR PROTEIN SNF7	
34892_at	Cluster Incl. AF016266:Homo sapiens TRAIL receptor 2 mRNA, complete cds /cds=(117,1439) /gb=AF016266 /gi=2529562 /ug=Hs.51233 /len=3972	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	8p22-p21
35016_at	Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080			

	/gi=184518 /ug=Hs.84298 /len=2080			
35078_at	Cluster Incl. X93093:H.sapiens LW gene /cds=(9,824) /gb=X93093 /gi=1491707 /ug=Hs.108287 /len=1243	ICAM4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group	19p13.2-cen
35154_at	Cluster Incl. W68046:zd42a12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-343294 /clone_end=3 /gb=W68046 /gi=1376935 /ug=Hs.25817 /len=575	BTBD2	BTB (POZ) domain containing 2	19p13.3
35204_at	Cluster Incl. U52840:Homo sapiens semaphorin F homolog mRNA, complete cds /cds=(637,3861) /gb=U52840 /gi=2772583 /ug=Hs.27621 /len=8056	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	5p15.2
35230_at	Cluster Incl. AF070530:Homo sapiens clone 24751 unknown mRNA /cds=(0,1252) /gb=AF070530 /gi=3387885 /ug=Hs.29344 /len=1560	CL24751	hypothetical protein, clone 24751	19p13.3
35260_at	Cluster Incl. AB020674:Homo sapiens mRNA for KIAA0867 protein, complete cds /cds=(152,1732) /gb=AB020674	MONDOA	KIAA0867 protein	12q21.31

at	/gi=4240222 /ug=Hs.52081 /len=4339			
35264_at	Cluster Incl. AF067139:Homo sapiens NADH-ubiquinone oxidoreductase NDUFS3 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds /cds=(12,806) /gb=AF067139 /gi=3337440 /ug=Hs.5273 /len=887	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	11p11.11
35282_r_at	Cluster Incl. M33680:Human 26-kDa cell surface protein TAPA-1 mRNA, complete cds /cds=(238,948) /gb=M33680 /gi=338677 /ug=Hs.54457 /len=1480	CD81	CD81 antigen (target of antiproliferative antibody 1)	11p15
35329_at	Cluster Incl. AF091084:Homo sapiens clone 638 unknown mRNA, complete sequence /cds=(30,413) /gb=AF091084 /gi=3860005 /ug=Hs.5825 /len=1065	LOC51706	cytochrome b5 reductase 1 (B5R.1)	1p36.13-q41
35340_at	Cluster Incl. AI819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2409932 /clone_end=3 /gb=AI819948 /gi=5439027 /ug=Hs.5947 /len=569	MEL	mel transforming oncogene (derived from cell line NK14)-RAB8 homolog	19p13.1
35350_at	Cluster Incl. AB011170:Homo sapiens mRNA for KIAA0598 protein, complete cds /cds=(581,2266) /gb=AB011170 /gi=3043719 /ug=Hs.6079 /len=4712	GALNAC4S-6ST	B cell RAG associated protein	10q26
35355_	Cluster Incl. AB020697:Homo sapiens mRNA for KIAA0890 protein, complete	DDX30	DEAD/H (Asp-Glu-Ala-	3p21.31

at	cds /cds=(143,3727) /gb=AB020697 /gi=4240268 /ug=Hs.6141 /len=3800		Asp/His) box polypeptide 30	1
35372_r_at	Cluster Incl. M17017:Human beta-thromboglobulin-like protein mRNA, complete cds /cds=(90,389) /gb=M17017 /gi=179579 /ug=Hs.624 /len=1639	IL8	interleukin 8	4q13-q21
35638_at	Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	CBFA2T1	"core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related"	8q22
35643_at	Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /gb=X76732 /gi=2706486 /ug=Hs.3164 /len=1586	NUCB2	nucleobindin 2	11p15.1-p14
35766_at	Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343) /gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412	KRT18	keratin 18	12q13
35813_at	Cluster Incl. AA192359:zp91c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-627574 /clone_end=3 /gb=AA192359 /gi=1781699 /ug=Hs.69235 /len=715	TRN-SR	transportin-SR	7q32.2-q32.3
35823_at	Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671)	PPIB	peptidylprolyl isomerase B (cyclophilin B)	15q21-q22

at	/gb=M63573 /gi=337998 /ug=Hs.699 /len=893		(cyclophilin B)	
35919_at	Cluster Incl. J05068:human transcobalamin I mRNA, complete cds /cds=(75,1376) /gb=J05068 /gi=307478 /ug=Hs.2012 /len=1537	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	11q11-q12
35939_s_at	Cluster Incl. L20433:Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588 /len=3824	POU4F1	POU domain, class 4, transcription factor 1	13q21.1-q22
35940_at	Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492	POU4F1	POU domain, class 4, transcription factor 1	13q21.1-q22
35941_f_at	Cluster Incl. U91329:Human kinesin-like motor protein KIF1C mRNA, complete cds /cds=(113,3424) /gb=U91329 /gi=2738148 /ug=Hs.211611 /len=4058	KIF1C	kinesin family member 1C	17p13
35995_at	Cluster Incl. AF067656:Homo sapiens ZW10 interactor Zwint mRNA, complete cds /cds=(24,857) /gb=AF067656 /gi=3901271 /ug=Hs.42650 /len=1639	ZWINT	ZW10 interactor	10q21-q22
36021_at	"Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409			

	/gi=4500194 /ug=Hs.44865 /len=1419"			
36095_at	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110	DKFZP586N1922	DKFZP586N1922 protein	19q13.1
36103_at	Cluster Incl. D90144:Homo sapiens gene for LD78 alpha precursor, complete cds /cds=(86,364) /gb=D90144 /gi=219905 /ug=Hs.73817 /len=781	SCYA3	small inducible cytokine A3 (homologous to mouse Mip-1a)	17q11-q21
36123_at	Cluster Incl. D87292:Homo sapiens mRNA for rhodanese, complete cds /cds=(48,941) /gb=D87292 /gi=1877030 /ug=Hs.74097 /len=1137	TST	thiosulfate sulfurtransferase (rhodanese)	22q13.1
36139_at	"Cluster Incl. AL050289:Homo sapiens mRNA; cDNA DKFZp586G0522 (from clone DKFZp586G0522) /cds=(179,1876) /gb=AL050289 /gi=4886510 /ug=Hs.7446 /len=2364"	C6orf5	chromosome 6 open reading frame 5	6q21
36155_at	Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(316,1590) /gb=D87465 /gi=1665814 /ug=Hs.74583 /len=5316	KIAA0275	KIAA0275 gene product	10pter-q25.3
36165_at	Cluster Incl. W51774:zc48b04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-325519 /clone_end=5 /gb=W51774 /gi=1349666 /ug=Hs.74649 /len=678	COX6C	cytochrome c oxidase subunit VIc	8q22-q23

361_at	Y13620 /FEATURE= /DEFINITION=HSRNABCL9 Homo sapiens mRNA for BCL9 gene	BCL9	B-cell CLL/lymphoma 9	1q21
36239_at	Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407 /len=3301	POU2AF1	POU domain, class 2, associating factor 1	11q23.1
36464_at	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	SGP28	specific granule protein (28 kDa)	6p12.3
36536_at	Cluster Incl. AF070614:Homo sapiens clone 24732 unknown mRNA, partial cds /cds=(0,1147) /gb=AF070614 /gi=3283878 /ug=Hs.61490 /len=1734	SCHIP1	schwannomin-interacting protein 1	3q26.1
36553_at	Cluster Incl. AA669799:ag36c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1118886 /clone_end=3 /gb=AA669799 /gi=2631298 /ug=Hs.6315 /len=679	ASMTL	acetylserotonin O-methyltransferase-like	Xp22.3
36571_at	Cluster Incl. X68060:H.sapiens topIIb mRNA for topoisomerase IIb /cds=(0,4865) /gb=X68060 /gi=37230 /ug=Hs.75248 /len=4866	TOP2B	topoisomerase (DNA) II beta (180kD)	3p24
36588_at	Cluster Incl. AB018353:Homo sapiens mRNA for KIAA0810 protein, partial cds /cds=(0,2475) /gb=AB018353 /gi=3882340 /ug=Hs.7531 /len=4047	KIAA0810	KIAA0810 protein	

36601_at	Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102	VCL	vinculin	10q22.1-q23
36607_at	Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606			
36608_at	Cluster Incl. D55654:Human mRNA for cytosolic malate dehydrogenase, complete cds /cds=(55,1059) /gb=D55654 /gi=1255603 /ug=Hs.75375 /len=1267	MDH1	malate dehydrogenase 1, NAD (soluble)	2p16
36629_at	Cluster Incl. AI635895:tz82a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2295060 /clone_end=3 /gb=AI635895 /gi=4687225 /ug=Hs.75450 /len=1082	DSIPI	delta sleep inducing peptide, immunoreactor	Xp21.1-q25
36638_at	Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312	CTGF	connective tissue growth factor	6q23.1
36644_at	Cluster Incl. D29963:Homo sapiens mRNA for CD151, complete cds /cds=(84,845) /gb=D29963 /gi=2073384 /ug=Hs.75564 /len=1486	CD151	CD151 antigen	11p15.5
36661_s_at	Cluster Incl. X06882:Human gene for CD14 differentiation antigen /cds=(105,1232) /gb=X06882 /gi=29736 /ug=Hs.75627 /len=1356	CD14	CD14 antigen	5q31.1

	/gi=29736 /ug=Hs.75627 /len=1356			
36667_at	Cluster Incl. U47025:Human fetal brain glycogen phosphorylase B mRNA, complete cds /cds=(34,2565) /gb=U47025 /gi=1172225 /ug=Hs.75658 /len=4055	PYGB	"phosphorylase, glycogen; brain"	20p11.2-p11.1
36690_at	Cluster Incl. M10901:Human glucocorticoid receptor alpha mRNA, complete cds /cds=(132,2465) /gb=M10901 /gi=183032 /ug=Hs.75772 /len=4788	NR3C1	nuclear receptor subfamily 3, group C, member 1	5q31
36709_at	Cluster Incl. Y00093:H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95 /cds=(64,3555) /gb=Y00093 /gi=35175 /ug=Hs.51077 /len=4654	ITGAX	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	16p11.2
36710_at	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	CAMP	cathelicidin antimicrobial peptide	3p21.3
36749_at	Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633			
36766_at	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	14q24-q31

36773_f_at	Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	6p21.3
36790_at	Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	TPM1	tropomyosin 1 (alpha)	15q22.1
36798_g_at	Cluster Incl. J04168:Human leukosialin mRNA, complete cds /cds=(95,1297) /gb=J04168 /gi=187118 /ug=Hs.80738 /len=2288	SPN	sialophorin (gpL115, leukosialin, CD43)	16p11.2
36802_at	Cluster Incl. M23197:Human differentiation antigen (CD33) mRNA, complete cds /cds=(12,1106) /gb=M23197 /gi=180097 /ug=Hs.83731 /len=1437	CD33	CD33 antigen (gp67)	19q13.3
36809_at	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	CLC	Charot-Leyden crystal protein	19q13.1
36843_at	Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein, complete cds /cds=(296,3424) /gb=AB005666 /gi=2389008 /ug=Hs.7019 /len=3885	SIPA1	signal-induced proliferation-associated gene 1	11q13.3
36873_	Cluster Incl. D16532:Human gene for very low density lipoprotein receptor,			

at	5flanking and /cds=(615,3236) /gb=D16532 /gi=407220 /ug=Hs.73729 /len=3853			
36878_f_at	Cluster Incl. M60028:Human MHC class II HLA-DQ-beta (DQB1,DQw9), complete cds /cds=(57,842) /gb=M60028 /gi=188114 /ug=Hs.73931 /len=1192	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	6p21.3
36881_at	Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein beta subunit /cds=(27,794) /gb=X71129 /gi=297901 /ug=Hs.74047 /len=835	ETFB	electron-transfer-flavoprotein, beta polypeptide	19q13.3
36894_at	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964			
36900_at	Cluster Incl. U52426:Homo sapiens GOK (STIM1) mRNA, complete cds /cds=(565,2622) /gb=U52426 /gi=2264345 /ug=Hs.74597 /len=4040	STIM1	stromal interaction molecule 1	11p15.5
36936_at	Cluster Incl. U58766:Human FX protein mRNA, complete cds /cds=(74,1039) /gb=U58766 /gi=1381178 /ug=Hs.75801 /len=1330	TSTA3	tissue specific transplantation antigen P35B	8q24.3
36945_at	Cluster Incl. X94910:Homo sapiens mRNA for ERp28 protein /cds=(11,796) /gb=X94910 /gi=3413292 /ug=Hs.75841 /len=892	C12orf8	chromosome 12 open reading frame 8	12q24.13

36952_at	Cluster Incl. D16480:Homo sapiens mRNA for mitochondrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenese alpha-subunit of trifunctional protein, complete cds /cds=(27,2318) /gb=D16480 /gi=493657 /ug=Hs.75860 /len=2690	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/ 3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	2p23
36963_at	Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324 /ug=Hs.75888 /len=1536	PGD	phosphogluconate dehydrogenase	1p36.3-p36.13
36973_at	Cluster Incl. U41371:Human spliceosome associated protein (SAP 145) mRNA, complete cds /cds=(48,2666) /gb=U41371 /gi=1173904 /ug=Hs.75916 /len=2820	SF3B2	splicing factor 3b, subunit 2, 145kD	11q13.1
36980_at	Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,1096) /gb=U03105 /gi=476094 /ug=Hs.75969 /len=2061	B4-2	proline-rich protein with nuclear targeting signal	6q16.1
36996_at	Cluster Incl. U41635:Human OS-9 precurosor mRNA, complete cds /cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736	OS-9	amplified in osteosarcoma	12q13
37001_	Homo sapiens /REF=M23254 /DEF=Cluster Incl. :Human Ca2-	CAPN2	calpain 2, (m/II) large subunit	1q41-q42

at	activated neutral protease large subunit (CANP) mRNA, complete cds /cds=(130,2232) /gb= /gi=511636 /ug=Hs.76288 /len=3213 /LEN=3435	2	large subunit	q42
37015_at	Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	9q21
37018_at	Cluster Incl. AI189287:qd05c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1722822 /clone_end=3 /gb=AI189287 /gi=3740496 /ug=Hs.7644 /len=738	H1F2	H1 histone family, member 2	6p21.3
37021_at	Cluster Incl. X16832:Human mRNA for cathepsin H (EC 3.4.22.16) /cds=(34,1041) /gb=X16832 /gi=29709 /ug=Hs.76476 /len=1399	CTSH	cathepsin H	15q24-q25
37023_at	Cluster Incl. J02923:Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds /cds=(74,1957) /gb=J02923 /gi=189501 /ug=Hs.76506 /len=3175	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	13q14.3
37026_at	Cluster Incl. AF001461:Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA, complete cds /cds=(30,881) /gb=AF001461 /gi=3378030 /ug=Hs.76526 /len=1354	COPEB	core promoter element binding protein	10p15
37027_at	Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /cds=(0,3835) /gb=M80899	AHNAK	AHNAK nucleoprotein (desmoyokin)	11q12-q13

at	/gi=178282 /ug=Hs.76549 /len=4051		(desmoyokin)	
37029_at	Homo sapiens /REF=X83218 /DEF=Cluster Incl. :H.sapiens mRNA for ATP synthase /cds=(36,677) /gb=/gi=1008079 /ug=Hs.76572 /len=750 /LEN=826	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	21q22.11
37039_at	Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199	HLA-DRA	major histocompatibility complex, class II, DR alpha	6p21.3
37054_at	Cluster Incl. J04739:Human bactericidal permeability increasing protein (BPI) mRNA, complete cds /cds=(30,1493) /gb=J04739 /gi=179528 /ug=Hs.89535 /len=1813	BPI	bactericidal/permeability-increasing protein	20q11.23-q12
37099_at	Cluster Incl. AI806222:wf26e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2356746 /clone_end=3 /gb=AI806222 /gi=5392788 /ug=Hs.100194 /len=563	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	13q12
37147_at	Cluster Incl. AF020044:Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds /cds=(179,1150) /gb=AF020044 /gi=2828595 /ug=Hs.105927 /len=1391	SCGF	"stem cell growth factor; lymphocyte secreted C-type lectin"	19q13.3

37149_s_at	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607			
37159_at	Cluster Incl. U79259:Human clone 23945 mRNA, complete cds /cds=(636,1403) /gb=U79259 /gi=1710213 /ug=Hs.10700 /len=1683	DJ159A19.3	hypothetical protein	1p36.13
37263_at	Cluster Incl. U55206:Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds /cds=(59,1015) /gb=U55206 /gi=2957143 /ug=Hs.78619 /len=1265	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygamma glutamyl hydrolase)	8q12.1
37311_at	Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242			
37326_at	"Cluster Incl. U93305:Homo sapiens A4 differentiation-dependent protein (A4), triple LIM domain protein (LMO6), and synaptophysin (SYP) genes, complete cds; and calcium channel alpha-1 subunit (CACNA1F) gene, partial cds /cds=(75,533) /gb=U93305 /gi=270759"			
37333_at	Cluster Incl. X63692:H.sapiens mRNA for DNA (cytosin-5)-methyltransferase /cds=(237,5087) /gb=X63692	DNMT1	DNA (cytosine-5-)-methyltransfera	19p13.2

at	/gi=1632818 /ug=Hs.77462 /len=5408		se 1	
37344_at	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079	HLA-DMA	major histocompatibility complex, class II, DM alpha	6p21.3
37384_at	Cluster Incl. D13640:Human mRNA for KIAA0015 gene, complete cds /cds=(106,1470) /gb=D13640 /gi=286006 /ug=Hs.77961 /len=5134	KIAA0015	KIAA0015 gene product	22q11.22
37399_at	Cluster Incl. D17793:Human mRNA for KIAA0119 gene, complete cds /cds=(51,1022) /gb=D17793 /gi=457407 /ug=Hs.78183 /len=1204	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	10p15-p14
37403_at	Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X05908 /gi=34387 /ug=Hs.78225 /len=1399	ANXA1	annexin A1	9q12-q21.2
37407_s_at	Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	MYH11	myosin, heavy polypeptide 11, smooth muscle	16p13.13-p13.12
37408_at	Cluster Incl. AB014609:Homo sapiens mRNA for KIAA0709 protein, complete cds /cds=(116,4555) /gb=AB014609 /gi=3327231 /ug=Hs.7835 /len=5641	KIAA0709	endocytic receptor (macrophage mannose receptor family)	17q24.1

			receptor family)	
37417_at	Cluster Incl. M36542:Human lymphoid-specific transcription factor mRNA, complete cds /cds=(54,1445) /gb=M36542 /gi=339495 /ug=Hs.1101 /len=2048	POU2F2	POU domain, class 2, transcription factor 2	19q13.31
37579_at	Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881	PIR121	cytoplasmic FMRP interacting protein 2	5q34
37600_at	Cluster Incl. U68186:Human extracellular matrix protein 1 mRNA, complete cds /cds=(103,1725) /gb=U68186 /gi=2660683 /ug=Hs.81071 /len=1819	ECM1	extracellular matrix protein 1	1q21
37615_at	Cluster Incl. D86962:Human mRNA for KIAA0207 gene, complete cds /cds=(781,2547) /gb=D86962 /gi=1503997 /ug=Hs.81875 /len=5431	GRB10	growth factor receptor-bound protein 10	7p12-p11.2
37625_at	Cluster Incl. U52682:Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds /cds=(125,1477) /gb=U52682 /gi=1378108 /ug=Hs.82132 /len=5320	IRF4	interferon regulatory factor 4	6p25-p23
37657_at	Cluster Incl. Y16270:Homo sapiens PALM gene, exon 1 and joined CDS /cds=(145,1308) /gb=Y16270 /gi=3219601 /ug=Hs.78482 /len=2823			

37669_s_at	Cluster Incl. U16799:Human Na,K-ATPase beta-1 subunit mRNA, complete cds /cds=(45,950) /gb=U16799 /gi=806753 /ug=Hs.78629 /len=1476	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	1q22-q25
37701_at	Cluster Incl. L13463:Human helix-loop-helix basic phosphoprotein (G0S8) mRNA, complete cds /cds=(32,667) /gb=L13463 /gi=292054 /ug=Hs.78944 /len=1345	RGS2	regulator of G-protein signalling 2, 24kD	1q31
37739_at	Cluster Incl. M86737:Human high mobility group box (SSRP1) mRNA, complete cds /cds=(274,2403) /gb=M86737 /gi=184241 /ug=Hs.79162 /len=2825	SSRP1	structure specific recognition protein 1	11q12
37747_at	Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U05770 /gi=2182176 /ug=Hs.79274 /len=1597			
37755_at	Cluster Incl. AB023169:Homo sapiens mRNA for KIAA0952 protein, complete cds /cds=(359,1927) /gb=AB023169 /gi=4589547 /ug=Hs.7935 /len=4856	KIAA0952	KIAA0952 protein	20p12.1
37762_at	Cluster Incl. Y07909:H.sapiens mRNA for Progression Associated Protein /cds=(218,691) /gb=Y07909 /gi=1542882 /ug=Hs.79368 /len=2774	EMP1	epithelial membrane protein 1	12p12.3
37775_	Cluster Incl. W25951:17d10 Homo sapiens cDNA /gb=W25951		septin 6	Xq24

at	/gi=1306236 /ug=Hs.123282 /len=738			
37809_at	Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411	HOXA9	homeo box A9	7p15-p14
37811_at	Cluster Incl. AF042792:Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds /cds=(161,3598) /gb=AF042792 /gi=2781438 /ug=Hs.127436 /len=5463	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	3p21.3
37897_s_at	Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493903 /clone_end=3 /gb=AI985964 /gi=5813241 /ug=Hs.82961 /len=487	TFF3	trefoil factor 3 (intestinal)	21q22.3
37926_at	Cluster Incl. D14520:Human mRNA for GC-Box binding protein BTEB2, complete cds /cds=(558,1217) /gb=D14520 /gi=303596 /ug=Hs.84728 /len=1301	KLF5	Kruppel-like factor 5 (intestinal)	13q21.32
37954_at	Cluster Incl. X16662:Human mRNA for vascular anticoagulant-beta (VAC-beta) /cds=(106,1089) /gb=X16662 /gi=37638 /ug=Hs.87268 /len=1940	ANXA8	annexin A8	10q11.2
37967_at	Cluster Incl. AF000424:Homo sapiens LST1 mRNA, cLST1/C splice variant, complete cds /cds=(225,500) /gb=AF000424 /gi=2145063	LY117	lymphocyte antigen 117	6p21.3

	/ug=Hs.88411 /len=635			
37992_s_at	Cluster Incl. AI436567:ti03b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2129369 /clone_end=3 /gb=AI436567 /gi=4282731 /ug=Hs.89761 /len=680	ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	19p13.3
38006_at	Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds /cds=(20,751) /gb=M37766 /gi=187518 /ug=Hs.901 /len=1058	CD48	CD48 antigen (B-cell membrane protein)	1q21.3-q22
38017_at	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107			
38037_at	Cluster Incl. M60278:Human heparin-binding EGF-like growth factor mRNA, complete cds /cds=(261,887) /gb=M60278 /gi=183866 /ug=Hs.799 /len=2342	DTR	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)	5q23
38063_at	Cluster Incl. U00952:Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA /cds=UNKNOWN /gb=U00952 /gi=405054 /ug=Hs.8068 /len=1047			
38095_i_at	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	6p21.3

	/ug=Hs.814 /len=1501		II, DP beta 1	
38096_f_at	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	6p21.3
38097_at	Cluster Incl. AF010313:Homo sapiens Pig8 (PIG8) mRNA, complete cds /cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165	PIG8	etoposide-induced mRNA	11q24
38112_g_at	"Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224"	CSPG2	chondroitin sulfate proteoglycan 2 (versican)	5q14.3
38116_at	Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836	KIAA0101	KIAA0101 gene product	15q22.1
38147_at	Cluster Incl. AL023657:Homo sapiens SH2D1A cDNA, formerly known as DSHP /cds=(299,685) /gb=AL023657 /gi=3153107 /ug=Hs.151544 /len=2530	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	Xq25-q26
38194_s_at	Cluster Incl. M63438:Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds /cds=(0,1049) /gb=M63438 /gi=184847	IGKC	immunoglobulin kappa constant	2p12

	/ug=Hs.156110 /len=1244			
38225_at	Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively spliced, partial cds /cds=(0,284) /gb=AF052728 /gi=3549258 /ug=Hs.165664 /len=767	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	7q35-q36
38233_at	Cluster Incl. AF093265:Homo sapiens homer-3 mRNA, complete cds /cds=(90,1166) /gb=AF093265 /gi=3834620 /ug=Hs.166146 /len=1407	HOMER-3	Homer, neuronal immediate early gene, 3	19p13.12
38269_at	"Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630) /gb=AL050147 /gi=4884153 /ug=Hs.91146 /len=1837"	PKD2	protein kinase D2	19q13.2
38312_at	"Cluster Incl. AL050002:Homo sapiens mRNA; cDNA DKFZp564O222 (from clone DKFZp564O222) /cds=UNKNOWN /gb=AL050002 /gi=4884256 /ug=Hs.94795 /len=1546"			
38319_at	Cluster Incl. AA919102:ol84h02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gi=3058992 /ug=Hs.95327 /len=622	CD3D	CD3D antigen, delta polypeptide (TiT3 complex)	11q23
38336_at	Cluster Incl. AB023230:Homo sapiens mRNA for KIAA1013 protein, partial cds /cds=(0,3188) /gb=AB023230 /gi=4589675 /ug=Hs.96427 /len=4783	KIAA1013	KIAA1013 protein	3

	/gi=4589675 /ug=Hs.96427 /len=4783			
38361_g_at	Cluster Incl. AI688812:wd41c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2330692 /clone_end=3 /gb=AI688812 /gi=4900106 /ug=Hs.99491 /len=504	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	11q13
38391_at	Cluster Incl. M94345:Homo sapiens macrophage capping protein mRNA, complete cds /cds=(49,1095) /gb=M94345 /gi=187455 /ug=Hs.82422 /len=1221	CAPG	capping protein (actin filament), gelsolin-like	2cen-q24
38414_at	Cluster Incl. U05340:Human p55CDC mRNA, complete cds /cds=(110,1609) /gb=U05340 /gi=468031 /ug=Hs.82906 /len=1686	CDC20	CDC20 (cell division cycle 20, S. cerevisiae, homolog)	9q13-q21
38415_at	Cluster Incl. U14603:Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence /cds=(423,926) /gb=U14603 /gi=894158 /ug=Hs.82911 /len=1526	PTP4A2	protein tyrosine phosphatase type IVA, member 2	1p35
38435_at	Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921	PRDX4	peroxiredoxin 4	Xp22.13
38465_at	Cluster Incl. M37721:Human peptidylglycine alpha-amidating monooxygenase mRNA, complete cds /cds=(188,3112) /gb=M37721	PAM	peptidylglycine alpha-amidating monooxygenase	5q14-q21

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	/gi=189594 /ug=Hs.83920 /len=3748			
38472_at	Cluster Incl. D63477:Human mRNA for KIAA0143 gene, partial cds /cds=(0,2658) /gb=D63477 /gi=1469867 /ug=Hs.84087 /len=5286	KIAA0143	KIAA0143 protein	8q24.22
38485_at	Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549 /len=553	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI)	4q28.2-q31.1
38487_at	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777			
38577_at	Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429			
38578_at	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	TNFRSF7	tumor necrosis factor receptor superfamily, member 7	12p13
38653_at	Cluster Incl. D11428:Homo sapiens mRNA for PMP-22(PAS-II/SR13/Gas-3), complete cds /cds=(188,670) /gb=D11428 /gi=220009 /ug=Hs.103724 /len=1806	PMP22	peripheral myelin protein 22	17p12-p11.2

38666_at	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	PSCD1	pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1)	17q25
38695_at	Cluster Incl. AA203303:zx55b01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446377 /clone_end=5 /gb=AA203303 /gi=1799194 /ug=Hs.10758 /len=876	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	5q11.1
38705_at	Cluster Incl. AI310002:qo77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1914548 /clone_end=3 /gb=AI310002 /gi=4004873 /ug=Hs.108332 /len=656	UBE2D2	ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5)	5p14.2-q23.3
38728_at	Cluster Incl. D86978:Human mRNA for KIAA0225 gene, partial cds /cds=(0,6043) /gb=D86978 /gi=1504029 /ug=Hs.84790 /len=6237	KIAA0225	KIAA0225 protein	7q33
38730_at	Homo sapiens /REF=AB020671 /DEF=Cluster Incl. : mRNA for KIAA0864 protein, partial cds /cds=(0,3656) /gb= /gi=4240216 /ug=Hs.84883 /len=4319 /LEN=4481	KIAA0864	KIAA0864 protein	17p11.2
38735_at	Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete cds /cds=(631,1866) /gb=AB011085 /gi=3043549 /ug=Hs.85053 /len=7758	KIAA0513	KIAA0513 gene product	16q24.1

38747_at	Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616			
38767_at	Cluster Incl. AF041037:Homo sapiens novel antagonist of FGF signaling (sprouty-1) mRNA, partial cds /cds=(0,419) /gb=AF041037 /gi=2827283 /ug=Hs.88044 /len=1586	SPRY1	sprouty (Drosophila) homolog 1 (antagonist of FGF signaling)	4
38780_at	Cluster Incl. J04794:Human aldehyde reductase mRNA, complete cds /cds=(60,1037) /gb=J04794 /gi=178480 /ug=Hs.89529 /len=1132	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	1p33-p32
38791_at	Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936 /ug=Hs.89674 /len=1668	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	1p36.1
38808_at	Cluster Incl. D64154:Human mRNA for Mr 110,000 antigen, complete cds /cds=(46,1269) /gb=D64154 /gi=994759 /ug=Hs.90107 /len=1375	GP110	cell membrane glycoprotein, 110000M(r) (surface antigen)	20q13.33
38812_at	Cluster Incl. X79683:H.sapiens LAMB2 mRNA for beta2 laminin /cds=(165,5561) /gb=X79683 /gi=663206 /ug=Hs.90291 /len=5673	LAMB2	laminin, beta 2 (laminin S)	3p21
388	Cluster Incl. AF039103:Homo sapiens	HTATI	HIV-1 Tat	11p15.

24_at	Tat-interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297	P2	interactive protein 2, 30 kDa	1
38833_at	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	6p21.3
38858_at	Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) mRNA, complete cds /cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.188021 /len=4070	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	7q35-q36
38879_at	Cluster Incl. D83664:Human mRNA for CAAF1 (calcium-binding protein in amniotic fluid 1), complete cds /cds=(68,346) /gb=D83664 /gi=1502286 /ug=Hs.19413 /len=466	S100A12	S100 calcium-binding protein A12 (calgranulin C)	1q21
38893_at	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136			
38894_g_a	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains			

t	genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136			
38895_i_at	Cluster Incl. X77094:H.sapiens mRNA for p40phox /cds=(130,1149) /gb=X77094 /gi=458543 /ug=Hs.196352 /len=1245	NCF4	neutrophil cytosolic factor 4 (40kD)	22q13.1
38917_at	Cluster Incl. X73617:H.sapiens mRNA for T-cell receptor delta /cds=UNKNOWN /gb=X73617 /gi=402624 /ug=Hs.2014 /len=2343			
38949_at	Cluster Incl. L01087:Human protein kinase C-theta (PRKCT) mRNA, complete cds /cds=(94,2214) /gb=L01087 /gi=558098 /ug=Hs.211593 /len=2754	PRKCQ	protein kinase C, theta	10p15
38963_i_at	Cluster Incl. U12707:Human Wiskott-Aldrich syndrome protein (WASP) mRNA, complete cds /cds=(34,1542) /gb=U12707 /gi=695150 /ug=Hs.2157 /len=1806	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	Xp11.4-p11.21
38992_at	Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502 /ug=Hs.110713 /len=2699	DEK	DEK oncogene (DNA binding)	6p23
38994_at	Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913)	STATI2	STAT induced STAT inhibitor-2	12q

at	/gb=AF037989 /gi=3265032 /ug=Hs.110776 /len=1937			
39061_at	Cluster Incl. D28137:Human mRNA for BST-2, complete cds /cds=(9,551) /gb=D28137 /gi=457563 /ug=Hs.118110 /len=996	BST2	bone marrow stromal cell antigen 2	19p13.2
39062_at	Cluster Incl. AL008726:dJ337O18.2 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C)) /cds=(133,1575) /gb=AL008726 /gi=3183870 /ug=Hs.118126 /len=1946			
39070_at	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	SNL	singed (Drosophila)-like (sea urchin fascin homolog like)	7p22
39089_at	Cluster Incl. Y07604:H.sapiens mRNA for nucleoside-diphosphate kinase /cds=(11,574) /gb=Y07604 /gi=1945761 /ug=Hs.9235 /len=879	NME4	non-metastatic cells 4, protein expressed in	16p13.3
39118_at	Cluster Incl. L08069:Human heat shock protein, E. coli DnaJ homologue mRNA, complete cds /cds=(82,1275) /gb=L08069 /gi=306713 /ug=Hs.94 /len=1438	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	9p13-p12
39136_at	Cluster Incl. AB017642:Homo sapiens mRNA for oxidative-stress responsive 1, complete cds /cds=(342,1925) /gb=AB017642 /gi=4519628	OSR1	oxidative-stress responsive 1	3p22-p21.3

	/ug=Hs.95220 /len=4519			
39165_at	Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819	NIFU	nitrogen fixation cluster-like	12q24.1
39170_at	"Cluster Incl. AL049957:Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323) /cds=UNKNOWN /gb=AL049957 /gi=4884209 /ug=Hs.99766 /len=2180"			
39179_at	Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=940510 /ug=Hs.99962 /len=1637	PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	11q12
39262_at	Cluster Incl. U79266:Human clone 23627 mRNA, complete cds /cds=(184,1041) /gb=U79266 /gi=1710225 /ug=Hs.23642 /len=1561	HSU79266	protein predicted by clone 23627	11q13.1
39301_at	Cluster Incl. X85030:H.sapiens mRNA for skeletal muscle-specific calpain /cds=(0,2465) /gb=X85030 /gi=791039 /ug=Hs.239689 /len=2466	CAPN3	calpain 3, (p94)	15q15.1-q21.1
39327_at	Cluster Incl. D86983:Human mRNA for KIAA0230 gene, partial cds /cds=(0,4490) /gb=D86983 /gi=1504039 /ug=Hs.118893 /len=5510	D2S448	Melanoma associated gene	2pter-p25.1

39358_at	Cluster Incl. U37146:Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds /cds=(495,4982) /gb=U37146 /gi=1045654 /ug=Hs.120980 /len=5970			
39610_at	Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520	HOXB2	homeo box B2	17q21-q22
39649_at	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236	ARHGAP4	Rho GTPase activating protein 4	Xq28
39670_at	"Cluster Incl. AL050034:Homo sapiens mRNA; cDNA DKFZp566G0224 (from clone DKFZp566G0224) /cds=(0,1380) /gb=AL050034 /gi=4884274 /ug=Hs.33573 /len=1762"	ADPRTL3	"ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 3"	3p22.2-p21.1
39689_at	Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2014362 /clone_end=3 /gb=AI362017 /gi=4113638 /ug=Hs.135084 /len=778	CST3	cystatin C (amyloid angiopathy and cerebral hemorrhage)	20p11.2
39730_at	Cluster Incl. X16416:Human c-abl mRNA encoding p150 protein /cds=(147,3539) /gb=X16416 /gi=28236 /ug=Hs.146355 /len=5527	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	9q34.1
39755_	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on			

at	chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802			
39756_g_at	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802			
39775_at	Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827			
39801_at	Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	7q22
39814_s_at	Cluster Incl. AI052724:oz27a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676542 /clone_end=3 /gb=AI052724 /gi=3308715 /ug=Hs.109201 /len=682	LOC51635	CGI-86 protein	14q23.1
39824_at	Cluster Incl. AI391564:tg16b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2108907 /clone_end=3		ESTs, Weakly similar to A28996 proline-	

at	/gb=AI391564 /gi=4217568 /ug=Hs.110820 /len=442		rich protein M14 precursor - mouse [M.musculus]	
39827_at	Cluster Incl. AA522530:ni38d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-979127 /clone_end=3 /gb=AA522530 /gi=2263242 /ug=Hs.111244 /len=891	FLJ20500	hypothetical protein	10pter-q26.12
39860_at	Cluster Incl. U05040:Human FUSE binding protein mRNA, complete cds /cds=(26,1960) /gb=U05040 /gi=460151 /ug=Hs.118962 /len=2325		Homo sapiens far upstream element (FUSE) binding protein 1 (FUBP1), mRNA	
39921_at	Cluster Incl. AI526089:DU3.2-7.H07.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI526089 /gi=4440207 /ug=Hs.1342 /len=788	COX5B	cytochrome c oxidase subunit Vb	2cen-q13
39929_at	Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505	KIAA0922	KIAA0922 protein	4q31.3
39968_at	Cluster Incl. U50136:Human leukotriene C4 synthase (LTC4S) gene, complete cds /cds=(96,548) /gb=U50136 /gi=1314482 /ug=Hs.456 /len=665			
39993_	Cluster Incl. D11466:Homo sapiens mRNA for PIG-A protein, complete cds	PIGA	phosphatidylinositol glycan,	Xp22.1

at	/cds=(85,1539) /gb=D11466 /gi=219993 /ug=Hs.51 /len=3589		class A (paroxysmal nocturnal hemoglobinuria)	
40081_at	Cluster Incl. L26232:Human phospholipid transfer protein mRNA, complete cds /cds=(87,1568) /gb=L26232 /gi=468325 /ug=Hs.154854 /len=1750	PLTP	phospholipid transfer protein	20q12-q13.1
40159_r_at	Cluster Incl. M55067:Human 47-kD autosomal chronic granulomatous disease protein mRNA, complete cds /cds=(22,1194) /gb=M55067 /gi=189050 /ug=Hs.1583 /len=1349	NCF1	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1)	7q11.23
40198_at	Cluster Incl. L06132:Human voltage-dependent anion channel isoform 1 (VDAC) mRNA, complete cds /cds=(99,950) /gb=L06132 /gi=340198 /ug=Hs.149155 /len=1806	VDAC 1	voltage-dependent anion channel 1	5q31
40281_at	Cluster Incl. D63878:Human mRNA for KIAA0158 gene, complete cds /cds=(258,1343) /gb=D63878 /gi=961447 /ug=Hs.155595 /len=3433	NEDD 5	neural precursor cell expressed, developmentally down-regulated 5	2q37
40282_s_at	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	DF	D component of complement (adipsin)	19p13.3

40396_at	Cluster Incl. U49395:Human ionotropic ATP receptor P2X5a mRNA, complete cds /cds=(52,1317) /gb=U49395 /gi=1552521 /ug=Hs.77807 /len=1956	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	17p13
40407_at	Cluster Incl. U28386:Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds /cds=(132,1721) /gb=U28386 /gi=899538 /ug=Hs.159557 /len=1976	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	17q23.1-q23.3
40419_at	Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035			
40456_at	"Cluster Incl. AL049963:Homo sapiens mRNA; cDNA DKFZp564A132 (from clone DKFZp564A132) /cds=UNKNOWN /gb=AL049963 /gi=4884213 /ug=Hs.16726 /len=1322"			
40493_at	Cluster Incl. L05424:Human hyaluronate receptor (CD44) gene /cds=(136,2211) /gb=L05424 /gi=950415 /ug=Hs.169610 /len=2905			
40509_at	Cluster Incl. J04058:Human electron transfer flavoprotein alpha-subunit mRNA, complete cds /cds=(0,1001) /gb=J04058 /gi=182250 /ug=Hs.169919 /len=1266	ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	15q23-q25
405	Cluster Incl. D25538:Human mRNA for	ADCY	adenylate	16q12-

85_at	KIAA0037 gene, complete cds /cds=(265,3507) /gb=D25538 /gi=436217 /ug=Hs.172199 /len=6196	7	cyclase 7	q13
40610_at	Cluster Incl. AI743507:wf72a06.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-2361106 /clone_end=3 /gb=AI743507 /gi=5111795 /ug=Hs.173518 /len=733	ZFR	zinc finger RNA binding protein	5p13.3
40698_at	Cluster Incl. X96719:H.sapiens mRNA for AICL (activation-induced C-type lectin) /cds=(132,581) /gb=X96719 /gi=1632815 /ug=Hs.85201 /len=739	CLECSF2	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	12p13-p12
40718_at	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	CTSW	cathepsin W (lymphopain)	11q13.1
40723_at	Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010059 /gi=4688891 /ug=Hs.88012 /len=1232	SIT	SHP2 interacting transmembrane adaptor	9p13-p12
40763_at	Cluster Incl. U85707:Human leukemogenic homolog protein (MEIS1) mRNA, complete cds /cds=(65,1237) /gb=U85707 /gi=2058550 /ug=Hs.170177 /len=2511	MEIS1	Meis1 (mouse) homolog	2p14-p13

40767_at	Cluster Incl. M59499:Human lipoprotein-associated coagulation inhibitor (LACI) gene /cds=(2,916) /gb=M59499 /gi=187205 /ug=Hs.170279 /len=3599			
40775_at	Cluster Incl. AL021786:Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs /cds=(0,680) /gb=AL021786 /gi=2853186 /ug=Hs.17109 /len=1389			
40786_at	Cluster Incl. U37352:Human protein phosphatase 2A Balpha1 regulatory subunit mRNA, complete cds /cds=(88,1632) /gb=U37352 /gi=1203811 /ug=Hs.171734 /len=4064	PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	3p21
40817_at	Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650	NUCB1	nucleobindin 1	19q13.2-q13.4
40856_at	Cluster Incl. U29953:Human pigment epithelium-derived factor gene, complete cds /cds=(136,1224) /gb=U29953 /gi=1144298 /ug=Hs.173594 /len=1511			
40864_at	Cluster Incl. D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN /gb=D25274 /gi=464185 /ug=Hs.173737 /len=1232			

	/gi=464185 /ug=Hs.173737 /len=1232			
40865_at	Cluster Incl. U51166:Human G/T mismatch-specific thymine DNA glycosylase mRNA, complete cds /cds=(399,1631) /gb=U51166 /gi=1378106 /ug=Hs.173824 /len=3410	TDG	thymine-DNA glycosylase	12q24.1
40936_at	Cluster Incl. AI651806:wb55f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2309611 /clone_end=3 /gb=AI651806 /gi=4735797 /ug=Hs.19280 /len=609	CRIM1	cysteine-rich motor neuron 1	2p21
41096_at	Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446	S100A8	S100 calcium-binding protein A8 (calgranulin A)	1q21
41138_at	Cluster Incl. M16279:Human MIC2 mRNA, complete cds /cds=(177,734) /gb=M16279 /gi=188542 /ug=Hs.177543 /len=1238	MIC2	antigen identified by monoclonal antibodies 12E7, F21 and O13	Xp22.32
41153_f_at	Cluster Incl. AF102803:untitled /cds=(2,2722) /gb=AF102803 /gi=4092760 /ug=Hs.178452 /len=3668			
41155_at	Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=(4,2799) /gb=U03100 /gi=414981 /ug=Hs.178452 /len=3526	CTNNA1	catenin (cadherin-associated protein), alpha 1 (102kD)	5q31

			(102kD)	
41156_g_at	Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=(4,2799) /gb=U03100 /gi=414981 /ug=Hs.178452 /len=3526	CTNNA1	catenin (cadherin-associated protein), alpha 1 (102kD)	5q31
41163_at	Cluster Incl. AL109672:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 755868 /cds=(98,751) /gb=AL109672 /gi=5689836 /ug=Hs.179516 /len=1378	P24B	integral type I protein	15q24-q25
41164_at	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	IGHM	immunoglobulin heavy constant mu	14q32.33
41165_g_at	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	IGHM	immunoglobulin heavy constant mu	14q32.33
41166_at	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325			
41177_at	Cluster Incl. AW024285:wt69d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512715 /clone_end=3 /gb=AW024285 /gi=5877815	FLJ12443	hypothetical protein FLJ12443	5p15.33

	/ug=Hs.179882 /len=550			
41191_at	Cluster Incl. AB023209:Homo sapiens mRNA for KIAA0992 protein, partial cds /cds=(0,2318) /gb=AB023209 /gi=4589627 /ug=Hs.180347 /len=4347	KIAA0992	palladin	4q32.3
41193_at	Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390	DUSP6	dual specificity phosphatase 6	12q22-q23
41200_at	Cluster Incl. Z22555:H.sapiens encoding CLA-1 mRNA /cds=(69,1598) /gb=Z22555 /gi=397606 /ug=Hs.180616 /len=2552	CD36L1	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	12q24.31
41220_at	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	MSF	MLL septin-like fusion	17q25
41273_at	Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /clone_end=5 /gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695			
41338_at	Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523			

41396_at	Cluster Incl. AB006629:Homo sapiens mRNA for KIAA0291 gene, partial cds /cds=(0,2856) /gb=AB006629 /gi=2564329 /ug=Hs.104717 /len=4943	CYLN2	cytoplasmic linker 2	7q11.23
41470_at	Cluster Incl. AF027208:Homo sapiens AC133 antigen mRNA, complete cds /cds=(37,2634) /gb=AF027208 /gi=2688948 /ug=Hs.112360 /len=3794	PROML1	prominin (mouse)-like 1	4p15.33
41471_at	Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	S100A9	S100 calcium-binding protein A9 (calgranulin B)	1q21
41503_at	Cluster Incl. AB020661:Homo sapiens mRNA for KIAA0854 protein, complete cds /cds=(304,2817) /gb=AB020661 /gi=4240196 /ug=Hs.30209 /len=4089	KIAA0854	KIAA0854 protein	8q24.13
41535_at	Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor protein (doc-1) mRNA, complete cds /cds=(522,869) /gb=AF006484 /gi=2738496 /ug=Hs.3436 /len=1608	CDK2AP1	CDK2-associated protein 1	12q24.31
41547_at	Cluster Incl. AF047472:Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA, complete cds /cds=(70,1056) /gb=AF047472 /gi=2921872 /ug=Hs.40323 /len=2585	BUB3	BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog	10q26
41609_at	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162	HLA-DMB	major histocompatibility complex, class	6p21.3

at	/len=1362		II, DM beta	
41654_at	Cluster Incl. X02994:Human mRNA for adenosine deaminase (adenosine aminohydrolase, EC 3.5.4.4) /cds=(95,1186) /gb=X02994 /gi=28379 /ug=Hs.1217 /len=1498	ADA	adenosine deaminase	20q12-q13.11
41660_at	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	GTSE 1	G-2 and S-phase expressed 1	22q13.2-q13.3
41694_at	Cluster Incl. M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M17754 /gi=179512 /ug=Hs.1276 /len=1881	BN51T	BN51 (BHK21) temperature sensitivity complementing	8q21
41723_s_at	Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	6p21.3
41734_at	Cluster Incl. AB020677:Homo sapiens mRNA for KIAA0870 protein, complete cds /cds=(436,1998) /gb=AB020677 /gi=4240228 /ug=Hs.18166 /len=4484	KIAA0870	KIAA0870 protein	8q24.3
41747_s_at	Cluster Incl. U49020:Human myocyte-specific enhancer factor 2A (MEF2A) gene, first coding /cds=(142,1662) /gb=U49020 /gi=1197536			

	/ug=Hs.182280 /len=5329			
41763_g_at	Cluster Incl. D64015:Homo sapiens mRNA for T-cluster binding protein, complete cds /cds=(157,954) /gb=D64015 /gi=2281005 /ug=Hs.182741 /len=1737	TIAL1	TIA1 cytotoxic granule-associated RNA-binding protein-like 1	10q
41796_at	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	PLCE2	phospholipase C, epsilon 2	3p24.3
41808_at	Cluster Incl. AF052102:Homo sapiens clone 23926 mRNA sequence /cds=UNKNOWN /gb=AF052102 /gi=3360409 /ug=Hs.5671 /len=1884			
41809_at	Cluster Incl. AI656421:tt50h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2244259 /clone_end=3 /gb=AI656421 /gi=4740400 /ug=Hs.5671 /len=566	MGC4175	hypothetical protein MGC4175	7q21.1-q21.2
41847_at	Cluster Incl. AA214546:zr92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516	IL24	interleukin 24	1q32
432_s_at	X02883 /FEATURE=cds /DEFINITION=HSTCRAC Human gene for T-cell receptor alpha chain C region	TRA	T cell receptor alpha locus	14q11.2
484_at	U59302 /FEATURE= /DEFINITION=HSU59302 Human	NCOA1	nuclear receptor coactivator 1	2p23

_at	steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	1	coactivator 1	
529 _at	U15932 /FEATURE= /DEFINITION=HSU15932 Human dual-specificity protein phosphatase mRNA, complete cds	DUSP 5	dual specificity phosphatase 5	10q25
538 _at	S53911 /FEATURE= /DEFINITION=S53911 CD34=glycoprotein expressed in lymphohematopoietic progenitor cells {alternatively spliced, truncated form} [human, UT7, mRNA, 2657 nt]	CD34	CD34 antigen	1q32
585 _at	M30938 /FEATURE=mRNA#2 /DEFINITION=HUMKUP Human Ku (p70/p80) subunit mRNA, complete cds	XRCC 5	"X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)"	2q35
605 _at	L78833 /FEATURE=exon#36 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds			
706 _at	Glucocorticoid Receptor, Beta			
767 _at	AF001548 /FEATURE=mRNA /DEFINITION=HUAF001548 Human			

_at	Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence			
820 _at	U77604 /FEATURE= /DEFINITION=HSU77604 Homo sapiens microsomal glutathione S-transferase 2 (MGST2) mRNA, complete cds	MGST 2	microsomal glutathione S-transferase 2	4q28-q31
854 _at	S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]	BLK	B lymphoid tyrosine kinase	8p23-p22
931 _at	L08177 /FEATURE= /DEFINITION=HUMGPCRB Human EBV induced G-protein coupled receptor (EBI2) mRNA, complete cds	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	13q32.3
932 _i_at	L11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds	ZNF91	zinc finger protein 91 (HPF7, HTF10)	19p13.1-p12
933 _f_at	L11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds	ZNF91	zinc finger protein 91 (HPF7, HTF10)	19p13.1-p12
958 _s_	Rna Polymerase II, 14.5 Kda Subunit			

at				
AFFX-HUMRGE/M10098_M_at	M10098 Human 18S rRNA gene, complete (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)			

Table 22:

Pairwise Comparisons

Classification	nBM	CLL	CML	ALL	AML	
nBM		KIA0952, BNL	IRF4, HLA-DMB	PLSCR1; KCNH2 KIAA0467*	PLSCR1, CAMP	n=8
CLL	100% (1.00)		TRB, HLA-DMB	NOCA1, U92981*	POU2AF1, TNFRSF7	n=8
CML	100% (1.00)	100% (1.00)		CLC, TALD01	DEFA3, LCN2, SGP28*	n=10
ALL	100% (0.97)	100% (1.00)	100% (1.00)		OS-9*, LEF1, MSF PPGE, APLP2	n=18
AML	100% (1.00)	100% (1.00)	100% (0.96)	97% (0.95)		n=59
	n=8	n=8	n=10	n=18	n=59	
	% = accuracy in leave-one-out cross validation					
	() = confidence					

Table 23:

Golub				diffgenes			
A -	Samples: 18 / 85			A -	samples: 18 / 85		
Accuracy	0,87			accuracy	0,96		
Confidenc e	0,77			confidenc e	0,88		
Failed	6,19,22,26,78,79,80,81,82,83,84,85,99			failed	5,6,19,22		
Gene	Signal-to-noise	p	decision limit	gene	signal-to-noise	p	decision limit
g1	-1,14	0*	482,01	g1	-1,14	0	
g2	-1,06	0*	192,17	g2	-1,06	0*	98,50
g3	-0,97	0*	207,67	g3	-0,97	0	
g4	0,94	0*	205,05	g4	0,94	0	
g5	-0,93	0*	1818,11	g5	-0,93	0	
g6	0,93	0*	451,74	g6	0,93	0	
g7	-0,91	0*	23,84	g7	-0,91	0	
g8	-0,90	0*	225,72	g8	-0,90	0	

g9	0,90	0*	43,85	g9	0,90	0	
g10	0,89	0*	210,78	g10	0,89	0	
g11	-0,88	0*	118,63	g11	-0,88	0	
g12	0,87	0*	55,39	g12	0,87	0*	67,80
g13	0,87	0*	127,15	g13	0,87	0*	164,10
g14	0,86	0*	222,04	g14	0,86	0	
g15	0,85	0*	68,52	g15	0,85	0	
g16	-0,85	0*	546,97	g16	-0,85	0	
g17	0,84	0*	1242,77	g17	0,84	0	
g18	-0,84	0*	162,61	g18	-0,84	0	
g19	-0,83	0*	385,39	g19	-0,83	0	
g20	0,46	0*	105,38	g20	0,46	0	

Table 24:

Classes	t(15;17) vs. t(8;21)	t(15;17) vs. inv(16)	inv(16) vs. t(8;21)	inv(16) vs. remainder	t(8;21) vs. remainder	t(15;17) vs. remainder
Accuracy	1.00	1.00	1.00	1.00	1.00	1.00
Prediction strength	0.91	0.96	0.93	0.95	0.98	0.91
M65066				-1.52		
AL049933						-2.12
AF010310						1.89
N90866						-2.34
M26326	2.85				-2.56	

	N99340			8.43			
	M25915						1.63
P(g,c)	AF013570		-6.84	7.78	6.99		
	AI207842	3.08	3.08				3.08
	X16665			6.56	6.56		
	X96719						-2.36
	AF013611	2.68					
	W72424						-2.05

Table 25

GenBank accession No.	Approved UCL/HGNC/HUGO database symbol	Description	identified according to Golub et al.	identified utilizing multiple-tree classifiers
M65066	*PRKAR1B*	cAMP-dependent protein kinase regulatory subunit RI-beta	X	
AL049933	*GNAI1*	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	X	
AF010310	*PIG6**	proline oxidase homolog	X	
N90866	*CDW52*	CDW52 antigen (CAMPATH-1 antigen)	X	
M26326	*KRT18*	keratin, type i cytoskeletal 18	X	X
N99340	*DKFZP586N1922**	DKFZP586N1922 protein	X	X
M25915	*CLU*	clusterin precursor	X	
AI207842	*PTGDS*	prostaglandin-h2 d-isomerase precursor	X	
X16665	*HOXB2*	homeobox protein hox-b2	X	X
X96719	*CLECSF2*	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	X	X
AF013611	*CTSW*	cathepsin w (lymphopain) precursor	X	X
W72424	*S100A9*	calgranulin b (migration inhibitory factor-related protein 14)	X	
AF013570	*MYH11*	myosin heavy chain, smooth muscle isoform	X	X
AF001548	*MYH11*	myosin heavy chain, smooth muscle isoform		X

X53742	*FBLN1*	fibulin-1		X
U37122	*ADD3*	gamma adducin		X
J03853	*ADRA2C*	alpha-2c-1 adrenergic receptor		X
Y10183	*ALCAM*	CD166 antigen precursor (activated leukocyte-cell adhesion molecule)		X
AB002313	*PLXNB2*	plexin B2		X
X78817	*ARHGAP4*	rho GTPase activating protein 4		X
X54486	*SERPING1*	plasma protease c1 inhibitor precursor		X
L19872	*AHR*	aryl hydrocarbon receptor		X
M15395	*ITGB2*	CD18, integrin beta-2 precursor		X
AF045229	*RGS10*	regulator of g-protein signaling 10		X
D43638	*CBFA2T1*	MTG8 protein (ETO protein)		X
M25280	*SELL*	l-selectin precursor (lymph node homing receptor)		X
W25986	*DKFZP564K0822* *	hypothetical protein DKFZp564K0822		X
M36035	*BZRP*	peripheral-type benzodiazepine receptor		X
X64624	*POU4F1*	brain-specific homeobox/pou domain protein 3a		X
M18728	*CEACAM6*	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)		X
M77349	*TGFBI*	transforming growth factor-beta induced protein ig-h3 precursor		X

M80899	*AHNAK*	neuroblast differentiation associated protein ahnak		X
M13560	*CD74*	CD74 antigen, (invariant polypeptide of major histocompatibility complex, class II antigen-associated)		X
X62744	*HLA-DMA*	major histocompatibility complex, class II, DM alpha, RING6		X
M32578	*HLA-DRB1*	HLA class II histocompatibility antigen, dr-1(dw14) beta chain precursor		X
X00457	*HLA-DPA1*	HLA class II histocompatibility antigen, dp alpha chain precursor		X
J00194	*HLA-DRA*	HLA class II histocompatibility antigen, dr alpha chain precursor		X

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Table 26: Comparisons of protein expression and mRNA abundance in acute myeloid leukemia as assessed by flow cytometry and microarray analysis

Antigen	Number of comparisons	Both FC and MA positive	Both FC and MA negative	MA positive and FC negative	FC positive and MA negative
Myeloperoxidase	25	**25**	-	-	-
CD13	25	**24**	-	-	1
CD33	25	**24**	-	-	1
CD45	21	**21**	-	-	-
HLA-DR	10	**10**	-	-	-
CD135	4	**3**	-	1	-
CD61	19	-	**19**	-	-
CD10	15	-	**15**	-	-
CD235a	14	-	**12**	2	-
NG2	11	-	**11**	-	-
CD22	5	-	**5**	-	-
CD133	4	-	**4**	-	-
CD79a	2	-	**1**	1	-
CD14	23	**6**	**14**	3	-
CD34	22	**17**	**4**	1	-
CD2	22	**16**	**3**	3	-
CD7	22	**14**	**8**	-	-
CD15	19	**15**	**1**	3	-
CD3	9	**4**	**4**	1	-
Lactoferrin	13	**8**	**2**	3	-
CD116	6	**4**	**2**	-	-
CD11b	7	**5**	**2**	-	-
CD19	12	**5**	**2**	5	-
CD36	22	**2**	**14**	-	6
CD38	9	**4**	**1**	-	4
CD4	18	**6**	**7**	2	3
CD56	23	**2**	**17**	-	4
CD64	23	**15**	**4**	3	1
TdT	20	-	**17**	2	1
Total	**450 (100%)**	**230 (51.1%)**	**169 (37.6%)**	**30 (6.7%)**	**21 (4.7%)**
		399 (88.7%) congruent		**51 (11.4%) not congruent**	

Protein expression and mRNA abundance were compared in 25 patients. "Number of comparisons" indicates the number of patients analyzed for the respective antigens (maximum number, 25 patients)

Table 27

Affymetrix_ID	Description_microarray	Symbol	Description_NetAffx	Chromosome
1087_at	M60459 /FEATURE= /DEFINITION=HUMERYTH Human erythropoietin receptor mRNA, complete cds	EPOR	erythropoietin receptor	19p13.3-p13.2
1747_at	AD000092 /FEATURE=cds#2 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence	unknown cDNA*	?	
1752_at	AD000092 /FEATURE=cds#6 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence	unknown cDNA*	?	
180_at	S82470 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	LENG4*	leukocyte receptor cluster (LRC) member 4	19q13.4
206_at	M84424 /FEATURE=expanded_cds /DEFINITION=HUMCTSE09 Human cathepsin E (CTSE) gene, exon 9 and	CTSE	cathepsin E	

	complete cds			
31381_at	Cluster Incl. AF076483:Homo sapiens peptidoglycan recognition protein precursor (PGRP) mRNA, complete cds /cds=(44,634) /gb=AF076483 /gi=3342532 /ug=Hs.137583 /len=690	PGLYRP	peptidoglycan recognition protein	19q13.2-q13.3
31682_s_at	Cluster Incl. D32039:Human pgH3 mRNA for proteoglycan PG-M(V3), complete cds /cds=(105,2072) /gb=D32039 /gi=1008912 /ug=Hs.234753 /len=2087	CSPG2	chondroitin sulfate proteoglycan 2 (versican)	5q14.3
31749_f_at	Cluster Incl. Z98744:histone H2A /cds=(7,399) /gb=Z98744 /gi=3080457 /ug=Hs.131954 /len=499	H2AFN	H2A histone family, member N	6p22-p21.3
32323_at	Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cds=(8,736) /gb=M63582 /gi=190297 /ug=Hs.182231 /len=1457	TRH	thyrotropin-releasing hormone	3q13.3-q21
33093_at	Cluster Incl. AF077346:Homo sapiens interleukin-18 receptor accessory protein-like mRNA, complete cds /cds=(483,2282) /gb=AF077346 /gi=3851059 /ug=Hs.158315 /len=2681	IL18RAP	interleukin 18 receptor accessory protein	2p24.3-p24.1
33584_at	Cluster Incl. U35146:Human p56 KKIAMRE protein kinase (KKIAMRE), complete cds /cds=(0,1481) /gb=U35146 /gi=1517819 /ug=Hs.158512 /len=1482	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	4
34110_g_at	Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296	PIG6*	proline oxidase homolog	

	/ug=Hs.211605 /len=888			
34139_at	Cluster Incl. AL049651:Human DNA sequence from clone 753D10 on chromosome 20 Contains genes for SSTR4(somatostatin receptor 4) and THBD(thrombomodulin), ESTs, STSs, GSSs and CpG islands /cds=(98,1264) /gb=AL049651 /gi=4741619 /ug=Hs.226015 /len=1427	SSTR4	somatostatin receptor 4	20p11.2
34800_at	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N0910 /clone_end=3 /gb=AL039458 /gi=5408506 /ug=Hs.4193 /len=849	LIG1	ortholog of mouse integral membrane glycoprotein LIG-1	
34960_g_at	Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds (H107 epitope) /cds=(213,1178) /gb=M15059 /gi=182447 /ug=Hs.1416 /len=1530	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23A)	19p13.3
35179_at	Cluster Incl. AB009598:Homo sapiens mRNA for glucuronyltransferase I, complete cds /cds=(29,1036) /gb=AB009598 /gi=3892639 /ug=Hs.26492 /len=1441	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	11q12.2
35426_at	Cluster Incl. AC004410:Homo sapiens chromosome 19, fosmid 39554 /cds=(0,1196) /gb=AC004410 /gi=2959558 /ug=Hs.167352 /len=1197	LOC56928*	hypothetical protein from EUROIMAGE 42353	19p13.3
35552_at	Cluster Incl. AI041180:ov77e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1643360 /clone_end=3 /gb=AI041180	PCYT1B	phosphate cytidylyltransferase 1, choline,	Xp22.22

	/gi=3280374 /ug=Hs.132794 /len=810		beta isoform	
35766_at	Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343) /gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412	KRT18	keratin 18	12q13
36021_at	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	LEF1	lymphoid enhancer-binding factor 1	4q23-q25
36052_at	Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145 /ug=Hs.4852 /len=1284	ADD2	adducin 2 (beta)	2p14-p13
36095_at	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110	DKFZP586N1922*	DKFZP586N1922 protein	19q13.1
36372_at	Cluster Incl. U51333:Human hexokinase III (HK3) mRNA, complete cds /cds=(74,2845) /gb=U51333 /gi=1255787 /ug=Hs.159237 /len=3049	HK3	hexokinase 3 (white cell)	5q35.2
36464_at	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	SGP28*	specific granule protein (28 kDa)	6p12.3
36657_at	Cluster Incl. AA883870:am26f01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1467961 /clone_end=3 /gb=AA883870 /gi=2993400 /ug=Hs.75615 /len=599	APOC2	apolipoprotein C-II	19q13.2

36710_at	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	CAMP	cathelicidin antimicrobial peptide	3p21.3
36780_at	Cluster Incl. M25915:Human complement cytolysis inhibitor (CLI) mRNA, complete cds /cds=(198,1544) /gb=M25915 /gi=180619 /ug=Hs.75106 /len=1651	CLU	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	8p21-p12
38487_at	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777	FLJ12442*	hypothetical protein FLJ12442	
38975_at	Cluster Incl. AF062534:Homo sapiens genethonin 1 mRNA, complete cds /cds=(127,1203) /gb=AF062534 /gi=3851521 /ug=Hs.109590 /len=2340	GENX-3414*	genethonin 1	4q24-q25
39070_at	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	SNL	singed (Drosophila)-like (sea urchin fascin homolog like)	7p22
39221_at	Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds	LILRB2	leukocyte immunoglobulin -like receptor,	19q13.4

	/cds=(208,2001) /gb=AF004231 /gi=2343110 /ug=Hs.22405 /len=2863		subfamily B (with TM and ITIM domains), member 2	
39307_s_at	Cluster Incl. X81637:H.sapiens clathrin light chain b gene /cds=UNKNOWN /gb=X81637 /gi=963046 /ug=Hs.239782 /len=5938	CLTB	clathrin, light polypeptide	4q21-qter
39775_at	Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827	SERPING1	complement component 1 inhibitor	11q12-q13.1
40282_s_at	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	DF	D component of complement (adipsin)	19p13.3
40365_at	Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	19p13.3
40763_at	Cluster Incl. U85707:Human leukemogenic homolog protein (MEIS1) mRNA, complete cds /cds=(65,1237) /gb=U85707 /gi=2058550 /ug=Hs.170177 /len=2511	MEIS1	Meis1 (mouse) homolog	2p14-p13
41045_at	Cluster Incl. U77643:Homo sapiens K12 protein precursor mRNA, complete cds /cds=(118,864) /gb=U77643 /gi=2062390 /ug=Hs.95655 /len=2000	SECTM1	secreted and transmembrane 1	17q25
41448_	Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170O19 from 7p15-p21	HOXA10	homeo box A10	7p15-p14

at	/cds=(0,1247) /gb=AC004080 /gi=2822164 /ug=Hs.110637 /len=1248			
41815_at	Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	SYNE-2*	synaptic nuclei expressed gene 2	14q23.2

Table 28a

classes	BM - t(8;21)	BM - t(15;17)	BM - inv(16)	BM - t(11q23)/MLL	BM - AML
accuracy	*1.00*	*1.00*	*1.00*	*1.00*	*1.00*
prediction strenght	*0.88*	*0.91*	*0.99*	*0.89*	*0.89*
Symbol	P(g,c) values	P(g,c) values	P(g,c) values	P(g,c) values	P(g,c) values
EPOR		7.36	7.36		2.74
unknown cDNA*		-6.46			
unknown cDNA*		-2.76			
LENG4*		-2.92			
CTSE		3.35		2.51	2.39
PGLYRP		7.39			
CSPG2		7.39			
H2AFN				-5.02	
TRH	-2.12				

IL18RAP				4.79	
CDKL2		-3.12			
PIG6*		-2.92			
SSTR4		16.61			
LIG1					3.06
FCER2		4.72			
B3GAT3		-2.04			
LOC56928*				-8.39	-1.70
PCYT1B	3.56				
KRT18		-3.02			
LEF1				3.26	3.26
ADD2		5.63			
DKFZP586N1922*			-8.84		
HK3		6.55			
SGP28*					3.04
APOC2		-5.33		-4.16	
CAMP		6.40			
CLU		-2.71			

FLJ12442*		-2.16			
GENX-3414*				1.97	
SNL		-3.64			
LILRB2		9.75			
CLTB				-4.38	
SERPING1		-2.48			
DF		-2.95			-1.73
GNA15		-2.69			
MEIS1				-4.22	
SECTM1		7.07			
HOXA10				-3.18	
SYNE-2*				3.36	

Table 28b: In total 269 cases with leukemia or normal bone marrow (BM) were analyzed. 248 of 269 (92.2%) cases were assigned to the correct leukemia type in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL t(4;11)	ALL t(8;14)	ALL B not Ph	ALL Ph	T-ALL	AML +8	AML complex	AML normal	AML t(8;21)	AML t(15;17)	AML inv(16)	AML MLL	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL t(4;11)	9															9	100.00	90.00
ALL t(8;14)		3					1									4	75.00	100.00
ALL B not Ph			8	1												9	88.89	80.00
ALL Ph			1	14												15	93.33	87.50
T-ALL					8		1									9	88.89	100.00
AML +8						6		4								10	0.60	100.00
AML complex	1			1			30	3							1	36	83.33	90.91
AML normal			1				1	58				2				62	93.55	85.29
AML t(8;21)									13							13	100.00	100.00
AML t(15;17)										20						20	100.00	100.00
AML inv(16)											12					12	100.00	100.00
AML MLL								2				13				15	86.67	86.67
CLL								1					31			32	96.88	1.00
CML														14		14	100.00	100.00
normal BM															9	9	100.00	90.00
total	10	3	10	16	8	6	33	68	13	20	12	15	31	14	10	269		

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Table 28c: In total 3766 individual assignments of leukemia and normal bone marrow were analyzed. 3745 of 3766 assignments (99.4%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL t(4;11)	ALL t(8;14)	ALL B not Ph	ALL Ph	T-ALL	AML +8	AML complex	AML normal	AML t(8;21)	AML t(15;17)	AML inv(16)	AML MLL	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL t(4;11)	126															126	100.00	99.21
ALL t(8;14)		55					1									56	98.21	100.00
ALL B not Ph			125	1												126	99.21	98.43
ALL Ph			1	209												210	99.52	99.05
T-ALL					125		1									126	99.21	100.00
AML +8						136		4								140	97.14	100.00
AML complex	1			1			498	3							1	504	98.81	99.40
AML normal			1				1	864				2				868	99.54	98.86
AML t(8;21)									182							182	100.00	100.00
AML t(15;17)										280						280	100.00	100.00
AML inv(16)											168					168	100.00	100.00
AML MLL								2				208				210	99.05	99.05
CLL								1					447			448	99.78	100.00
CML														196		196	100.00	100.00
normal BM															126	126	100.00	99.21
total	127	55	127	211	125	136	501	874	182	280	168	210	447	196	127	3766		

Table 29

Analysis of the listed 14 leukemia subgroups and normal bone marrow (BM) according to the method as described by Golub et al. in pairwise comparison

	N
ALL t(4;11)	9
ALL t(8;14)	4
ALL B not Ph	9
ALL Ph	15
T-ALL	9
AML +8	10
AML complex	36
AML normal	62
AML t(8;21)	13
AML t(15;17)	20
AML inv(16)	12
AML MLL	15
CLL	32
CML	14
normal BM	9

5

ALL t(4;11) vs. all other	samples: 9 / 260			
accuracy	1			
confidence	0.983255511396901			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
215925_s_at	2.15211119031413	0		
225592_at	2.10479676639873	0		NRM
205821_at	2.06781828794101	0		D12S2489E
209168_at	2.03682741085015	0		GPM6B
225563_at	2.0365845909197	0		
209170_s_at	1.99341681464758	0		GPM6B
219033_at	1.98127277039877	0*	3296.75	FLJ21308
227407_at	1.9806645400311	0*	2368.95	
226496_at	1.94883167321783	0		
219463_at	1.92861464656998	0		C20orf103
203796_s_at	1.90484126349741	0		BCL7A
210934_at	1.78273564893858	0		BLK
221969_at	1.72749112194125	0		PAX5
239393_at	1.72516948033426	0		
238750_at	1.71981673787555	0		
239214_at	1.67607810398359	0*	645.75	
218469_at	1.65073049955565	0		CKTSF1B1
226244_at	1.64755028976206	0		
218384_at	1.64357646019602	0		CRHSP-24
209815_at	1.64023870547228	0		PTCH

t(4;11) vs. t(15;17)	samples: 9 / 20			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221969_at	5.83664657385464	0*	1301	PAX5
207697_x_at	5.35854600658567	0		LILRB2
203948_s_at	-5.11890143327711	0		MPO
224918_x_at	-4.9355306862525	0		MGST1
203949_at	-4.8364973202297	0		MPO
231736_x_at	-4.46563746824662	0		MGST1
235101_at	4.28876186377802	0		KIAA1014
202481_at	4.05195275593644	0		SDR1
219463_at	3.9253737114322	0		C20orf103
201540_at	3.81769665767171	0		FHL1
238583_at	-3.81099135622948	0		
205382_s_at	-3.80101585016411	0		DF
226878_at	3.74369099536436	0		
210934_at	3.72127171897839	0		BLK
226545_at	3.69021106148297	0		
38487_at	-3.54247992575908	0		FLJ12442
220798_x_at	-3.50808230625528	0		FLJ11535
232201_at	3.50091671488931	0		NKD2
204069_at	3.4252967216987	0		MEIS1
244261_at	3.40910490910101	0		

t(4;11) vs. inv(16)	samples: 9 / 12			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225653_at	-6.57614058007186	0*	129.2	
221969_at	5.83664657385464	0		PAX5
231259_s_at	-5.68009935369819	0		CCND2
203949_at	-4.47845706407372	0		MPO
200951_s_at	-4.24994685464806	0		CCND2
219463_at	3.9253737114322	0		C20orf103
203948_s_at	-3.82832616186979	0		MPO
200953_s_at	-3.81507848947069	0		CCND2
217979_at	3.7506313191621	0		NET-6
210934_at	3.72127171897839	0		BLK
204214_s_at	-3.64249678228396	0		RAB32
203973_s_at	-3.54203246324105	0		CEBPD
232201_at	3.50091671488931	0		NKD2
216860_s_at	3.46199526723217	0		GDF11
244261_at	3.40910490910101	0		
201360_at	-3.40410310063102	0		CST3
226496_at	3.36372190983709	0		
238824_at	3.31690199423555	0		
217966_s_at	-3.29280071064851	0		C1orf24
38340_at	2.62428006100593	0		HIP12

ALL t(4;11) vs. AML MLL	samples: 9 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221969_at	4.924403129677	0*	1534.5	PAX5
226795_at	4.12248256776444	0		
205821_at	4.05458217339808	0		D12S2489E
201360_at	-3.44934876199386	0		CST3
244261_at	3.40910490910101	0		
217979_at	3.33945130505483	0		NET-6
204215_at	3.27742574573237	0		MGC4175
211404_s_at	-3.1044343641572	0		APLP2
217223_s_at	3.09813118817326	0		
206255_at	3.06828641368978	0		BLK
214875_x_at	-2.95163557135368	0		APLP2
201828_x_at	-2.94392957130376	0		CXX1
208702_x_at	-2.9259192302265	0		APLP2
208456_s_at	2.83112443648876	0		RRAS2
219229_at	-2.78106365052986	0		SLC21A11
210487_at	2.65572482698711	0		DNTT
210192_at	2.63764031456982	0		ATP8A1
226496_at	2.63678458715383	0		
203796_s_at	2.63294411410401	0		BCL7A
212207_at	2.62364024475935	0		KIAA1025

ALL t(4;11) vs. CLL	samples: 9 / 32			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210045_at	6.76734853184964	0*	142.15	IDH2
204798_at	4.99101493214162	0		MYB
225592_at	4.17686594916951	0		NRM
202503_s_at	4.02396247600866	0		KIAA0101
219463_at	3.9253737114322	0		C20orf103
201540_at	3.7195174107357	0		FHL1
226545_at	3.4985271993093	0		
223276_at	3.36058308258119	0		NID67
209267_s_at	3.33868760455037	0		LOC64116
201416_at	3.27673886279907	0		SOX4
224710_at	3.27404618682988	0		RAB34
218384_at	3.26299093107225	0		CRHSP-24
209365_s_at	3.22987740485106	0		ECM1
219869_s_at	3.18151227716348	0		LOC64116
218942_at	-3.1335063798458	0		FLJ22055
209825_s_at	3.12344649016037	0		UMPK
201417_at	3.10175892236352	0		
238022_at	3.08645149251292	0		
212281_s_at	3.07915047956129	0		MAC30
204069_at	3.04751039522855	0		MEIS1

ALL t(4;11) vs. CML	samples: 9 / 14			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221969_at	5.83664657385464	0*	1301	PAX5
207000_s_at	4.65703873448273	0		PPP3CC
212484_at	4.34689222808594	0		MTVR
201485_s_at	4.25216281704109	0		RCN2
204214_s_at	-4.24363288728321	0		RAB32
203796_s_at	4.18407933075926	0		BCL7A
218223_s_at	4.16804739438629	0		LOC51177
226795_at	4.12248256776444	0		
205821_at	4.05458217339808	0		D12S2489E
221755_at	3.99463418568195	0		
219463_at	3.9253737114322	0		C20orf103
202332_at	3.87997129184981	0		CSNK1E
210254_at	-3.85534735854191	0		
209619_at	3.77477243739775	0		CD74
226878_at	3.74369099536436	0		
205557_at	-3.71054014877636	0		BPI
225713_at	3.59398617666668	0		KIAA1898
206440_at	-3.54851691296324	0		VELI1
232201_at	3.50091671488931	0		NKD2
204215_at	3.43706276144109	0		MGC4175

ALL t(4;11) vs. normal BM	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201828_x_at	-6.82241973614495	0*	285.3	CXX1
210045_at	6.76734853184964	0		IDH2
214950_at	6.24435639089538	0		
237431_at	5.31661820706767	0		
225792_at	-5.04037264761662	0		
205624_at	-4.8793192574965	0		CPA3
201540_at	4.79436840204501	0		FHL1
204214_s_at	-4.53807365704691	0		RAB32
218916_at	4.52409549429394	0		FLJ23436
200832_s_at	-4.29237917192722	0		SCD
203796_s_at	4.18407933075926	0		BCL7A
205051_s_at	-4.13944949609416	0		KIT
202332_at	4.13816009401715	0		CSNK1E
228176_at	-4.13090953290361	0		
226795_at	4.12248256776444	0		
208754_s_at	4.00220842620578	0		NAP1L1
221755_at	3.99463418568195	0		
228424_at	-3.92813180248343	0		NAALADASEL
219463_at	3.9253737114322	0		C20orf103
212967_x_at	3.92366867855542	0		NAP1L1

ALL t(4;11) vs. ALL t(8;14)	samples: 9 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210045_at	6.76734853184964	0*	142.15	IDH2
240106_at	6.10571301118426	0		
202853_s_at	-5.88804457870992	0		RYK
242434_at	-5.60754470569171	0		
237431_at	5.31661820706767	0		
201540_at	4.94655082712075	0		FHL1
215855_s_at	4.71299810202736	0		
212357_at	4.18767818184794	0		KIAA0280
204798_at	4.12313508850913	0		MYB
226795_at	4.12248256776444	0		
77508_r_at	4.0317985345148	0		FLJ23282
46142_at	3.95748459279267	0		FLJ12681
225277_at	3.7552029934786	0		
210934_at	3.72127171897839	0		BLK
215537_x_at	3.53324247477066	0		
232201_at	3.50091671488931	0		NKD2
214505_s_at	3.42260996379197	0		FHL1
244261_at	3.40910490910101	0		
208614_s_at	3.34565043119022	0		FLNB
210298_x_at	3.30171221592859	0.01		FHL1

ALL t(4;11) vs. ALL B not Ph	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
237431_at	5.31661820706767	0*	49	
219033_at	3.19032095561144	0		FLJ21308
219463_at	2.69567768562793	0		C20orf103
204069_at	2.54127866831197	0		MEIS1
201105_at	2.30596776500018	0		LGALS1
200907_s_at	2.19034049161844	0		KIAA0992
242414_at	2.08870062415486	0		
222492_at	-2.04226084466602	0		FLJ21324
230441_at	-2.03717805375485	0		
235291_s_at	2.0210425168076	0		
225592_at	2.01329642963674	0		NRM
200906_s_at	1.9632986862999	0		
201153_s_at	1.93254941630797	0		MBNL
201152_s_at	1.93227192981893	0		MBNL
241985_at	-1.91875000661653	0		
213894_at	1.89533012552966	0		KIAA0960
243756_at	1.82938790694615	0		
225563_at	1.82046495626766	0		
232231_at	1.8138577510169	0		
240581_at	1.80942575017411	0		

ALL t(4;11) vs. ALL Ph	samples: 9 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204069_at	3.31118886883646	0*	482.55	MEIS1
219033_at	3.24786485857293	0		FLJ21308
219463_at	2.78353259146178	0		C20orf103
221969_at	2.4416835946504	0		PAX5
201874_at	2.38057857279198	0		FLJ21047
209170_s_at	2.31526351178702	0		GPM6B
233500_x_at	2.23629715560156	0		LLT1
205899_at	2.23375311954146	0		CCNA1
242414_at	2.21567202901383	0		
205821_at	2.10144186601662	0		D12S2489E
205055_at	2.04951650013049	0		ITGAE
209168_at	2.02899949049115	0		GPM6B
226939_at	1.99568402107224	0		
209354_at	-1.9938191217443	0		TNFRSF14
200906_s_at	1.9632986862999	0		
225563_at	1.88712595721941	0		
237431_at	1.87880985981148	0		
34210_at	-1.86187594200254	0		CDW52
202853_s_at	-1.84984316383277	0		RYK
209167_at	1.84829764568262	0		GPM6B

ALL t(4;11) vs. T-ALL	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221969_at	5.83664657385464	0*	1301	PAX5
237431_at	5.31661820706767	0		
213772_s_at	4.80540935532116	0		GGA2
219463_at	3.9253737114322	0		C20orf103
210934_at	3.72127171897839	0		BLK
242292_at	-3.53231266693437	0		
226496_at	3.49024496949904	0		
244261_at	3.40910490910101	0		
205640_at	3.04306419050975	0		ALDH3B1
219033_at	3.03434195473282	0		FLJ21308
209168_at	3.02932118514235	0		GPM6B
205821_at	2.9956567374574	0		D12S2489E
235706_at	2.99518505957364	0		CPM
225592_at	2.98114633774562	0		NRM
225314_at	-2.87525509857994	0		
209170_s_at	2.832580891342	0		GPM6B
215925_s_at	2.79328349720245	0		
204069_at	2.67025815490556	0		MEIS1
210192_at	2.63764031456982	0		ATP8A1
217080_s_at	2.60699026264913	0		HOMER-2B

ALL t(4;11) vs. AML +8	samples: 9 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201828_x_at	-4.66708459109445	0*	226.35	CXX1
221969_at	3.82090922998168	0		PAX5
244261_at	3.40910490910101	0		
210024_s_at	-3.20983153576119	0		UBE2E3
219013_at	-3.19035252569463	0		FLJ21634
226496_at	3.13934828480165	0		
205821_at	3.04595286153542	0		D12S2489E
219229_at	-3.04273361188054	0		SLC21A11
222422_s_at	-3.02123752629534	0		MGC10924
233138_at	2.95580347805273	0		
206255_at	2.76163042569406	0		BLK
217979_at	2.7584725396168	0		NET-6
203796_s_at	2.72124988867035	0		BCL7A
214761_at	2.62282117562643	0		OAZ
227407_at	2.55763093921665	0		
209365_s_at	2.53044674597142	0		ECM1
228379_at	2.52915026244479	0		
204214_s_at	-2.51760565011465	0		RAB32
202626_s_at	-2.5141028457265	0		LYN
244876_at	2.46777854429452	0		

ALL t(4;11) vs. AML complex	samples: 9 / 36			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221969_at	4.27209531988207	0*	1815.1	PAX5
210934_at	3.72127171897839	0		BLK
244261_at	3.40910490910101	0		
219463_at	3.31691046444078	0		C20orf103
206255_at	2.78386884086495	0		BLK
226496_at	2.68550006340332	0		
209170_s_at	2.55250295984436	0		GPM6B
209168_at	2.44311832949527	0		GPM6B
215925_s_at	2.34663986373513	0		
226244_at	2.33002353009868	0		
219033_at	2.29968992798521	0		FLJ21308
205821_at	2.2854186259635	0		D12S2489E
232201_at	2.05970386931189	0		NKD2
209167_at	2.05931372040727	0		GPM6B
244876_at	2.04904743648645	0		
212658_at	-2.00156707557967	0		LHFPL2
227407_at	1.9737052609863	0		
202853_s_at	-1.93859575890205	0		RYK
203796_s_at	1.92961910857241	0		BCL7A
214761_at	1.92608972571974	0		OAZ

ALL t(4;11) vs. AML normal	samples: 9 / 62			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221969_at	4.52880455396521	0*	1791.55	PAX5
210934_at	3.72127171897839	0		BLK
205821_at	2.95344549198955	0		D12S2489E
206255_at	2.91976312133621	0		BLK
226496_at	2.83306188482026	0		
215925_s_at	2.5921353451626	0		
244261_at	2.54559007441965	0		
244876_at	2.46777854429452	0		
203796_s_at	2.38175636157975	0		BCL7A
209815_at	2.31390268701643	0		PTCH
204215_at	2.24841200417248	0		MGC4175
227407_at	2.2323195471751	0		
214761_at	2.22867492056937	0		OAZ
226244_at	2.1571079710692	0		
225563_at	2.13989749649066	0		
225592_at	2.10215542418477	0		NRM
35974_at	2.05472986731736	0		LRMP
217979_at	2.03188116697557	0		NET-6
230292_at	2.02307533754428	0		
209168_at	2.01872981119451	0		GPM6B

ALL t(4;11) vs. AML t(8;21)	samples: 9 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212484_at	4.34689222808594	0*	121.4	MTVR
221969_at	4.27496053785902	0		PAX5
203796_s_at	4.18407933075926	0		BCL7A
219463_at	3.9253737114322	0		C20orf103
210934_at	3.72127171897839	0		BLK
232201_at	3.50091671488931	0		NKD2
244261_at	3.40910490910101	0		
204069_at	3.34624733362178	0		MEIS1
204214_s_at	-3.30583121065186	0		RAB32
225592_at	3.20386305207036	0		NRM
206255_at	3.14140321370378	0		BLK
212658_at	-3.07377549400227	0		LHFPL2
226496_at	3.07152636043149	0		
233138_at	2.95580347805273	0		
227041_at	2.93637529041438	0		
212480_at	2.90213688157125	0		KIAA0376
203795_s_at	2.86560617331268	0		BCL7A
202853_s_at	-2.76308096012904	0		RYK
203949_at	-2.76134156327152	0		MPO
219033_at	2.72927502272681	0		FLJ21308

AML t(15;17) vs. all other	samples: 20 / 249			
accuracy	1			
confidence	0.984095291727473			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214450_at	2.5552572465358	0		CTSW
38487_at	2.48122703820417	0*	5275.3	FLJ12442
212953_x_at	2.383904085321	0		CALR
224794_s_at	2.04094710734487	0		LOC51148
221004_s_at	2.02822882303862	0		ITM3
204150_at	1.96620111034732	0		STAB1
203948_s_at	1.77090499793556	0*	13772.15	MPO
219837_s_at	1.67874985207037	0		C17
205382_s_at	1.63444144003612	0		DF
241383_at	1.6305764545467	0		
216032_s_at	1.61454780261863	0		SDBCAG84
200654_at	1.60202170245338	0		P4HB
220798_x_at	1.58679638297009	0		FLJ11535
208852_s_at	1.58602299942644	0		CANX
203074_at	1.57040201174593	0		ANXA8
200656_s_at	1.55688359776913	0		P4HB
209344_at	1.55490125921714	0		TPM4
205624_at	1.52362814764187	0		CPA3
64942_at	1.52358978934783	0		
AFFX-HUMGAPDH/M33197_5_at HG-U133A	1.05449125226594	0		GAPD

AML t(15;17) vs. AML inv(16)	samples: 20 / 12			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204661_at	-3.70847055085953	0*	1899.15	CDW52
209732_at	-3.23538966029247	0		CLECSF2
241742_at	-3.11768531834572	0		PRAM-1
38487_at	3.08138549900179	0		FLJ12442
238022_at	3.0278549438122	0		
204563_at	-2.99471501611954	0		SELL
34210_at	-2.99398735377828	0		CDW52
203535_at	-2.97123029136408	0		S100A9
217478_s_at	-2.93655072055469	0		
214450_at	2.92945546081029	0		CTSW
211991_s_at	-2.91096104465505	0		HLA-DPA1
208306_x_at	-2.87060964824031	0		HLA-DRB4
213779_at	2.84856846381654	0		
211990_at	-2.76844422327205	0		HLA-DPA1
221004_s_at	2.72545702224706	0		ITM3
209312_x_at	-2.66880572066538	0		HLA-DRB1
219789_at	-2.64334906817191	0		NPR3
204425_at	-2.62831954360607	0		ARHGAP4
205076_s_at	-2.59502309617401	0		CRA
64942_at	2.28304127550384	0		

AML t(15;17) vs. AML MLL	samples: 20 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205624_at	3.0741697102978	0*	2052.6	CPA3
38487_at	2.78111206643545	0		FLJ12442
203948_s_at	2.68497999695567	0		MPO
221004_s_at	2.64526084301972	0		ITM3
200951_s_at	2.52924582612911	0		CCND2
206761_at	2.52586949939666	0		TACTILE
203949_at	2.44678680592608	0		MPO
214651_s_at	-2.42192013365627	0		HOXA9
200952_s_at	2.39696270141848	0		CCND2
64942_at	2.28304127550384	0		
200953_s_at	2.24845652213108	0		CCND2
204150_at	2.2435902165197	0		STAB1
212953_x_at	2.22414089725316	0		CALR
233072_at	2.22380780245302	0		KIAA1857
214450_at	2.16984309325722	0		CTSW
224794_s_at	2.14479331910386	0		LOC51148
205349_at	2.12589700684588	0		GNA15
212509_s_at	2.11142192746438	0		
224839_s_at	2.07810412712239	0		GPT2
210788_s_at	2.07490438621852	0		LOC51635

AML t(15;17) vs. CLL	samples: 20 / 32			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203949_at	6.8835946674069	0*	5834.85	MPO
203948_s_at	5.89121269767824	0		MPO
206871_at	4.93321162912793	0		ELA2
226043_at	4.54092115946342	0		AGS3
213854_at	4.34395164475566	0		SYNGR1
224918_x_at	4.34201320024004	0		MGST1
206111_at	4.19970662571818	0		RNASE2
200654_at	4.03204616783544	0		P4HB
231736_x_at	4.00585801175558	0		MGST1
224838_at	-3.92476184954236	0		
211990_at	-3.92005265639026	0		HLA-DPA1
238583_at	3.81099135622948	0		
221004_s_at	3.79791980511322	0		ITM3
212400_at	-3.75779674692328	0		
211709_s_at	3.73806507086654	0		SCGF
214575_s_at	3.66149641725929	0		AZU1
205382_s_at	3.59180789007477	0		DF
238022_at	3.5791572544895	0		
212953_x_at	3.54883221957949	0		CALR
38487_at	3.51682772737691	0		FLJ12442

AML t(15;17) vs. CML	samples: 20 / 14			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201029_s_at	4.80190269912041	0*	4487.95	MIC2
212531_at	-4.73996757450677	0		LCN2
206676_at	-4.32531789709243	0		CEACAM8
216379_x_at	-4.27706524116979	0		
209771_x_at	-4.21950511119586	0		CD24
207269_at	-3.91601606801308	0		DEFA4
205557_at	-3.83288724786037	0		BPI
202018_s_at	-3.78757135021052	0		LTF
38487_at	3.67170603901023	0		FLJ12442
211657_at	-3.58933972989264	0		
205382_s_at	3.52725281328905	0		DF
220798_x_at	3.50808230625528	0		FLJ11535
209772_s_at	-3.45628903280328	0		CD24
221004_s_at	3.42707462770742	0		ITM3
203535_at	-3.38406746753723	0		S100A9
205863_at	-3.37594312179774	0		S100A12
204174_at	-3.3757799683273	0		ALOX5AP
203757_s_at	-3.33946937382462	0		CEACAM6
225386_s_at	-3.31814635286046	0		LOC92906
64942_at	2.28304127550384	0		

AML t(15;17) vs. normal BM	samples: 20 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225792_at	-5.04037264761662	0*	76.45	
202018_s_at	-5.02314565371121	0		LTF
223280_x_at	-4.43579892206636	0		MS4A6A
212531_at	-4.09661809496392	0		LCN2
203535_at	-3.97435355306196	0		S100A9
205382_s_at	3.87917813251128	0		DF
224356_x_at	-3.8624083855044	0		MS4A6A
201029_s_at	3.64114093559717	0		MIC2
219471_at	-3.59149059254273	0		FLJ21562
223391_at	-3.55822107244772	0		LOC81537
225897_at	-3.53074009879907	0		
209831_x_at	3.47754001947329	0		DNASE2
230526_at	-3.32964763857134	0		FLJ20015
221004_s_at	3.30073847019088	0		ITM3
38487_at	3.26067308155523	0		FLJ12442
207697_x_at	-3.24955398927113	0		LILRB2
203645_s_at	-3.22408073656527	0		CD163
201506_at	-3.1496662320639	0		TGFBI
239278_at	-3.14559842984954	0		
201640_x_at	3.1436907617525	0		CLPTM1

AML t(15;17) vs. ALL t(8;14)	samples: 20 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212400_at	-6.34509116618667	0*	124.35	
239835_at	-4.64446812677972	0		KIAA1842
213854_at	4.34395164475566	0		SYNGR1
209765_at	-3.90392395971701	0		ADAM19
212953_x_at	3.6338360358333	0		CALR
220798_x_at	3.50808230625528	0		FLJ11535
202723_s_at	-3.43565959824609	0		FOXO1A
205382_s_at	3.38600016039015	0		DF
205059_s_at	3.37067676532123	0		IDUA
38487_at	3.30566285802216	0		FLJ12442
235823_at	-3.22388670008998	0		
214450_at	3.19435746487831	0		CTSW
201640_x_at	3.1436907617525	0		CLPTM1
242774_at	-3.10884740483827	0		SYNE-2
205624_at	3.08135190030361	0		CPA3
221004_s_at	3.04980072799641	0		ITM3
202262_x_at	3.00631284337625	0		DDAH2
227525_at	-2.99175282480629	0		LOC113263
227173_s_at	-2.97620214103741	0		BACH2
46142_at	2.45069282884032	0		FLJ12681

AML t(15;17) vs. ALL B not Ph	samples: 20 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205382_s_at	3.94103663553541	0*	3034.4	DF
214450_at	3.7272017152315	0		CTSW
220798_x_at	3.50808230625528	0		FLJ11535
209831_x_at	3.47754001947329	0		DNASE2
212953_x_at	3.01141919123014	0		CALR
231736_x_at	2.98271279100376	0		MGST1
211990_at	-2.92818453065756	0		HLA-DPA1
241383_at	2.90001109867359	0		
224918_x_at	2.89999004151056	0		MGST1
205624_at	2.84403833450845	0		CPA3
38487_at	2.72794873611638	0		FLJ12442
200654_at	2.71316195189784	0		P4HB
221004_s_at	2.68426024071363	0		ITM3
208689_s_at	2.62363368134519	0		RPN2
221739_at	2.61870113363546	0		IL27
203679_at	2.54794444503946	0		IL1RL1LG
217716_s_at	2.27011720191064	0		SEC61A1
208852_s_at	2.24073987327423	0		CANX
220744_s_at	2.21509524546031	0		WDR10
55093_at	1.63667373135171	0		KIAA1402

AML t(15;17) vs. ALL Ph	samples: 20 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
211990_at	-3.8327925790289	0		HLA-DPA1
220798_x_at	3.50808230625528	0*	41	FLJ11535
224918_x_at	3.50754573671859	0		MGST1
214450_at	3.50155234311803	0		CTSW
231736_x_at	3.3802502122888	0		MGST1
205624_at	3.21024990481945	0		CPA3
203373_at	-3.1946557461653	0		STATI2
205382_s_at	3.14485336319038	0		DF
212953_x_at	2.86696122083705	0		CALR
203948_s_at	2.80859584810434	0		MPO
238583_at	2.78542343697266	0		
209732_at	-2.73475243434259	0		CLECSF2
233072_at	2.63743334734262	0		KIAA1857
209619_at	-2.55642326842901	0		CD74
226545_at	-2.50061887472005	0		
238022_at	2.48587783472615	0		
210487_at	-2.48460923232205	0		DNTT
200654_at	2.41521499865532	0		P4HB
209831_x_at	2.34522293184427	0		DNASE2
225790_at	2.31674527318944	0		

AML t(15;17) vs. T-ALL	samples: 20 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203949_at	5.76493681986315	0*	6205	MPO
203948_s_at	5.52731611865475	0		MPO
224918_x_at	5.05683576581082	0		MGST1
231736_x_at	4.44324813542895	0		MGST1
213854_at	4.34395164475566	0		SYNGR1
205382_s_at	4.13724322163424	0		DF
206871_at	4.09729897232645	0		ELA2
206111_at	3.61313451786675	0		RNASE2
242292_at	-3.53231266693437	0		
214575_s_at	3.51522052980985	0		AZU1
220798_x_at	3.50808230625528	0		FLJ11535
38487_at	3.40780715783254	0		FLJ12442
200654_at	3.36034425167829	0		P4HB
235101_at	-3.27592263847035	0		KIAA1014
208689_s_at	3.18547214467073	0		RPN2
212953_x_at	3.18316032369792	0		CALR
204348_s_at	3.06277487805438	0		AK3
201537_s_at	2.82382291089523	0		DUSP3
214450_at	2.81907045269144	0		CTSW
204150_at	2.73329912927614	0		STAB1

AML t(15;17) vs. AML +8	samples: 20 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214450_at	3.0865086945171	0*	1926.7	CTSW
212953_x_at	2.71319553382926	0		CALR
236787_at	2.4273500798775	0		
200952_s_at	2.39696270141848	0		CCND2
205624_at	2.38480346275743	0		CPA3
38487_at	2.38251622694176	0		FLJ12442
205614_x_at	2.24846130719191	0		MST1
206761_at	2.20501899975366	0		TACTILE
216320_x_at	2.16690689445934	0		
224794_s_at	2.14479331910386	0		LOC51148
233072_at	2.07721746169547	0		KIAA1857
221004_s_at	2.05892662897696	0		ITM3
227326_at	2.04924504239987	0		
221980_at	2.01752809990056	0		
225547_at	-1.98126007880124	0		
210145_at	-1.95455412087558	0		PLA2G4A
212509_s_at	1.92046303571342	0		
209344_at	1.90906303754685	0		TPM4
201029_s_at	1.87538506046111	0		MIC2
204150_at	1.87343002266891	0		STAB1

AML t(15;17) vs. AML complex	samples: 20 / 36			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205382_s_at	2.47024872277389	0		DF
212953_x_at	2.44599456599903	0*	4652.35	CALR
64942_at	2.28304127550384	0		
214450_at	2.2627370518124	0		CTSW
38487_at	2.15395063071356	0		FLJ12442
224794_s_at	2.14479331910386	0		LOC51148
220798_x_at	2.06303065394458	0		FLJ11535
216032_s_at	2.05259440043708	0		SDBCAG84
203948_s_at	2.04245448483567	0		MPO
209732_at	-1.90630142681759	0		CLECSF2
230526_at	-1.90204644112897	0		FLJ20015
238022_at	1.89121106100583	0		
200654_at	1.73209407132843	0		P4HB
204150_at	1.72000809746397	0		STAB1
213447_at	-1.71480861978241	0		IPW
206847_s_at	-1.68023930751716	0		HOXA7
203074_at	1.65576107663154	0		ANXA8
219837_s_at	1.65191807395586	0		C17
200931_s_at	-1.6356222023809	0		VCL
AFFX-HUMGAPDH/M33197_5_at HG-U133A	1.15678566237816	0		GAPD

AML t(15;17) vs. AML normal	samples: 20 / 62			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212953_x_at	2.64618373092816	0*	4541.1	CALR
214450_at	2.28653040002124	0		CTSW
203948_s_at	2.28093863578688	0		MPO
38487_at	2.27897339525457	0		FLJ12442
224794_s_at	2.14479331910386	0		LOC51148
233072_at	2.02319157581908	0		KIAA1857
221004_s_at	2.01169552990941	0		ITM3
236787_at	1.97410536661333	0		
209732_at	-1.93278822451406	0		CLECSF2
214651_s_at	-1.88045707977072	0		HOXA9
216032_s_at	1.84310066944834	0		SDBCAG84
227326_at	1.83154138034996	0		
200952_s_at	1.79422847402715	0		CCND2
208852_s_at	1.77896258332914	0		CANX
200654_at	1.77731955574697	0		P4HB
204150_at	1.77067560905128	0		STAB1
64942_at	1.71976456537364	0		
203949_at	1.69386661503752	0		MPO
235753_at	-1.67072227461966	0		
209344_at	1.65496211687573	0		TPM4

AML t(15;17) vs. AML t(8;21)	samples: 20 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214450_at	3.53862069365814	0*	1809.95	CTSW
38487_at	3.30334484935728	0		FLJ12442
209732_at	-3.18277220746091	0		CLECSF2
204150_at	2.73329912927614	0		STAB1
201596_x_at	2.73162867034962	0		KRT18
213944_x_at	2.5862372690463	0		
230526_at	-2.42276930706474	0		FLJ20015
212509_s_at	2.33481477262277	0		
211990_at	-2.3270695509372	0		HLA-DPA1
204319_s_at	-2.25060861801642	0		RGS10
205614_x_at	2.24846130719191	0		MST1
216320_x_at	2.16690689445934	0		
224794_s_at	2.14479331910386	0		LOC51148
224839_s_at	2.07810412712239	0		GPT2
227326_at	2.04924504239987	0		
238365_s_at	2.03674279873081	0		
228827_at	-2.03460798747208	0		
228570_at	2.03169244854036	0		
205349_at	2.02142471684528	0		GNA15
200986_at	2.01484061650733	0		SERPING1

AML inv(16) vs. all other	samples: 12 / 257			
accuracy	1			
confidence	0.786321619312236			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201497_x_at	1.74852845185764	0		MYH11
231310_at	1.47164364462932	0		
241525_at	1.40464277333052	0		
233555_s_at	1.36141951191384	0*	462.05	
224724_at	1.35707926936144	0		KIAA1247
200665_s_at	1.34209700274375	0		SPARC
202370_s_at	-1.29245470192814	0		CBFB
222862_s_at	1.26048366428059	0		AK5
200675_at	-1.23914248971997	0		CD81
205076_s_at	1.22017942852008	0		CRA
201496_x_at	1.21510481759962	0		MYH11
223385_at	1.2113380867898	0		CYP2S1
221486_at	-1.19152063013451	0		
223471_at	-1.18312106893472	0		
206135_at	1.18181935093584	0		KIAA0535
206956_at	1.17922310970084	0		BGLAP
235359_at	1.16409001423194	0		
202016_at	1.15872909212242	0*	1	MEST
201324_at	1.15017496156271	0		EMP1
AFFX-HUMRGE/M10098_5_at - HG-U133B	0.737113176900438	0		

AML inv(16) vs. AML MLL	samples: 12 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
200951_s_at	4.24994685464806	0*	75.6	CCND2
228058_at	3.25212044058077	0		
219271_at	2.57049778814556	0		FLJ12691
231259_s_at	2.43255056573718	0		CCND2
214651_s_at	-2.30388406553935	0		HOXA9
202551_s_at	2.25890379783091	0		CRIM1
205453_at	2.23059959679219	0		HOXB2
200953_s_at	2.19700687874039	0		CCND2
213737_x_at	-2.16186095833837	0		
235818_at	2.13054793207832	0		
225653_at	2.10834669134201	0		
232636_at	-2.07022186491858	0		
202746_at	2.06211630393441	0		
200665_s_at	2.03751489015447	0		SPARC
203949_at	2.01364277991339	0		MPO
202552_s_at	1.96670486082105	0		CRIM1
223471_at	-1.96529988161274	0		
201828_x_at	-1.9593150488894	0		CXX1
235359_at	1.95403665761428	0		
202747_s_at	1.9384101680124	0		ITM2A

AML inv(16) vs. CLL	samples: 12 / 32			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203949_at	6.95021247410033	0*	3746.5	MPO
211709_s_at	5.18681505358433	0		SCGF
203948_s_at	4.72760268663435	0		MPO
231310_at	4.35158499850242	0		
226043_at	4.31805631251135	0		AGS3
201417_at	3.83165504179581	0		
209365_s_at	3.8293529362527	0		ECM1
224838_at	-3.72164043642693	0		
243000_at	3.63182045730937	0		
223382_s_at	3.56679694464951	0		NIN283
201163_s_at	3.21223463217947	0		IGFBP7
202862_at	3.20454480816595	0		FAH
231982_at	3.1934694742924	0		
201162_at	3.15702502490111	0		IGFBP7
218942_at	-3.1335063798458	0		FLJ22055
212827_at	-3.11017349120191	0		IGHM
224710_at	3.04332806808412	0		RAB34
208864_s_at	3.01671716600197	0		TXN
211787_s_at	2.90916234544607	0		EIF4A1
205382_s_at	2.90564641349051	0		DF

AML inv(16) vs. CML	samples: 12 / 14			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201029_s_at	4.31890554977499	0*	4017	MIC2
209365_s_at	3.8293529362527	0		ECM1
226844_at	3.75460881300519	0		
209771_x_at	-3.55889840129944	0		CD24
206440_at	-3.54851691296324	0		VELI1
233138_at	3.4735123827114	0		
216379_x_at	-3.43948341863688	0		
227749_at	3.41648620394084	0		
209772_s_at	-3.3477199485593	0		CD24
210982_s_at	3.24778523856649	0		HLA-DRA
218942_at	-3.24708603988632	0		FLJ22055
206676_at	-3.24497920147189	0		CEACAM8
204661_at	3.10482803895821	0		CDW52
212531_at	-3.09841450182506	0		LCN2
208306_x_at	3.05465357697194	0		HLA-DRB4
208890_s_at	2.99789197915585	0		PLXNB2
216015_s_at	2.9548034027314	0		
223839_s_at	-2.95162251991881	0		
207802_at	-2.93213346323135	0		SGP28
34210_at	2.86220111493221	0		CDW52

AML inv(16) vs. normal BM	samples: 12 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225792_at	-5.04037264761662	0*	76.45	
224975_at	-5.01918026903577	0		NFIA
224976_at	-4.534006778733	0		NFIA
238652_at	4.21116590562832	0		
209365_s_at	3.8293529362527	0		ECM1
223044_at	-3.73370982362517	0		SLC11A3
226326_at	-3.6960030140107	0		
200832_s_at	-3.67575949264708	0		SCD
213288_at	-3.55635098156803	0		
230988_at	-3.46948918999612	0		
205382_s_at	3.29073930292859	0		DF
201417_at	3.27682718704937	0		
225897_at	-3.21286424500781	0		
226299_at	3.21097313269574	0		pknbeta
210933_s_at	3.17596755096177	0		MGC4655
218094_s_at	3.1307319856851	0		C20orf35
201029_s_at	3.10235325372561	0		MIC2
210036_s_at	-3.09612221936927	0		KCNH2
212667_at	3.07883651171274	0		SPARC
40189_at	2.32056421839438	0		SET

AML inv(16) vs. ALL t(8;14)	samples: 12 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214558_at	5.11198812058407	0*	75.15	GPR12
227525_at	-4.9287188464128	0		LOC113263
211852_s_at	4.75980688856888	0		ATRN
238652_at	4.21116590562832	0		
206090_s_at	4.11779253006199	0		DISC1
237864_at	3.94349147195948	0		
225051_at	-3.89930170229982	0		
209365_s_at	3.8293529362527	0		ECM1
223382_s_at	3.56679694464951	0		NIN283
201278_at	3.38592358815787	0		DAB2
219654_at	3.25519407914616	0		PTPLA
202074_s_at	-3.24311911278957	0		OPTN
231982_at	3.1934694742924	0		
231310_at	3.18344789439715	0		
210933_s_at	3.17596755096177	0		MGC4655
222062_at	3.12204176758762	0		WSX1
242774_at	-3.10884740483827	0		SYNE-2
244257_at	3.09069018899455	0		
212667_at	3.07883651171274	0		SPARC
225305_at	2.99842864962803	0		

AML inv(16) vs. ALL B not Ph	samples: 12 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205382_s_at	3.44559828536398	0*	2092.2	DF
206772_at	3.36924689882826	0		PTHR2
228058_at	3.25212044058077	0		
218094_s_at	3.1307319856851	0		C20orf35
223385_at	3.07706676910952	0		CYP2S1
204858_s_at	2.96720397750981	0		ECGF1
227556_at	2.66258700650327	0		ATP1B1
212463_at	-2.65372355495687	0		
201360_at	2.63414688358486	0		CST3
205997_at	2.6308573171159	0		ADAM28
231310_at	2.60181313279404	0		
203973_s_at	2.4714469340582	0		CEBPD
200872_at	2.42523459110761	0		S100A10
200661_at	2.42407433324859	0		PPGB
227415_at	-2.35663515228965	0		
219358_s_at	2.31004642323513	0		CENTA2
202016_at	2.30727907426241	0		MEST
208248_x_at	2.27797183411701	0		APLP2
212188_at	2.26974263089413	0		LOC115207
205076_s_at	2.257959447417	0		CRA

AML inv(16) vs. ALL Ph	samples: 12 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
231310_at	3.26954611223081	0*	119.2	
203373_at	-3.07194642697668	0		STATI2
210487_at	-2.57922739606335	0		DNTT
209735_at	-2.57442202182339	0		ABCG2
223314_at	-2.46037319479876	0		MGC11352
227276_at	2.31171718422321	0		TEM7R
205382_s_at	2.30057319708762	0		DF
200872_at	2.27656979916265	0		S100A10
200985_s_at	-2.25258857041194	0		CD59
207224_s_at	2.24976284058658	0		SIGLEC7
208702_x_at	2.21820176325777	0		APLP2
209975_at	2.21237181448127	0		CYP2E
219452_at	2.18614057488219	0		LOC64174
224918_x_at	2.18042008960618	0		MGST1
200661_at	2.15820911658542	0		PPGB
205076_s_at	2.1576215121228	0		CRA
203092_at	-2.1346943506478	0		TIMM44
217979_at	-2.13131555913964	0		NET-6
228058_at	2.11586185512013	0		
210609_s_at	2.1104858897821	0		PIG3

AML inv(16) vs. T-ALL	samples: 12 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203949_at	5.55902965521097	0*	4116.65	MPO
205640_at	4.30508511818292	0		ALDH3B1
203948_s_at	4.299250186967	0		MPO
204484_at	-3.92079658637056	0		PIK3C2B
223482_at	3.8867405806948	0		TMPIT
205382_s_at	3.78294993092265	0		DF
242292_at	-3.53231266693437	0		
224918_x_at	3.39770561886615	0		MGST1
228058_at	3.25212044058077	0		
210314_x_at	3.15624540914219	0		TNFSF13
216015_s_at	2.9548034027314	0		
206380_s_at	2.92913137540268	0		PFC
202944_at	2.90807873450708	0		NAGA
231736_x_at	2.90529949191742	0		MGST1
209500_x_at	2.88541455460133	0		TNFSF13
205312_at	2.86437379660673	0		SPI1
211495_x_at	2.85808523976773	0		TNFSF13
211101_x_at	2.82479786118477	0		LILRA2
219763_at	2.71839322196283	0		KIAA1608
225510_at	2.68685955542078	0		CHN1

AML inv(16) vs. AML +8	samples: 12 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233138_at	3.4735123827114	0*	54.25	
209365_s_at	3.00986865470169	0		ECM1
202283_at	2.6160707896185	0		SERPINF1
218942_at	-2.45751904192227	0		FLJ22055
201828_x_at	-2.21365274281998	0		CXX1
200951_s_at	2.02357943949022	0		CCND2
226120_at	-2.01082485261142	0		LOC123016
203188_at	-1.9379696222037	0		B3GNT6
202085_at	-1.9147903697218	0		TJP2
206135_at	1.90877055638373	0		KIAA0535
210024_s_at	-1.90335978018863	0		UBE2E3
204661_at	1.83776082826379	0		CDW52
241525_at	1.83006374766269	0		
208710_s_at	-1.80896001968559	0		AP3D1
34210_at	1.75572696362264	0		CDW52
201497_x_at	1.74852845185764	0		MYH11
212236_x_at	1.74679406476776	0		
213810_s_at	1.69077455623534	0		FLJ10342
212250_at	-1.62885302351785	0		
AFFX-r2-Hs18SrRNA-5_at				
HG-U133A	1.32018767826727	0		

AML inv(16) vs. AML complex	samples: 12 / 36			
accuracy	1			
confidence	0.957308305034528			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203092_at	-1.77664454556306	0		TIMM44
209190_s_at	1.75723541848141	0*	1593.8	DIAPH1
201497_x_at	1.74852845185764	0*	134.75	MYH11
205076_s_at	1.73951655525411	0		CRA
241525_at	1.71682483225979	0		
213779_at	-1.71354352282537	0		
210982_s_at	1.70318998731519	0		HLA-DRA
200985_s_at	-1.64643993864436	0		CD59
212463_at	-1.6457941052799	0		
200675_at	-1.61546783522649	0*	707.85	CD81
218942_at	-1.59347299102441	0		FLJ22055
200984_s_at	-1.56833724351535	0		CD59
208894_at	1.54975491884609	0		HLA-DRA
202265_at	-1.53139324627965	0		BMI1
224724_at	1.5143785002027	0		KIAA1247
210715_s_at	-1.49004107536748	0		SPINT2
213452_at	-1.48522101377482	0		ZNF184
205382_s_at	1.45942422076027	0		DF
201360_at	1.45905524413008	0		CST3
206135_at	1.45729112913321	0		KIAA0535

AML inv(16) vs. AML normal	samples: 12 / 62			
accuracy	1			
confidence	0.952958978230212			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
200951_s_at	1.82916486676122	0		CCND2
209365_s_at	1.79092214915991	0*	390.9	ECM1
214651_s_at	-1.77796050968374	0*	187.6	HOXA9
201497_x_at	1.74852845185764	0		MYH11
231310_at	1.62450567760929	0*	167.8	
223385_at	1.57142154491015	0		CYP2S1
206135_at	1.54931600211688	0		KIAA0535
235753_at	-1.54691446076282	0		
231259_s_at	1.52681305174601	0		CCND2
204661_at	1.46205490369508	0		CDW52
202370_s_at	-1.45859936190513	0		CBFB
213353_at	-1.44758735114725	0		ABCA5
209905_at	-1.42239381454703	0		HOXA9
200675_at	-1.38662888859944	0		CD81
207194_s_at	1.38591797740996	0		ICAM4
201324_at	1.36182933080382	0		EMP1
235818_at	1.35992709972839	0		
225510_at	1.35514122232308	0		CHN1
228834_at	1.35066870620531	0		TOB1
34210_at	1.33546826742244	0		CDW52

AML inv(16) vs. AML t(8;21)	samples: 12 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233138_at	3.4735123827114	0*	54.25	
202283_at	2.6160707896185	0		SERPINF1
201596_x_at	2.55517188589615	0		KRT18
233555_s_at	2.48943541958708	0		
226818_at	2.3621676751726	0		
212828_at	2.33130605042964	0		SYNJ2
227276_at	2.31171718422321	0		TEM7R
224724_at	2.30850265580909	0		KIAA1247
224764_at	2.25934489179779	0		ARHGAP10
224049_at	2.25244855640038	0		KCNK17
205453_at	2.23059959679219	0		HOXB2
226841_at	2.21329419316194	0		
209975_at	2.21237181448127	0		CYP2E
205076_s_at	2.21083117233863	0		CRA
202340_x_at	2.18671963481275	0		NR4A1
210314_x_at	2.17138407196792	0		TNFSF13
34689_at	2.16463995293403	0		TREX1
235359_at	2.12423469465025	0		
212188_at	2.11590883979512	0		LOC115207
205718_at	2.10547132123535	0		ITGB7

AML MLL vs. all other	samples: 15 / 254			
accuracy	0.977695167286245			
confidence	0.736329320600874			
failed:	3,6,7,11,155,212			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228083_at	1.21941234348391	0		
201105_at	1.20839678060713	0*	8795.05	LGALS1
205849_s_at	1.03753805567643	0		UQCRB
205472_s_at	1.03076838857205	0		DACH
208702_x_at	1.01256627546813	0		APLP2
225700_at	-1.01092153300039	0		
222982_x_at	-1.00741126543277	0*	1101	SLC38A2
238856_s_at	-0.990415633837559	0*	1	
214875_x_at	0.989164186017564	0		APLP2
209616_s_at	0.966839890517189	0		CES1
205471_s_at	0.957394713027089	0		DACH
211404_s_at	0.942572231076861	0		APLP2
213857_s_at	-0.933745825960995	0		CD47
204951_at	-0.925961455918277	0		ARHH
203544_s_at	-0.922231323262765	0		STAM
204082_at	0.910815804799754	0		PBX3
219360_s_at	0.902459945140701	0		TRPM4
235604_x_at	-0.895150647295372	0		
200742_s_at	0.89214325035062	0		CLN2
217520_x_at	0.891291087387708	0		

AML MLL vs. CLL	samples: 15 / 32			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
224838_at	-3.80748815117863	0*	1810.6	
212400_at	-2.86025920523167	0		
212827_at	-2.83572202473321	0		IGHM
223514_at	-2.79698500849851	0		CARD11
207168_s_at	2.78000663400662	0		H2AFY
208456_s_at	-2.77288752188536	0		RRAS2
206111_at	2.74648404080317	0		RNASE2
204951_at	-2.73367910105826	0		ARHH
204215_at	-2.70725768797715	0		MGC4175
41220_at	-2.64744893915855	0		MSF
227173_s_at	-2.60156567650878	0		BACH2
211404_s_at	2.58701495228114	0		APLP2
201163_s_at	2.58627447208644	0		IGFBP7
227829_at	-2.5720529437702	0		
202880_s_at	-2.55714780536776	0		PSCD1
224837_at	-2.52465899436623	0		FOXP1
209374_s_at	-2.50451803785685	0		IGHM
243780_at	-2.49073709912546	0		
212590_at	-2.45765382458849	0		
AFFX-HUMGAPDH/M33197_3_at HG-U133B	2.15372303795555	0		GAPD

AML MLL vs. CML	samples: 15 / 14			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
209771_x_at	-4.47855739740896	0*	4909	CD24
216379_x_at	-4.47782401977517	0		
212531_at	-4.20914790815671	0		LCN2
206676_at	-4.08016979869995	0		CEACAM8
205557_at	-3.89666780981116	0		BPI
209772_s_at	-3.7540800038095	0		CD24
211657_at	-3.35563391812807	0		
203757_s_at	-3.27728001846237	0		CEACAM6
202018_s_at	-3.2413562747036	0		LTF
205513_at	-3.11724133997788	0		TCN1
207269_at	-3.04676950166614	0		DEFA4
207802_at	-2.84753376114576	0		SGP28
236908_at	-2.83593202717857	0		
266_s_at	-2.75915771343774	0		CD24
201105_at	2.73676787442809	0		LGALS1
208890_s_at	2.63909820141829	0		PLXNB2
210244_at	-2.58291056673136	0		CAMP
214875_x_at	2.54486223713713	0		APLP2
236979_at	-2.51234802423843	0		
49306_at	1.35686961755716	0		AD037

AML MLL vs. normal BM	samples: 15 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225792_at	-5.04037264761662	0*	76.45	
227812_at	-4.50172833847856	0		
236908_at	-4.3851399912751	0		
225700_at	-4.20778530270981	0		
202018_s_at	-4.1218976881036	0		LTF
225804_at	3.78433665952281	0		
212531_at	-3.62189836886899	0		LCN2
208651_x_at	-3.08131561292721	0		CD24
209771_x_at	-2.80531442593767	0		CD24
216379_x_at	-2.74718662648409	0		
210244_at	-2.74600903663689	0		CAMP
226301_at	-2.70321745971481	0		dJ55C23.6
227151_at	2.68181697471281	0		
209160_at	-2.64474285212333	0		AKR1C3
225285_at	-2.56569832423798	0		
235818_at	-2.5546546541523	0		
226726_at	-2.52741579223109	0		LOC129642
207269_at	-2.43598973973471	0		DEFA4
226751_at	-2.41273912703748	0		DKFZP566K1924
58780_s_at	1.24593648437062	0		FLJ10357

AML MLL vs. ALL t(8;14)	samples: 15 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
227173_s_at	-2.97620214103741	0*	93.35	BACH2
225700_at	-2.97113581211542	0		
212400_at	-2.91449782508721	0		
227151_at	2.68181697471281	0		
205690_s_at	-2.63484847538673	0		G10
231552_at	2.60340424456959	0		
239647_at	2.56381751217569	0		
239835_at	-2.49692099181388	0		KIAA1842
226435_at	2.38716130768923	0		
226301_at	-2.38404537685874	0		dJ55C23.6
226607_at	2.34518225140996	0		L3MBTL
215785_s_at	-2.31901965008779	0		CYFIP2
225085_at	2.24977026547419	0		
214651_s_at	2.24855870756181	0		HOXA9
209765_at	-2.20363939375933	0		ADAM19
236606_at	-2.19711183569464	0		
218319_at	-2.1925818315627	0		PELI1
227525_at	-2.16383106825606	0		LOC113263
212538_at	-2.11358391570231	0		KIAA1058
228083_at	2.10218682980016	0		

AML MLL vs. ALL B not Ph	samples: 15 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201482_at	2.87636338319455	0*	363.95	QSCN6
201105_at	2.64910601922115	0		LGALS1
239647_at	2.56381751217569	0		
211404_s_at	2.31189269578112	0		APLP2
201360_at	2.27456235196276	0		CST3
214875_x_at	2.20140608739693	0		APLP2
266_s_at	-2.19196810995278	0		CD24
208702_x_at	2.17966631844281	0		APLP2
223469_at	2.13015217253256	0		MGC10812
209771_x_at	-2.12750959401045	0		CD24
208248_x_at	2.10716186347527	0		APLP2
230441_at	-2.03717805375485	0		
200742_s_at	2.01183913393136	0		CLN2
216379_x_at	-1.97574478072792	0		
204215_at	-1.96532146024999	0		MGC4175
208650_s_at	-1.93906624919753	0		CD24
214651_s_at	1.92853927147488	0		HOXA9
233813_at	-1.8799760260639	0		
208703_s_at	1.86864966354898	0		APLP2
58780_s_at	1.40471564488899	0		FLJ10357

AML MLL vs. ALL Ph	samples: 15 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210487_at	-2.66400596339357	0		DNTT
211404_s_at	2.5799328562955	0		APLP2
214875_x_at	2.53091704146699	0		APLP2
208702_x_at	2.442063176235	0		APLP2
214651_s_at	2.38931027314895	0		HOXA9
234107_s_at	2.17019003130007	0*	321.6	
201105_at	2.08770407459668	0		LGALS1
239647_at	2.02467198705529	0		
217979_at	-1.99927745769533	0		NET-6
213150_at	1.98436589229381	0		HOXA10
212012_at	-1.96026252932157	0		D2S448
207971_s_at	-1.95442302553682	0		KIAA0582
200742_s_at	1.93172870108821	0		CLN2
236606_at	-1.90758120714248	0		
235753_at	1.89768662161529	0		
232035_at	-1.87493486925109	0		H4FH
41220_at	-1.84432301556426	0		MSF
209771_x_at	-1.83370834497243	0		CD24
1007_s_at	-1.8257200735147	0		DDR1
201968_s_at	1.81818231032019	0		PGM1

AML MLL vs. T-ALL	samples: 15 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
242292_at	-3.53231266693437	0*	19.4	
243154_at	-3.1306973304726	0		
219891_at	3.05552709838153	0		FLJ20208
211404_s_at	2.9355923181049	0		APLP2
209499_x_at	2.75677919960856	0		TNFSF13
211495_x_at	2.73018317509301	0		TNFSF13
208702_x_at	2.59886997802643	0		APLP2
214875_x_at	2.52933264502392	0		APLP2
206111_at	2.43695278026584	0		RNASE2
209500_x_at	2.41035664982945	0		TNFSF13
210314_x_at	2.38921906328214	0		TNFSF13
225003_at	2.37212829914098	0		MBC3205
218122_s_at	-2.30056189156697	0		SENP2
204484_at	-2.28386643829897	0		PIK3C2B
205640_at	2.26383232065516	0		ALDH3B1
201105_at	2.26087708407154	0		LGALS1
200743_s_at	2.25956196871586	0		CLN2
222698_s_at	2.23788003936299	0		IMPACT
200742_s_at	2.2220970534291	0		CLN2
201537_s_at	2.16766347414866	0		DUSP3

AML MLL vs. AML +8	samples: 15 / 10			
accuracy	1			
confidence	0.8689072208975			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
200056_s_at - HG-U133A	-1.60303643777462	0		C1D
212250_at	-1.47262825515036	0		
228024_at	-1.43968630786794	0		PAK1
205355_at	-1.39534301157978	0		ACADSB
225700_at	-1.39419450937928	0.01		
234726_s_at	1.36257922965513	0		
202619_s_at	-1.34323877280623	0		PLOD2
205453_at	-1.29520111839967	0		HOXB2
202823_at	-1.28255326311509	0		TCEB1
210749_x_at	-1.26893758929818	0		DDR1
227786_at	-1.24020773870069	0		TRAP25
212479_s_at	-1.23922427261637	0*	437.3	FLJ13910
219312_s_at	-1.21983738431424	0		RINZF
218172_s_at	-1.21403337241271	0*	285.95	PRO2577
200867_at	-1.2110165320696	0*	531	
202956_at	-1.21043821718202	0*	550.6	BIG1
213902_at	-1.19710457307816	0		ASAH
239597_at	1.19444081572455	0		
214789_x_at	-1.19367799101574	0		SRP46
AFFX-r2-Ec-bioD-3_at - HG-U133B	0.789398697044362	0		

AML MLL vs. AML complex	samples: 15 / 36			
accuracy	1			
confidence	0.928537448772464			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228083_at	1.83691594955677	0		
201105_at	1.56013660814198	0		LGALS1
201377_at	-1.5390279619994	0		KIAA0144
201358_s_at	-1.46121373620596	0		COPB
203387_s_at	-1.43200690176451	0		KIAA0603
201585_s_at	-1.42612880048733	0		SFPQ
222982_x_at	-1.4232823410753	0		SLC38A2
202746_at	-1.40541613814493	0*	277.15	
204951_at	-1.38290450200254	0*	224.05	ARHH
203725_at	-1.35090921185734	0		GADD45A
203544_s_at	-1.33195316834084	0		STAM
225804_at	1.3109814684568	0		
203386_at	-1.30903268579411	0		KIAA0603
201359_at	-1.3066438308133	0		COPB
201830_s_at	-1.29170882160348	0		NET1
218041_x_at	-1.27263528593652	0		PRO1068
223318_s_at	1.27042416454958	0		MGC10974
212222_at	-1.26786775770503	0		KIAA0077
201829_at	-1.26235979300155	0		NET1
239647_at	1.09622576767215	0		

AML MLL vs. AML normal	samples: 15 / 62			
accuracy	0.948051948051948			
confidence	0.903617550418171			
failed:	3,4,72,76			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205453_at	-1.38558116676561	0*	203.25	HOXB2
222465_at	-1.29236441992376	0		C15orf15
225406_at	-1.29036630213613	0*	191.3	TSG
200829_x_at	-1.1349148684836	0		ZNF207
225326_at	-1.12776286034489	0		KIAA1311
200056_s_at - HG-U133B	-1.12696320763032	0		C1D
238856_s_at	-1.09612740485765	0		
227786_at	-1.08912698999125	0		TRAP25
200673_at	-1.08754065564232	0		LAPTM4A
226250_at	-1.08598948671591	0		
233559_s_at	1.08564709559314	0		FENS-1
228904_at	-1.07283266172579	0		
227680_at	-1.06344466244967	0		
223982_s_at	-1.06119523760418	0		IPLA2
202377_at	-1.05377199670316	0		HSOBRGRP
225700_at	-1.04818024157045	0		
209160_at	-1.04660040264575	0		AKR1C3
229232_at	-1.04476453216419	0		
231870_s_at	-1.04348230442961	0		LOC51068
201105_at	1.03632090944134	0		LGALS1

AML MLL vs. AML t(8;21)	samples: 15 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214651_s_at	2.42114497347366	0		HOXA9
201105_at	2.17374439391796	0*	3881.25	LGALS1
228827_at	-2.03460798747208	0		
206009_at	-2.02655766969028	0		ITGA9
228083_at	1.99768244710951	0		
213150_at	1.98436589229381	0		HOXA10
50221_at	1.94810783752319	0		
221581_s_at	1.89677192380517	0		WBSCR5
235753_at	1.88396584115232	0		
206622_at	-1.79659162526109	0		TRH
209905_at	1.76718971964498	0		HOXA9
204069_at	1.75588643276789	0		MEIS1
209160_at	-1.75500319419551	0		AKR1C3
235818_at	-1.70111545046162	0		
223498_at	1.67798456165549	0		
211404_s_at	1.67488607654784	0		APLP2
209500_x_at	1.66210516483391	0		TNFSF13
203949_at	-1.65967693892027	0		MPO
214875_x_at	1.65852470588382	0		APLP2
56256_at	1.09757984221605	0		LOC51092

CLL vs. all other	samples: 32 / 237			
accuracy	0.996282527881041			
confidence	1			
failed:	11			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
224838_at	2.72658457901213	0		
239287_at	2.21787255431445	0*	630.55	
223514_at	2.1294564890461	0		CARD11
44790_s_at	2.04322734300157	0		FLJ21562
212590_at	2.0395652222237	0		
223287_s_at	2.01927297186102	0		FOXP1
228390_at	2.01736536531344	0		
219471_at	2.0123024445387	0		FLJ21562
208456_s_at	2.00649246957273	0		RRAS2
243780_at	1.99741020732395	0		
201998_at	1.97818562004593	0		SIAT1
223391_at	1.97429784627482	0		LOC81537
208091_s_at	1.95442592300049	0		DKFZP564K0822
225927_at	1.94521013683932	0		MAP3K1
202589_at	-1.94332001129586	0		TYMS
229072_at	1.94278755168998	0		
229844_at	1.93701311168151	0		
214615_at	1.91900370555866	0		P2Y10
230768_at	1.89700621262016	0		
224837_at	1.88521474574714	0		FOXP1

CLL vs. CML	samples: 32 / 14			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210254_at	-4.88339464327865	0*	3718.45	
205557_at	-4.67296996074416	0		BPI
206111_at	-4.55904506479679	0		RNASE2
209619_at	4.54717160557061	0		CD74
202503_s_at	-4.46030015155587	0		KIAA0101
206871_at	-4.43465869214911	0		ELA2
203949_at	-4.36878588501229	0		MPO
202589_at	-4.25959896335016	0		TYMS
212268_at	-4.11824280019806	0		SERPINB1
212531_at	-4.10884128760506	0		LCN2
206676_at	-3.98482491918087	0		CEACAM8
204670_x_at	3.97453356450998	0		HLA-DRB5
210334_x_at	-3.95114669210453	0		BIRC5
200654_at	-3.73551197850169	0		P4HB
208306_x_at	3.6021607716515	0		HLA-DRB4
224838_at	3.57587529198941	0		
213572_s_at	-3.56773642902922	0		SERPINB1
207269_at	-3.5389139132598	0		DEFA4
212750_at	3.51249429987917	0		PPP1R16B
41577_at	3.13666804152596	0		PPP1R16B

CLL vs. normal BM	samples: 32 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204776_at	-4.80025506569938	0*	163.3	THBS4
210613_s_at	-4.76199342875923	0		SYNGR1
218662_s_at	-4.49242317171143	0		HCAP-G
202503_s_at	-4.2272639947421	0		KIAA0101
202580_x_at	-4.18939678293477	0		FOXM1
205051_s_at	-4.15661524563327	0		KIT
202018_s_at	-4.09501572722927	0		LTF
230988_at	-4.0486666186669	0		
206871_at	-4.04477996703664	0		ELA2
224975_at	-3.78270966714705	0		NFIA
227230_s_at	-3.69195069014622	0		KIAA1211
209714_s_at	-3.55884052493629	0		CDKN3
212531_at	-3.54256621978711	0		LCN2
214575_s_at	-3.53838586077798	0		AZU1
202589_at	-3.38277320357567	0		TYMS
223785_at	-3.37348567040386	0		FLJ10719
202705_at	-3.36111245088024	0		CCNB2
224976_at	-3.35971882977735	0		NFIA
210052_s_at	-3.33990497740824	0		C20orf1

CLL vs. ALL t(8;14)	samples: 32 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
202580_x_at	-7.18159480292423	0*	218.2	FOXM1
209891_at	-6.98895220029526	0		AD024
227039_at	3.70691051731571	0		AKAP13
218663_at	-3.68808195572391	0		HCAP-G
36004_at	3.51464925040429	0		IKBKG
226936_at	-3.44796352148406	0		
228211_at	3.34271829518438	0		
218355_at	-3.32490989672808	0		KIF4A
201761_at	-3.28097759120759	0		MTHFD2
205837_s_at	-3.18161701452463	0		GYPA
210052_s_at	-3.16637659493241	0		C20orf1
202095_s_at	-3.11748537316183	0		BIRC5
202503_s_at	-3.09625623775405	0		KIAA0101
212020_s_at	-3.09152886109552	0		MKI67
216833_x_at	-3.08262837314566	0		
228361_at	-3.05435230901633	0		
212022_s_at	-3.01225907956052	0		MKI67
227065_at	3.00267996592052	0		COL5A2
218039_at	-2.9948995053224	0		ANKT
36920_at	2.10655917810938	0		MTM1

CLL vs. ALL B not Ph	samples: 32 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225927_at	3.15130564055876	0*	1541.45	MAP3K1
213927_at	2.64985304902657	0		
201462_at	2.62143810029708	0		KIAA0193
224838_at	2.5941283416844	0		
213453_x_at	-2.18846578413759	0		GAPD
239287_at	2.18590081196116	0		
208091_s_at	2.12019333022318	0		DKFZP564K0822
201998_at	2.1165316341122	0		SIAT1
224848_at	-2.11049474415864	0		
202863_at	2.08665988043685	0		SP100
225592_at	-2.07634399767076	0		NRM
205805_s_at	2.04616469387812	0		ROR1
228390_at	2.03697588799482	0		
AFFX-HUMGAPDH/M33197_3_at - HG-U133B	-2.02578116307399	0		GAPD
220768_s_at	2.01657972292803	0		CSNK1G3
221858_at	2.00702836396881	0		KIAA0608
214786_at	2.00594347120247	0		MAP3K1
224570_s_at	-2.00161337456916	0		
202625_at	1.99700437780915	0		LYN
AFFX-r2-Hs18SrRNA-3_s_at - HG-U133B	0.670536484443349	0		

CLL vs. ALL Ph	samples: 32 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204663_at	-3.923285216392	0*	80.55	ME3
203373_at	-3.78247945374324	0		STATI2
225927_at	3.05858766321181	0		MAP3K1
223514_at	2.79698500849851	0		CARD11
210487_at	-2.66400596339357	0		DNTT
213927_at	2.64985304902657	0		
237337_at	2.52705433891484	0		
236280_at	2.49746424904494	0		
227900_at	2.49040043479395	0		
211709_s_at	-2.45092080989795	0		SCGF
224833_at	2.40705165058966	0		ETS1
226545_at	-2.40457551567713	0		
208091_s_at	2.38274758846201	0		DKFZP564K0822
235674_at	2.37963455734461	0		
234107_s_at	2.36302665773918	0		
223462_at	2.32337125093609	0		MGC4618
201462_at	2.3212369641096	0		KIAA0193
223391_at	2.30224083750022	0		LOC81537
212719_at	-2.29194173393375	0		SCOP

CLL vs. T-ALL	samples: 32 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201417_at	-3.83747798152129	0*	2230.95	
201416_at	-3.69716215884899	0		SOX4
221858_at	2.73818494452306	0		KIAA0608
213772_s_at	2.72201152228286	0		GGA2
224932_at	2.6366912338985	0		PRSS2
224847_at	-2.63602874545103	0		
201462_at	2.62143810029708	0		KIAA0193
224848_at	-2.60776696130397	0		
243780_at	2.49991585531364	0		
227900_at	2.49040043479395	0		
202625_at	2.4377901797746	0		LYN
228390_at	2.41659743191322	0		
201998_at	2.39630335572289	0		SIAT1
226545_at	-2.3815195487075	0		
204446_s_at	2.37716091038765	0		ALOX5
204192_at	2.34749349754959	0		CD37
219076_s_at	-2.31227318629435	0		PXMP2
206398_s_at	2.30227312148638	0		CD19
224838_at	2.29208011575118	0		
212827_at	2.28758794629918	0		IGHM

CLL vs. AML +8	samples: 32 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
224838_at	3.16933404672116	0		
223514_at	2.79698500849851	0		CARD11
212827_at	2.5676577800083	0		IGHM
201200_at	-2.5208800664045	0		CREG
242633_x_at	2.38085767453167	0		
208456_s_at	2.34106774724323	0		RRAS2
212590_at	2.3295599530646	0		
44790_s_at	2.32854069014676	0		FLJ21562
219471_at	2.27189811261511	0		FLJ21562
202441_at	-2.26915475899159	0		KEO4
209374_s_at	2.26352755463127	0		IGHM
243780_at	2.25989352775893	0		
204215_at	2.24311505389492	0*	906.65	MGC4175
223382_s_at	-2.21844659554677	0		NIN283
201163_s_at	-2.2061831531108	0		IGFBP7
224837_at	2.17714293481922	0		FOXP1
223391_at	2.1733535915887	0		LOC81537
208091_s_at	2.17150813050761	0		DKFZP564K0822
205933_at	2.16573909337041	0		SETBP1
239287_at	2.1598880074389	0		

CLL vs. AML complex	samples: 32 / 36			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
224838_at	2.78969388721613	0		
235674_at	2.37963455734461	0		
243780_at	2.32051881321218	0		
239287_at	2.24074490580899	0		
223514_at	2.18755403591948	0		CARD11
222680_s_at	-2.18354473266858	0*	203.95	RAMP
209619_at	2.13206191976271	0		CD74
202503_s_at	-2.11188972263141	0		KIAA0101
208456_s_at	2.10620770802115	0		RRAS2
208864_s_at	-2.10162761752294	0		TXN
212590_at	2.09310293747601	0		
201200_at	-2.05492899324696	0		CREG
212827_at	2.05442625446282	0		IGHM
224837_at	2.04951179193956	0		FOXP1
205805_s_at	2.04616469387812	0		ROR1
244261_at	2.03144018714413	0		
223287_s_at	2.0252763158281	0		FOXP1
208091_s_at	2.0139098675012	0		DKFZP564K0822
226989_at	2.00631003964875	0		
236854_at	1.99292097643003	0		

CLL vs. AML normal	samples: 32 / 62			
accuracy	0.98936170212766			
confidence	1			
failed:	11			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
224838_at	2.80936017892095	0*	2987.7	
243780_at	2.42900650257202	0		
223514_at	2.40431982389629	0		CARD11
201200_at	-2.28363968538296	0		CREG
201998_at	2.19987941765164	0		SIAT1
44790_s_at	2.18842053042545	0		FLJ21562
205049_s_at	2.18662155440889	0		CD79A
239287_at	2.17948863877979	0		
223287_s_at	2.16628667951355	0		FOXP1
223391_at	2.16298199717166	0		LOC81537
219471_at	2.13618332752253	0		FLJ21562
225175_s_at	2.12811708839772	0		CTL2
204215_at	2.11642877909845	0		MGC4175
236280_at	2.11271003733104	0		
208456_s_at	2.10890038745727	0		RRAS2
206398_s_at	2.09984081904119	0		CD19
212827_at	2.09850222830603	0		IGHM
228390_at	2.09600254213173	0		
229072_at	2.09351406943008	0		
214615_at	2.06329249104139	0		P2Y10

CLL vs. AML t(8;21)	samples: 32 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203949_at	-3.50330789770673	0		MPO
224838_at	3.25663434332492	0		
205192_at	3.21758439151756	0*	113.25	MAP3K14
211709_s_at	-2.95109939287116	0		SCGF
212827_at	2.84469338495376	0		IGHM
230768_at	2.8154401362934	0		
206009_at	-2.7972720292112	0		ITGA9
208091_s_at	2.63085873400942	0		DKFZP564K0822
208456_s_at	2.62810675193075	0		RRAS2
215215_s_at	-2.60039836996497	0		
203948_s_at	-2.56960807932381	0		MPO
201811_x_at	2.56895859687937	0		SH3BP5
243780_at	2.51082778037667	0		
212590_at	2.50058834205242	0		
227900_at	2.49040043479395	0		
226546_at	-2.44432895386159	0		
225927_at	2.44085004959256	0		MAP3K1
212589_at	2.43561411833392	0		RRAS2
228390_at	2.41659743191322	0		
225246_at	2.39661265710521	0		STIM2

CML vs. all other	samples: 14 / 255			
accuracy	0.981412639405205			
confidence	0.984251851969928			
failed:	4,6,10,14,115			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212531_at	2.20686225450673	0		LCN2
205557_at	2.19817622063178	0*	11581.65	BPI
206676_at	2.01751329912518	0		CEACAM8
209772_s_at	1.89825970350824	0*	3429.4	CD24
207802_at	1.84335905687648	0		SGP28
216379_x_at	1.76253321043545	0		
209771_x_at	1.75699226119665	0		CD24
203936_s_at	1.75554347155831	0		MMP9
211657_at	1.69149085236384	0		
203757_s_at	1.6780512743379	0		CEACAM6
210254_at	1.6590320804534	0		
202018_s_at	1.64680728641866	0		LTF
211275_s_at	1.62477051547664	0		GYG
205513_at	1.60415014432038	0		TCN1
205863_at	1.60339454990244	0		S100A12
223839_s_at	1.57424844312026	0		
210244_at	1.56058501019954	0		CAMP
206440_at	1.5590538838617	0		VELI1
207269_at	1.55083422089021	0		DEFA4
204174_at	1.53747851176966	0		ALOX5AP

CML vs. normal BM	samples: 14 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
227198_at	-3.96995770729437	0*	39.95	
204562_at	-3.83910818190111	0		IRF4
227749_at	-3.11980636745679	0		
228377_at	-2.65145492785893	0		KIAA1384
226713_at	-2.28229285614419	0		
209619_at	-2.27384420268273	0		CD74
227375_at	-2.22184735546056	0		DKFZP566D1346
204057_at	-2.13119125485664	0		ICSBP1
201506_at	-2.05058862618543	0		TGFBI
221558_s_at	-2.0055054625083	0		LEF1
227867_at	-2.00414646646454	0		
225331_at	-1.95134035825926	0		
223280_x_at	-1.95125537387335	0		MS4A6A
243780_at	-1.94601159348593	0		
228055_at	-1.94418493221925	0		
204670_x_at	-1.94197079510435	0		HLA-DRB5
208683_at	-1.93662356244796	0		CAPN2
210356_x_at	-1.92014292171279	0		MS4A2
209670_at	-1.89146017871026	0		TRA
AFFX-HUMGAPDH/M33197_3_at - HG-U133B	1.0887744230798	0		GAPD

CML vs. ALL t(8;14)	samples: 14 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
231215_at	-3.69904177219169	0*	17.25	
212400_at	-3.60679086659289	0		
239835_at	-3.24273732421016	0		KIAA1842
214439_x_at	-3.01379256143662	0		BIN1
227173_s_at	-2.97620214103741	0		BACH2
209619_at	-2.86528990843459	0		CD74
234660_s_at	-2.81161728678359	0		DIS3
202723_s_at	-2.69572816449622	0		FOXO1A
227700_x_at	-2.59859831428636	0		FLJ10709
219202_at	-2.52442131777509	0		FLJ22341
204638_at	-2.51835721417786	0		ACP5
222147_s_at	-2.47042047428454	0		
213772_s_at	-2.41552637854988	0		GGA2
203932_at	-2.39804753895984	0		HLA-DMB
205145_s_at	-2.34102992713809	0		MYL5
221969_at	-2.278395672233	0.01		PAX5
217521_at	2.26710710056045	0		
205541_s_at	-2.22303735713359	0		GSPT2
204661_at	-2.15814023268535	0		CDW52
242729_at	2.02602724250151	0		

CML vs. ALL B not Ph	samples: 14 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
206440_at	3.54851691296324	0*	69.75	VELI1
223839_s_at	2.95162251991881	0		
201482_at	2.5967465282815	0		QSCN6
223246_s_at	-2.53289104519377	0		STRBP
202477_s_at	-2.36949525800043	0		GCP2
227415_at	-2.35663515228965	0		
202819_s_at	-2.31208048847973	0		TCEB3
226876_at	2.29929647597952	0		
200654_at	2.2916645921996	0		P4HB
231472_at	-2.27133126588153	0		
217521_at	2.26710710056045	0		
218764_at	-2.26149206068996	0		MGC5363
219615_s_at	2.21717677908473	0		KCNK5
219111_s_at	-2.20588673666352	0		MGC2835
212268_at	2.20005764504112	0		SERPINB1
211275_s_at	2.1595066613388	0		GYG
211990_at	-2.15004013194548	0		HLA-DPA1
206676_at	2.13116752502457	0		CEACAM8
235818_at	2.13111499669481	0		
210254_at	2.07581294141343	0		

CML vs. ALL Ph	samples: 14 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
209619_at	-3.47132181247921	0*	5777.85	CD74
212778_at	-3.09966497846595	0		KIAA0602
201029_s_at	-3.08460906542498	0		MIC2
214317_x_at	-3.02953000176234	0		RPS9
202332_at	-2.9539112535883	0		CSNK1E
211990_at	-2.80086525597245	0		HLA-DPA1
203373_at	-2.76056827822619	0		STAT12
210487_at	-2.66400596339357	0		DNTT
226844_at	-2.53578669067924	0		
207971_s_at	-2.4877090389281	0		KIAA0582
206440_at	2.45272667930868	0		VELI1
205513_at	2.38968722893052	0		TCN1
211275_s_at	2.33552678870234	0		GYG
204670_x_at	-2.32905695313267	0		HLA-DRB5
205557_at	2.3286749741246	0		BPI
220000_at	2.32132983989275	0		SIGLEC5
212531_at	2.31169568945083	0		LCN2
204174_at	2.3066969794321	0		ALOX5AP
225386_s_at	2.25229241478444	0		LOC92906
206111_at	2.22277368410809	0		RNASE2

CML vs. T-ALL	samples: 14 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210254_at	4.72390509810889	0*	3562.85	
206111_at	4.12411957901486	0		RNASE2
205557_at	4.12268252311326	0		BPI
216379_x_at	4.09576684675689	0		
209771_x_at	4.04268115620178	0		CD24
204484_at	-3.92079658637056	0		PIK3C2B
203949_at	3.82080923209307	0		MPO
206871_at	3.79666500221894	0		ELA2
212268_at	3.66762573362107	0		SERPINB1
239071_at	-3.65785660037409	0		
209772_s_at	3.61720812003475	0		CD24
212531_at	3.55056769994448	0		LCN2
206440_at	3.54851691296324	0		VELI1
242292_at	-3.53231266693437	0		
206676_at	3.51041964854693	0		CEACAM8
218224_at	-3.28568428621792	0		PNMA1
211657_at	3.27814094785335	0		
231215_at	-3.27770330337019	0		
211275_s_at	3.26113496045954	0		GYG
203757_s_at	3.16440848129156	0		CEACAM6

CML vs. AML +8	samples: 14 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212531_at	3.91758233758871	0*	6654.5	LCN2
218151_x_at	-3.61342068798238	0		FLJ11856
203188_at	-2.49453997369644	0		B3GNT6
225014_at	-2.46286744087574	0		
223894_s_at	2.42404553998791	0		FTS
227999_at	-2.41422896946156	0		LOC170394
210244_at	2.30650676975445	0		CAMP
223226_x_at	-2.1556086960975	0		MGC3181
205849_s_at	-2.15471806280279	0		UQCRB
203936_s_at	2.12656987689311	0		MMP9
202080_s_at	-2.08086044698338	0		KIAA1042
212146_at	-2.00720003739628	0		KIAA0842
210749_x_at	-2.00702022115248	0		DDR1
220755_s_at	-1.97451125809376	0		
211743_s_at	1.88718047009153	0		PRG2
214317_x_at	-1.86316203101213	0		RPS9
214475_x_at	1.8601686492104	0		CAPN3
200094_s_at - HG-U133A	-1.83127854302456	0		EEF2
223939_at	1.81572736683912	0		GPR91
229934_at	1.65483415989943	0		

CML vs. AML complex	samples: 14 / 36			
accuracy	0.98			
confidence	1			
failed:	19			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
209772_s_at	2.25515756155772	0		CD24
212531_at	2.16780856655461	0*	10028.8	LCN2
210244_at	2.05958595591104	0		CAMP
205557_at	1.88114022725824	0		BPI
207802_at	1.84224616530014	0		SGP28
203936_s_at	1.83245146841284	0		MMP9
206676_at	1.82688412686061	0		CEACAM8
216379_x_at	1.82175067686641	0		
209771_x_at	1.71430561727442	0		CD24
202265_at	-1.71011447772371	0		BMI1
209186_at	-1.65481819707492	0		ATP2A2
201029_s_at	-1.6407978740451	0		MIC2
206440_at	1.62023824679434	0		VELI1
218144_s_at	-1.60220955278722	0		FLJ22056
212783_at	-1.60173956589805	0		DKFZp761B2423
225065_x_at	1.5634162479603	0		
214317_x_at	-1.51909514839257	0		RPS9
212232_at	-1.51499149327941	0		KIAA1014
223894_s_at	1.50378092313755	0		FTS
207269_at	1.49292374711871	0		DEFA4

CML vs. AML normal	samples: 14 / 62			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212531_at	3.52937454592387	0*	9007.35	LCN2
209772_s_at	2.62224687740926	0		CD24
207802_at	2.60464949585023	0		SGP28
205557_at	2.59981269961356	0		BPI
206676_at	2.51996784029752	0		CEACAM8
205513_at	2.39713364221477	0		TCN1
209771_x_at	2.3694290541236	0		CD24
216379_x_at	2.36313392615064	0		
211657_at	2.35374478763084	0		
203757_s_at	2.29281876629007	0		CEACAM6
202018_s_at	2.19711362051377	0		LTF
210254_at	2.16927497946765	0		
203021_at	2.12970551783084	0		SLPI
205863_at	2.10812748771569	0		S100A12
203936_s_at	2.07272259731953	0		MMP9
210244_at	2.03624546792529	0		CAMP
204351_at	2.0071543551955	0		S100P
211275_s_at	1.97937290056753	0		GYG
224967_at	1.96229148265436	0		
223894_s_at	1.92953251923329	0		FTS

CML vs. AML t(8;21)	samples: 14 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
207802_at	2.83774385104531	0		SGP28
201425_at	2.50825834074572	0		ALDH2
201029_s_at	-2.22223571455337	0*	3078.2	MIC2
205653_at	2.20106889451589	0		CTSG
202391_at	2.10168460148023	0		BASP1
209619_at	-2.0547003400447	0		CD74
228827_at	-2.03460798747208	0		
204670_x_at	-1.98893997185408	0		HLA-DRB5
212531_at	1.96994267101106	0		LCN2
203936_s_at	1.92996861752981	0		MMP9
225386_s_at	1.90963950502737	0		LOC92906
226878_at	-1.90647418854412	0		
201015_s_at	-1.90408812555782	0		JUP
201281_at	-1.88812152152812	0		ADRM1
210982_s_at	-1.87330616648773	0		HLA-DRA
210254_at	1.87025014628174	0		
201137_s_at	-1.84763478416102	0		HLA-DPB1
202545_at	1.81501795739179	0		PRKCD
228485_s_at	1.81223837093458	0		CDW92
231969_at	1.61927333154015	0		DKFZp762K222

normal BM vs. all other	samples: 9 / 260			
accuracy	0.970260223048327			
confidence	1			
failed:	1,3,4,5,7,8,9,234			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
202018_s_at	1.70014923965644	0		LTF
231241_at	1.68875870396623	0		
212531_at	1.61671894194992	0		LCN2
210244_at	1.4725412229519	0		CAMP
244652_at	1.41007652726897	0		
218916_at	-1.40959768522889	0		FLJ23436
208141_s_at	-1.39496085050899	0		MGC4293
218516_s_at	-1.39489208362807	0		FLJ20421
224976_at	1.38035857849962	0		NFIA
201396_s_at	-1.35501592670165	0		SGT
230988_at	1.27806474591682	0		
200631_s_at	-1.27257367942543	0		SET
224975_at	1.25475272090295	0		NFIA
203535_at	1.24698765220296	0		S100A9
227497_at	1.24053728574653	0*	317.95	
225792_at	1.2371690464102	0		
203367_at	-1.23177778244874	0		DUSP14
40189_at	-1.22367056036721	0		SET
225700_at	1.22315772266762	0		
223785_at	1.22097206282821	0		FLJ10719

normal BM vs. ALL t(8;14)	samples: 9 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
222147_s_at	-5.80632286389653	0*	48.2	
209380_s_at	4.30105342509009	0		ABCC5
230988_at	4.0486666186669	0		
227230_s_at	3.69195069014622	0		KIAA1211
201278_at	3.59730622800604	0		DAB2
205051_s_at	3.55673529468534	0		KIT
214558_at	3.49255759470258	0		GPR12
201988_s_at	3.46251302734757	0		CREBL2
223253_at	3.45322097101822	0		UCC1
204285_s_at	-3.35570555370453	0		PMAIP1
237006_at	3.14219078440997	0		
217047_s_at	3.00448756016945	0		
243020_at	2.97861252444615	0		
205690_s_at	-2.97763156027721	0		G10
234764_x_at	2.9597816169315	0		
209160_at	2.88288854646291	0.01		AKR1C3
239835_at	-2.82125904680112	0		KIAA1842
242434_at	-2.60351764410894	0.01		
228708_at	2.60104548908002	0.01		
229575_at	2.59826531472399	0		

normal BM vs. ALL B not Ph	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201506_at	3.72288560994884	0*	464.35	TGFBI
218718_at	3.24294310152425	0		PDGFC
205051_s_at	3.03451031560789	0		KIT
235818_at	2.5546546541523	0		
202382_s_at	2.39296453276424	0		GNPI
221802_s_at	2.32414568373485	0		KIAA1598
238066_at	2.17647785634866	0		RBP7
203645_s_at	2.13814112768782	0		CD163
227038_at	2.09057615422001	0		
225792_at	2.07680085776485	0		
202729_s_at	2.04654552970378	0		LTBP1
230441_at	-2.03717805375485	0		
212989_at	2.00592033097705	0		
201462_at	1.98840399134665	0		KIAA0193
227627_at	1.97570787395888	0		SGKL
204112_s_at	1.90974025156521	0		HNMT
204285_s_at	-1.90604496284052	0		PMAIP1
223044_at	1.88064158446644	0		SLC11A3
223839_s_at	1.86406616667336	0		
204225_at	1.85888952621093	0		HDAC4

normal BM vs. ALL Ph	samples: 9 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225792_at	5.04037264761662	0*	76.45	
224976_at	4.534006778733	0		NFIA
227230_s_at	3.69195069014622	0		KIAA1211
203373_at	-3.60116056485263	0		STATI2
202332_at	-3.19705046805115	0		CSNK1E
212778_at	-3.09966497846595	0		KIAA0602
230988_at	3.03359562676407	0		
218718_at	3.0129378014466	0		PDGFC
205624_at	2.79751505147013	0		CPA3
224975_at	2.78377945957649	0		NFIA
234107_s_at	2.7482082597836	0		
217988_at	-2.7439427550045	0		HEI10
202945_at	-2.67000372671022	0		FPGS
218916_at	-2.6636521234692	0		FLJ23436
223044_at	2.59882500535427	0		SLC11A3
226751_at	2.41273912703748	0		DKFZP566K1924
210487_at	-2.38376037071424	0		DNTT
201029_s_at	-2.37712949687212	0		MIC2
207971_s_at	-2.36738543730614	0		KIAA0582
203645_s_at	2.32470988727879	0		CD163

normal BM vs. T-ALL	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
231241_at	5.25713497545753	0*	52.3	
225792_at	5.04037264761662	0		
224976_at	4.534006778733	0		NFIA
204484_at	-3.92079658637056	0		PIK3C2B
218516_s_at	-3.89821124480393	0.01		FLJ20421
244652_at	3.8571916430704	0		
210613_s_at	3.6441364713354	0		SYNGR1
206488_s_at	3.59792987181253	0		CD36
201416_at	-3.57631738716755	0		SOX4
201417_at	-3.57222567838335	0		
218224_at	-3.56533208466192	0		PNMA1
206871_at	3.49320660549908	0		ELA2
214575_s_at	3.38517251606938	0		AZU1
221188_s_at	3.26852421442154	0		CIDEB
203104_at	3.11161266045758	0		CSF1R
226190_at	3.08925054797494	0		
202018_s_at	3.06471974822162	0		LTF
200631_s_at	-3.05905666007645	0		SET
224970_at	3.05809311507561	0		NFIA
212531_at	3.03461908631694	0		LCN2

normal BM vs. AML +8	samples: 9 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
231241_at	5.25713497545753	0*	52.3	
218916_at	-4.40926777727725	0		FLJ23436
218151_x_at	-3.61342068798238	0		FLJ11856
212531_at	3.35638912536087	0		LCN2
225014_at	-2.46286744087574	0		
210244_at	2.4347108722936	0		CAMP
227999_at	-2.41422896946156	0		LOC170394
220755_s_at	-2.40201593179233	0		
202945_at	-2.37212917164108	0		FPGS
214109_at	2.28939588941522	0		LRBA
225792_at	2.20832306168575	0		
238066_at	2.17647785634866	0		RBP7
217179_x_at	2.173252865121	0		
200631_s_at	-2.1126574466818	0		SET
234764_x_at	2.11173306630787	0		
225547_at	-2.10764119746987	0		
205849_s_at	-2.04438654979845	0		UQCRB
208141_s_at	-2.04344739454244	0		MGC4293
233613_x_at	2.02519262390017	0		

normal BM vs. AML complex	samples: 9 / 36			
accuracy	0.977777777777778			
confidence	1			
failed:	15			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
231241_at	2.20113810647196	0*	94.5	
210244_at	2.15797898100991	0		CAMP
226734_at	2.10647394623844	0		
218516_s_at	-2.0003648205556	0		FLJ20421
244652_at	1.9350839662771	0		
201595_s_at	-1.81799799553143	0		HT010
212531_at	1.80637620431712	0		LCN2
201396_s_at	-1.79606593499252	0		SGT
203092_at	-1.77664454556306	0		TIMM44
230795_at	-1.75873906279717	0		H4F2
228377_at	1.70396224015785	0		KIAA1384
208141_s_at	-1.66429492261381	0		MGC4293
202265_at	-1.62376492554641	0		BMI1
202018_s_at	1.60476985758804	0		LTF
218916_at	-1.58708293547372	0		FLJ23436
224406_s_at	1.57633156642315	0		IRTA2
209806_at	-1.57424329592102	0		H2B/S
208645_s_at	1.5695109709269	0		
200040_at - HG-U133A	-1.548128254162	0		KHDRBS1
AFFX-HSAC07/X00351_M_at - HG-U133A	1.11476993738169	0		ACTB

normal BM vs. AML normal	samples: 9 / 62			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212531_at	3.03296310695958	0*	8390.45	LCN2
202018_s_at	2.55569861815605	0		LTF
210244_at	2.12911144557531	0		CAMP
231241_at	1.90756814920388	0		
234764_x_at	1.88445719282136	0		
238066_at	1.84490304262637	0		RBP7
218516_s_at	-1.76767038599239	0		FLJ20421
214651_s_at	-1.75409579509524	0		HOXA9
207802_at	1.69982859144728	0		SGP28
203535_at	1.6861966835666	0		S100A9
224976_at	1.68580070345942	0		NFIA
235818_at	1.65829753113564	0		
226188_at	1.63500287325021	0		
208651_x_at	1.6330531805719	0		CD24
214523_at	1.61056786968333	0		CEBPE
206871_at	1.60161598002874	0		ELA2
224970_at	1.57809657249869	0		NFIA
210004_at	1.57705611671231	0		OLR1
208141_s_at	-1.55515435811455	0		MGC4293
215379_x_at	1.53008885935316	0		IGLJ3

normal BM vs. AML t(8;21)	samples: 9 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225792_at	5.04037264761662	0*	76.45	
224976_at	4.534006778733	0		NFIA
201425_at	3.96306688659586	0		ALDH2
201506_at	3.72288560994884	0		TGFBI
208146_s_at	3.28524851571637	0		CPVL
224970_at	3.05809311507561	0		NFIA
206488_s_at	2.8751017477522	0		CD36
226818_at	2.67802773991406	0		
224975_at	2.55138740597295	0		NFIA
227388_at	2.49815087819486	0		
217963_s_at	2.48471435523086	0		HCS
233613_x_at	2.45189729191801	0		
228766_at	2.45082385023982	0		
208908_s_at	2.41879730006023	0		CAST
212586_at	2.33228373164484	0		ARTS-1
221802_s_at	2.32414568373485	0		KIAA1598
224823_at	2.30113027005505	0		
213624_at	2.29634946162627	0		ASM3A
221731_x_at	2.26796857130761	0		CSPG2
225426_at	2.26611296861875	0		

ALL t(8;14) vs. ALL Ph	samples: 4 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204663_at	-3.923285216392	0*	80.55	ME3
203373_at	-3.79361888147031	0		STATI2
207971_s_at	-3.75632756767036	0		KIAA0582
221834_at	-3.73210732395713	0		
212535_at	-3.35180803492209	0		
210487_at	-2.66400596339357	0		DNTT
226607_at	-2.65303285070543	0		L3MBTL
214505_s_at	-2.30002142127038	0		FHL1
226545_at	-2.26350222846019	0		
201540_at	-2.21889045310099	0		FHL1
209253_at	-2.17983750831107	0		SCAM-1
228496_s_at	-2.17784383479245	0		CRIM1
213854_at	-2.14963630962421	0		SYNGR1
228211_at	-2.14770747938169	0		
212012_at	-2.10857376713896	0		D2S448
208217_at	-2.10769716540219	0		GABRR2
202519_at	-2.0579870997007	0		MONDOA
218836_at	2.05747195088222	0		FLJ22638
211031_s_at	-2.05686503189171	0		CYLN2
50277_at	1.4804958933411	0		GGA1

ALL t(8;14) vs. T-ALL	samples: 4 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
213772_s_at	4.99941703918842	0*	105.35	GGA2
236019_at	-4.8835710129593	0		
225277_at	-4.63399536600695	0		
40148_at	3.56542456382539	0		APBB2
228211_at	-3.35861431980337	0		
201334_s_at	3.32612092220108	0		ARHGEF12
201417_at	-2.74359054965603	0		
206241_at	-2.66958809534806	0		KPNA5
208918_s_at	2.59071326340578	0		FLJ13052
210038_at	-2.55792113825771	0		
225735_at	-2.54773299400117	0		
209253_at	-2.33749346955264	0		SCAM-1
202262_x_at	-2.29867528817227	0		DDAH2
225129_at	2.29232308514395	0		MDS026
221969_at	2.278395672233	0		PAX5
225080_at	2.24115131588386	0		MYO1C
218338_at	-2.22116851483018	0		EDR1
208664_s_at	-2.20362132175544	0		TTC3
201029_s_at	-2.14618908100153	0.01		MIC2
56256_at	1.43796973813133	0		LOC51092

ALL t(8;14) vs. AML +8	samples: 4 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
213159_at	-4.39324002240111	0*	42.05	KIAA0805
226607_at	-4.38967336864894	0		L3MBTL
205420_at	-3.4525752660757	0		PEX7
202137_s_at	-3.07008892450809	0		BS69
36004_at	-2.57531929513625	0.01		IKBKG
203731_s_at	-2.45523698701432	0		ZFP95
212349_at	-2.36608074328153	0		POFUT1
209253_at	-2.32838757070082	0.01		SCAM-1
213238_at	-2.28171034767303	0		ATP10D
223382_s_at	-2.21844659554677	0		NIN283
219291_at	-2.18210292149327	0		MDS009
212293_at	-2.11981778828952	0		KIAA0630
1729_at	-1.99780531744703	0		TRADD
225959_s_at	-1.99555471271853	0.01		NIN283
205690_s_at	1.97864646284407	0		G10
243579_at	1.96429396023857	0		MSI2
220564_at	1.95122068807877	0		FLJ11218
210896_s_at	-1.94074678448131	0		ASPH
221617_at	-1.92262620134603	0.02		

ALL t(8;14) vs. AML complex	samples: 4 / 36			
accuracy	0.975			
confidence	0.967090153309866			
failed:	4			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
36004_at	-1.99819054416994	0		IKBKG
228410_at	-1.91203372111762	0		GAB3
226291_at	-1.85352930781754	0		ALS2
239478_x_at	-1.83892006057297	0		
201278_at	-1.78640641972044	0		DAB2
213073_at	-1.78527733316412	0		KIAA0321
36920_at	-1.77637196930535	0		MTM1
237864_at	-1.75181406771053	0		
206550_s_at	-1.74071643864686	0.01		NUP155
213779_at	-1.71354352282537	0		
237006_at	-1.71319042514024	0		
206847_s_at	-1.68023930751716	0		HOXA7
213639_s_at	-1.6794904444526	0		KIAA0557
40148_at	1.6627909781575	0*	64	APBB2
210358_x_at	-1.62491966279342	0		MGC2306
205420_at	-1.62469403094415	0		PEX7
226499_at	-1.60847740357238	0		
212293_at	-1.56783564141892	0*	524.25	KIAA0630
228211_at	-1.5662932955074	0		
AFFX-r2-Hs28SrRNA-5_at				
HG-U133B	0.804899059460234	0		

ALL t(8;14) vs. AML normal	samples: 4 / 62			
accuracy	1			
confidence	0.94492014468957			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
242774_at	2.1771591988175	0		SYNE-2
226066_at	-2.1383489258559	0		
239478_x_at	-1.86376314754514	0		
40148_at	1.78834322080621	0*	53.3	APBB2
214651_s_at	-1.72987407199338	0		HOXA9
241421_at	-1.69137753712694	0		
225277_at	-1.68295316743627	0		
237864_at	-1.66733222775185	0		
231181_at	1.63598703935064	0		
227173_s_at	1.58512628703822	0		BACH2
228410_at	-1.58118628637501	0		GAB3
226607_at	-1.56767039969117	0		L3MBTL
206398_s_at	1.56041095418581	0		CD19
226590_at	-1.55939441513481	0.01		
223391_at	1.54577336325056	0		LOC81537
205420_at	-1.53228798256568	0		PEX7
240106_at	-1.53045374201368	0		
236019_at	-1.50700230486984	0		
214558_at	-1.50544788292166	0		GPR12
AFFX-HUMRGE/M10098_3_at - HG-U133B	0.698344697289208	0		

ALL t(8;14) vs. AML t(8;21)	samples: 4 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
40148_at	3.56542456382539	0*	32.75	APBB2
239835_at	3.10722969539603	0		KIAA1842
225277_at	-2.97531197185908	0		
225306_s_at	-2.20761036808439	0		
210664_s_at	-2.19905382124823	0		TFPI
218319_at	2.13133938217549	0		PELI1
212985_at	2.10403815234864	0		
238155_at	2.09456306072679	0		
221617_at	-2.04115820286726	0		
220307_at	-2.04090815318901	0		CD244
225250_at	2.04032419238326	0		STIM2
217080_s_at	-2.03866301670049	0		HOMER-2B
228827_at	-2.03460798747208	0		
214558_at	-2.02268322634707	0.01		GPR12
230650_at	-2.02205697080977	0		
226546_at	-2.00802538838226	0		
219478_at	-1.99876002437156	0		WFDC1
211709_s_at	-1.99340446769437	0		SCGF
219789_at	-1.96292007200438	0		NPR3
231181_at	1.9495774287402	0		

ALL B not Ph vs. all other	samples: 9 / 260			
accuracy	0.988847583643123			
confidence	0.749589637027985			
failed:	1,2,8			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
230441_at	1.31003692018591	0		
202382_s_at	-1.16916758328947	0		GNPI
229253_at	-1.06515235605176	0		CTMP
201482_at	-1.03614111933273	0		QSCN6
214116_at	-1.00681323467099	0		BTD
224435_at	0.992700829908313	0		MGC4248
229344_x_at	0.972107787450054	0		KIAA1238
229487_at	0.965321723620396	0*	1	
217559_at	0.963455203763842	0		RPL10L
212592_at	0.956367645094086	0*	4436.6	
209197_at	0.921039694411825	0*	637.1	KIAA0080
223469_at	-0.914920276631408	0*	1	MGC10812
224739_at	0.904429749740017	0*	1	MG61
218351_at	-0.898398261455524	0*	145.5	FLJ20502
220744_s_at	-0.893719737391747	0*	1	WDR10
213582_at	-0.888860830483358	0*	1	ATP11A
219615_s_at	-0.8878326695192	0*	1	KCNK5
203795_s_at	0.880543704938786	0		BCL7A
229817_at	0.879488726239199	0		DKFZP434M098
244876_at	0.877426806604064	0		

ALL B not Ph vs. ALL Ph	samples: 9 / 15			
accuracy	0.916666666666667			
confidence	1			
failed:	3,10			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
219358_s_at	-1.52735607926994	0		CENTA2
241383_at	-1.07499870203752	0.01		
213895_at	-1.05505220750298	0		EMP1
202123_s_at	-1.02481061931947	0*	753.7	ABL1
205911_at	-1.0236634987836	0		PTHR1
242223_at	1.02343172223498	0.01		
211709_s_at	-1.01491744255679	0		SCGF
234839_at	-1.00185285072786	0		
212150_at	-0.996731200580515	0		KIAA0143
221991_at	-0.987741661696868	0		NXPH3
218543_s_at	0.973909033712243	0		FLJ22693
201874_at	0.966766364385792	0		FLJ21047
212188_at	-0.947998533949464	0		LOC115207
241810_at	-0.944344027780102	0.01		
207520_at	-0.936622132674122	0		
213979_s_at	-0.935519171149618	0		CTBP1
229745_x_at	-0.93424475879621	0.01		
216680_s_at	-0.934196756237652	0		EPHB4
202572_s_at	0.924395823520243	0		KIAA0964
243228_at	0.916138491705783	0		

ALL B not Ph vs. T-ALL	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
242292_at	-3.53231266693437	0*	19.4	
36566_at	2.04687603382912	0		CTNS
230636_s_at	1.96129371358941	0		BTEB1
266_s_at	1.95685220231101	0		CD24
209771_x_at	1.95325312023269	0		CD24
219631_at	-1.90940390225071	0		FLJ12929
202113_s_at	1.86969444770264	0		SNX2
216379_x_at	1.84446878357139	0		
221969_at	1.82924887172424	0		PAX5
229487_at	1.78170685853126	0		
208650_s_at	1.77571318786079	0		CD24
218464_s_at	-1.71465707824422	0		FLJ10700
213944_x_at	1.69297405468728	0		
226496_at	1.65125933296341	0		
202206_at	-1.58502966518677	0		ARL7
205504_at	1.58481348793145	0		BTK
213539_at	-1.56405807954932	0		CD3D
211101_x_at	1.55958748994576	0.01		LILRA2
244876_at	1.55727218904507	0		
209772_s_at	1.54041193817483	0		CD24

ALL B not Ph vs. AML +8	samples: 9 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
229253_at	-2.32958521030012	0		CTMP
230441_at	2.03717805375485	0		
202382_s_at	-2.02017770346207	0		GNPI
209135_at	-1.93398721370049	0		ASPH
229487_at	1.78170685853126	0		
236656_s_at	1.74257382856431	0		
206438_x_at	-1.68325155133202	0		FLJ12975
207403_at	-1.66596170819766	0		IRS4
219615_s_at	-1.66280630807372	0		KCNK5
51192_at	-1.66236513015575	0		SSH-3
208248_x_at	-1.64870519570629	0*	1987.65	APLP2
218109_s_at	-1.60915618696108	0		FLJ14153
206295_at	-1.5980305395866	0		IL18
219013_at	-1.59551449458991	0		FLJ21634
217979_at	1.59385936644152	0		NET-6
208674_x_at	-1.58849840915584	0		DDOST
213474_at	1.58394324440508	0		
218351_at	-1.58117397105311	0		FLJ20502
235422_at	1.57754106652849	0		FALZ
227709_at	1.573035497361	0		RCN1

ALL B not Ph vs. AML				
complex	samples: 9 / 36			
accuracy	1			
confidence	0.975685516889171			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
230441_at	2.03717805375485	0		
218168_s_at	-1.58072460849855	0*	584.1	CABC1
219615_s_at	-1.55121221944569	0		KCNK5
200620_at	-1.52004960803633	0		C1orf8
229487_at	1.50364388130017	0		
218718_at	-1.4701929847603	0		PDGFC
203372_s_at	1.43481740588652	0		STATI2
205997_at	-1.40495787127453	0		ADAM28
221969_at	1.3801763712428	0		PAX5
209628_at	-1.36215023734312	0		P15-2
243362_s_at	1.346548683162	0		LEF1
219362_at	-1.34586251735194	0		FLJ22643
244876_at	1.32930450347737	0		
227038_at	-1.3285550634404	0		
215001_s_at	-1.31302949268385	0		GLUL
202382_s_at	-1.31028007399306	0		GNPI
211574_s_at	-1.27970708025177	0		MCP
203373_at	1.2683089746763	0		STATI2
206847_s_at	-1.25861755739009	0		HOXA7
90610_at	0.53320359867076	0.01		LRRN1

ALL B not Ph vs. AML normal	samples: 9 / 62			
accuracy	0.985915492957746			
confidence	1			
failed:	51			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
230441_at	1.6244512124777	0		
229487_at	1.5789226463723	0		
244876_at	1.55727218904507	0		
230659_at	1.54315361034532	0		KIAA0212
214651_s_at	-1.46222218442109	0		HOXA9
221969_at	1.45958458157821	0*	695.5	PAX5
222915_s_at	1.43752454061174	0		BANK
204215_at	1.3973053569742	0		MGC4175
223469_at	-1.39620868523075	0		MGC10812
205997_at	-1.3950951014202	0		ADAM28
229253_at	-1.35885129348099	0		CTMP
209905_at	-1.35690502004825	0		HOXA9
236656_s_at	1.33665521300451	0		
205382_s_at	-1.33068263294683	0		DF
214761_at	1.3284704024734	0		OAZ
235753_at	-1.3151317291794	0		
218351_at	-1.29563799307181	0		FLJ20502
243362_s_at	1.29364059417566	0		LEF1
201482_at	-1.28902191317183	0		QSCN6
217979_at	1.28815999568218	0		NET-6

ALL B not Ph vs. AML t(8;21)	samples: 9 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
202382_s_at	-2.19898458962526	0*	48.7	GNPI
230441_at	2.03717805375485	0		
228827_at	-2.03460798747208	0		
219478_at	-1.99876002437156	0		WFDC1
218718_at	-1.92298631566524	0		PDGFC
203795_s_at	1.88483347573406	0		BCL7A
229487_at	1.78170685853126	0		
241383_at	-1.74636612447809	0		
236656_s_at	1.74257382856431	0		
235818_at	-1.70111545046162	0		
239278_at	1.69632987254595	0		
204647_at	-1.69400429479148	0		HOMER-3
213944_x_at	1.69297405468728	0		
217989_at	-1.69293289781308	0		LOC51170
205528_s_at	-1.64467496425566	0		CBFA2T1
38269_at	1.6387714295779	0		PKD2
201644_at	1.59860594123581	0		TSTA3
206622_at	-1.58757343463781	0		TRH
204319_s_at	-1.57313966435531	0		RGS10

ALL Ph vs. all other	samples: 15 / 254			
accuracy	0.973977695167286			
confidence	1			
failed:	5,6,10,12,13,14,139			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210487_at	1.46744760454294	0		DNTT
203373_at	1.40251061555498	0		STATI2
234107_s_at	-1.30126819904145	0		
224772_at	1.2067398887062	0		MGC14961
201540_at	1.17259032247018	0		FHL1
202123_s_at	1.11803958640816	0		ABL1
202052_s_at	1.1015960943329	0		RAI14
207971_s_at	1.09522659077439	0		KIAA0582
218589_at	1.08650464406846	0		P2Y5
210299_s_at	1.08531672501274	0		FHL1
227584_at	1.05386625392045	0		
223314_at	1.04772672325566	0		MGC11352
203355_s_at	1.04604188199321	0		KIAA0942
212975_at	1.04561133965056	0		KIAA0870
214505_s_at	1.03851430654898	0		FHL1
222154_s_at	1.03658126355559	0		DKFZP564A2416
209679_s_at	1.00639728893477	0		LOC57228
230659_at	1.0054326445936	0		KIAA0212
1007_s_at	1.00231733413632	0		DDR1
227998_at	0.995615703854239	0*	3687.45	MGC17528

ALL Ph vs. T-ALL	samples: 15 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
218224_at	-2.4418494296856	0		PNMA1
213854_at	2.14963630962421	0		SYNGR1
221969_at	2.06978634038245	0*	152.35	PAX5
205101_at	1.84182814954198	0		MHC2TA
213539_at	-1.83994967875006	0		CD3D
228988_at	-1.79658055608971	0		ZNF6
208894_at	1.79489847703276	0		HLA-DRA
209604_s_at	-1.75648531255811	0		GATA3
209619_at	1.72743796589982	0		CD74
209771_x_at	1.69086499548436	0		CD24
210982_s_at	1.68104679025052	0		HLA-DRA
229487_at	1.66237077940113	0		
235706_at	1.65050775066494	0		CPM
226878_at	1.64629305544324	0		
219631_at	-1.6447182870532	0		FLJ12929
216379_x_at	1.61950446576807	0		
232234_at	-1.6009007845449	0		C20orf24
210116_at	-1.58593866198308	0		SH2D1A
224772_at	1.58464619249453	0		MGC14961
213944_x_at	1.58085800202538	0		

ALL Ph vs. AML +8	samples: 15 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210487_at	2.5237441884906	0		DNTT
203373_at	1.87201491464778	0		STATI2
202626_s_at	-1.85118734150368	0		LYN
226545_at	1.80654821675707	0		
219229_at	-1.75947760308609	0		SLC21A11
201828_x_at	-1.75807186867031	0		CXX1
217979_at	1.75748092515514	0		NET-6
51192_at	-1.7460030120736	0		SSH-3
229302_at	1.73677596348294	0		
226438_at	-1.70384127791425	0		
227367_at	-1.69193353561271	0		
229487_at	1.66237077940113	0		
234107_s_at	-1.64136875764363	0*	340.6	
204672_s_at	-1.64125970689002	0		ANKRD6
202625_at	-1.61126391589076	0		LYN
231887_s_at	1.60675392068253	0		KIAA1274
218942_at	-1.59127524427508	0		FLJ22055
210749_x_at	1.58213182698513	0		DDR1
213150_at	-1.57881564631984	0		HOXA10
59697_at	1.03007856466368	0		

ALL Ph vs. AML complex	samples: 15 / 36			
accuracy	0.980392156862745			
confidence	1			
failed:	41			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203373_at	2.31025004347829	0		STATI2
206847_s_at	-1.68023930751716	0		HOXA7
203372_s_at	1.63947005879125	0		STATI2
234107_s_at	-1.61839900546276	0		
210487_at	1.52754184797369	0		DNTT
214651_s_at	-1.49910544616071	0*	250.95	HOXA9
209619_at	1.49461107113623	0		CD74
218718_at	-1.42002659230416	0		PDGFC
225660_at	1.39520949215218	0		SEMA6A
226878_at	1.38541949367152	0		
235753_at	-1.36744735557489	0		
229817_at	1.35899260632582	0		DKFZP434M098
229487_at	1.334779526707	0		
214761_at	1.33168680907428	0		OAZ
225782_at	-1.32289994708003	0		
209905_at	-1.31131029251837	0		HOXA9
235521_at	-1.3094635283322	0		HOXA3
221969_at	1.30539974000703	0		PAX5
213150_at	-1.28908316992088	0		HOXA10
243363_at	1.22268997650812	0		LEF1

ALL Ph vs. AML normal	samples: 15 / 62			
accuracy	1			
confidence	0.974929287250918			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214651_s_at	-1.85202940734635	0*	143.55	HOXA9
203373_at	1.62915723435284	0		STATI2
234107_s_at	-1.59102595714414	0		
229817_at	1.58719561744707	0		DKFZP434M098
235753_at	-1.57582123676185	0		
224772_at	1.55894528337306	0		MGC14961
210487_at	1.55488151717647	0		DNTT
212012_at	1.4856092975255	0		D2S448
223449_at	1.48450202420019	0		SEMA6A
209905_at	-1.46906077761321	0		HOXA9
213150_at	-1.46604197311664	0		HOXA10
212975_at	1.45775514780451	0		KIAA0870
221969_at	1.42534915280476	0		PAX5
206847_s_at	-1.42447895990314	0		HOXA7
214761_at	1.42199062015385	0		OAZ
229487_at	1.42117416701658	0		
217979_at	1.40224984357617	0		NET-6
225660_at	1.39520949215218	0		SEMA6A
212013_at	1.38743332601863	0*	595.1	D2S448
223314_at	1.38610020402626	0		MGC11352

ALL Ph vs. AML t(8;21)	samples: 15 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210487_at	2.25266231447204	0		DNTT
203373_at	2.24099300433703	0		STATI2
228827_at	-2.03460798747208	0*	162.15	
226545_at	1.91066898371188	0		
224928_at	1.88688841526862	0		
218718_at	-1.86717048634787	0		PDGFC
221581_s_at	1.85128137775803	0		WBSCR5
201811_x_at	1.82001958474325	0		SH3BP5
201486_at	1.78302051564335	0		RCN2
207655_s_at	1.77674162168543	0		BLNK
223467_at	1.77014181133384	0		RASD1
224764_at	1.76474506640734	0		ARHGAP10
218237_s_at	1.7513955350881	0		SLC38A1
212535_at	1.73463136017207	0		
202123_s_at	1.72757337414589	0		ABL1
50221_at	1.71143815565141	0		
202600_s_at	1.69190236878682	0		NRIP1
208146_s_at	1.67349162864443	0		CPVL
210151_s_at	1.66867162916475	0		DYRK3
229487_at	1.66237077940113	0		

T-ALL vs. all other	samples: 9 / 260			
accuracy	0.988847583643123			
confidence	0.974096654425726			
failed:	2,8,239			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
213539_at	1.47540002688666	0		CD3D
230588_s_at	1.40173530720654	0		MCPR
209604_s_at	1.29998211445613	0*	1756.45	GATA3
233589_x_at	-1.29177430222739	0*	1	
201416_at	1.28847513298777	0		SOX4
228988_at	1.22715826655642	0		ZNF6
205640_at	-1.20119307753531	0		ALDH3B1
201417_at	1.20045529988474	0		
228174_at	1.19343398440307	0		
206804_at	1.19196138585152	0		CD3G
218913_s_at	-1.18780274620161	0		LOC51291
221188_s_at	-1.17857568967097	0		CIDEB
221555_x_at	-1.15605774789743	0		CDC14B
229280_s_at	1.14891159995685	0		
219079_at	-1.1401640005663	0		b5&b5R
228242_at	1.13931660332537	0		
225003_at	-1.13574793214416	0		MBC3205
205504_at	-1.1269796752374	0		BTK
209499_x_at	-1.12273253976539	0		TNFSF13
226342_at	1.11835127434314	0		

T-ALL vs. AML +8	samples: 9 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233589_x_at	-5.40566971880279	0*	94.05	
211495_x_at	-3.24639126977955	0		TNFSF13
209499_x_at	-2.48173374690971	0		TNFSF13
201416_at	2.45175574451932	0		SOX4
227999_at	-2.41422896946156	0		LOC170394
205640_at	-2.36735951723515	0		ALDH3B1
218913_s_at	-2.26146566262815	0		LOC51291
242292_at	2.13276982228889	0		
227729_at	2.11399761533966	0		
206295_at	-2.10263843038377	0		IL18
218341_at	-2.09693358964157	0		FLJ11838
217989_at	-2.01015824384982	0		LOC51170
201200_at	-1.9921136873539	0		CREG
202626_s_at	-1.97579203488485	0		LYN
201417_at	1.94726816387174	0		
201985_at	-1.9229605331952	0		KIAA0196
219013_at	-1.91889126390119	0		FLJ21634
219329_s_at	-1.91383490407803	0		APR-3
230588_s_at	1.87407116981284	0		MCPR
39650_s_at	1.68662830524108	0		KIAA0435

T-ALL vs. AML complex	samples: 9 / 36			
accuracy	0.977777777777778			
confidence	1			
failed:	8			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
242292_at	1.76638958058548	0		
233589_x_at	-1.72473600410199	0		
201200_at	-1.67373612904555	0		CREG
221188_s_at	-1.58025708973943	0		CIDEB
214430_at	-1.57548239699241	0		GLA
203370_s_at	-1.49153229697191	0		ENIGMA
213101_s_at	-1.48624142663186	0		IL27
207543_s_at	-1.47703523852874	0*	244.15	P4HA1
200996_at	-1.46058173493331	0		ACTR3
228242_at	1.42599890928864	0		
200625_s_at	-1.41869234255251	0		CAP
212271_at	-1.41675681954144	0		MAPK1
213798_s_at	-1.3995900667655	0		CAP
218341_at	-1.38917958617976	0		FLJ11838
207809_s_at	-1.38033524444329	0		ATP6IP1
201416_at	1.36993537921948	0		SOX4
214017_s_at	-1.36371429454275	0		DDX34
210145_at	-1.35854949316142	0		PLA2G4A
221006_s_at	-1.35518233243855	0		MY014

T-ALL vs. AML normal	samples: 9 / 62			
accuracy	1			
confidence	0.957860143913647			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
230292_at	1.88640079114873	0*	209.2	
201200_at	-1.83242104341312	0		CREG
202479_s_at	1.72124560429389	0*	139	GS3955
213539_at	1.67079068669821	0		CD3D
224918_x_at	-1.58916954867569	0		MGST1
227999_at	-1.50019492619142	0		LOC170394
219812_at	1.47878284715341	0		MGC2463
228007_at	1.4773281277912	0		
231736_x_at	-1.46304321667415	0		MGST1
219079_at	-1.46035185202908	0		b5&b5R
204484_at	1.43138015243683	0		PIK3C2B
201537_s_at	-1.41942605715997	0		DUSP3
210613_s_at	-1.41293569747837	0		SYNGR1
217989_at	-1.41116959479258	0		LOC51170
207996_s_at	1.40679076628897	0		C18orf1
200765_x_at	-1.40654043227196	0		CTNNA1
205382_s_at	-1.40167577220905	0		DF
201463_s_at	-1.39170471415992	0		TALDO1
233589_x_at	-1.39076513944045	0		
39650_s_at	1.23989100884988	0		KIAA0435

T-ALL vs. AML t(8;21)	samples: 9 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
242292_at	3.53231266693437	0*	19.4	
203949_at	-3.12642743394317	0		MPO
203948_s_at	-2.45792853300794	0		MPO
217989_at	-2.43298080062421	0		LOC51170
223482_at	-2.33409794008859	0		TMPIT
203795_s_at	2.1853673808492	0		BCL7A
218224_at	2.09498423445912	0		PNMA1
217080_s_at	-2.03866301670049	0		HOMER-2B
236019_at	2.02213343587896	0		
219477_s_at	2.01911441063646	0		LOC55901
228988_at	2.01251275923737	0		ZNF6
201486_at	1.99987326641982	0		RCN2
219478_at	-1.99876002437156	0		WFDC1
228266_s_at	1.98746817521137	0		CGI-142
207996_s_at	1.96448548584508	0		C18orf1
222203_s_at	1.94383192684329	0		
205640_at	-1.93350841183487	0		ALDH3B1
210613_s_at	-1.93015512462768	0		SYNGR1
228174_at	1.9244800134633	0		
223474_at	1.91826574900603	0		C14orf4

AML +8 vs. all other	samples: 10 / 259			
accuracy	0.966542750929368			
confidence	1			
failed:	1,2,3,5,6,7,8,9,10			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212250_at	1.00891676230186	0		
218549_s_at	0.942516384676453	0		LOC51115
212449_s_at	0.88821669704833	0		LYPLA1
205849_s_at	0.882097788580276	0		UQCRB
222166_at	-0.873718781745549	0		
203007_x_at	0.87144371195471	0		
242975_s_at	-0.862022087552992	0		GNAS
208697_s_at	0.80816796889713	0		EIF3S6
201592_at	0.794789783421717	0		EIF3S3
218482_at	0.794345693087361	0		DC6
201985_at	0.784318906218296	0		KIAA0196
231101_at	-0.7838812614223	0		PPP2R5E
218642_s_at	0.776600267973484	0		MGC2217
201652_at	0.761703817525426	0		COPS5
201433_s_at	0.761252302206581	0		PTDSS1
217916_s_at	0.757235902578392	0		BM-009
226165_at	0.738121051467492	0*	1969.6	E2F5
203110_at	0.736663801658822	0		PTK2B
224804_s_at	-0.734849706050297	0		FLJ00005

AML +8 vs. AML complex	samples: 10 / 36			
accuracy	1			
confidence	0.855027999708228			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
222229_x_at	1.23332137897808	0		
208697_s_at	1.15066098039301	0		EIF3S6
205849_s_at	1.14869307530221	0		UQCRB
212586_at	1.11153173777253	0*	1231.4	ARTS-1
208646_at	1.07422424644875	0		
230795_at	-1.06732853628123	0		H4F2
202746_at	-1.03422849717783	0		
226545_at	-1.00972156245463	0*	100.15	
222166_at	-0.999828982909011	0*	1	
210715_s_at	-0.978857795907468	0*	573.3	SPINT2
228652_at	-0.974511468277957	0		
217979_at	-0.973647566321829	0*	234.35	NET-6
201548_s_at	-0.970651188910704	0*	289.85	PLU-1
202747_s_at	-0.952100249128964	0		ITM2A
201602_s_at	-0.951073671804128	0		PPP1R12A
205674_x_at	-0.945871996779656	0		FXYD2
244740_at	-0.942099475768156	0		
219518_s_at	-0.938970502867646	0		FLJ22637
227249_at	-0.931085853722028	0		NUDE1

AML +8 vs. AML normal	samples: 10 / 62			
accuracy	0.944444444444444			
confidence	1			
failed:	2,8,9,10			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214394_x_at	1.16987396866816	0		FLJ20897
203110_at	1.09167544137433	0		PTK2B
203007_x_at	1.00013993270134	0		
235124_at	-0.983829818030274	0		
212251_at	0.969996357896378	0*	4073.8	
242975_s_at	-0.968085578079267	0		GNAS
206781_at	-0.939680187764268	0		DNAJC4
225406_at	-0.924590937077397	0		TSG
218482_at	0.900623425034112	0		DC6
237291_at	-0.889981273455645	0.01		
235647_at	-0.87846991187601	0		
234726_s_at	-0.877362222213618	0		
225889_at	-0.85606834671728	0		
236837_x_at	-0.842273497900729	0		
222166_at	-0.840979666931678	0		
228092_at	-0.833074953827583	0		
212250_at	0.830552344097529	0		
226450_at	0.827753984186341	0		
238392_at	-0.812637849766076	0		
200655_s_at	0.811239676737242	0		CALM1

AML +8 vs. AML t(8;21)	samples: 10 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228827_at	-2.03460798747208	0*	162.15	
203188_at	1.98171895993959	0		B3GNT6
209522_s_at	1.87499941760774	0		CRAT
50221_at	1.77237042593137	0		
212586_at	1.70313290894867	0		ARTS-1
217816_s_at	1.69811663165145	0		pcnp
219084_at	1.68534097481951	0		NSD1
241370_at	1.66453119103938	0		
221581_s_at	1.64609943226078	0		WBSCR5
205528_s_at	-1.64467496425566	0		CBFA2T1
211341_at	-1.63310072579237	0		POU4F1
212250_at	1.62854737716103	0		
206940_s_at	-1.60737424398258	0		POU4F1
205529_s_at	-1.591491111654	0		CBFA2T1
213150_at	1.57881564631984	0		HOXA10
214394_x_at	1.57039311243451	0		FLJ20897
212895_s_at	1.56878968456679	0		ABR
218341_at	1.53928870336148	0		FLJ11838
204249_s_at	1.52597204656408	0		LMO2
214651_s_at	1.52240931149048	0		HOXA9

AML complex vs. all other	samples: 36 / 233			
accuracy	0.940520446096654			
confidence	0.921791251652985			
failed:	1,3,4,7,9,11,13,17,19,22,26,29,30,31,36,159			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
222229_x_at	-0.893099830348847	0		
200608_s_at	0.829215272839729	0*	1754.85	RAD21
219793_at	0.800006992121134	0*	82.35	SNX16
214700_x_at	0.78695642651388	0		
216652_s_at	0.767651877577316	0		
209523_at	0.752134816617307	0*	681.95	
203904_x_at	0.746250973896829	0		KAI1
209188_x_at	0.739903310934254	0		DR1
207654_x_at	0.732205254479051	0		DR1
223318_s_at	-0.730537441809073	0		MGC10974
201437_s_at	0.717807687112266	0		EIF4E
227056_at	-0.715710672900953	0		KIAA0141
209259_s_at	0.712514692902903	0		CSPG6
216304_x_at	0.711429386769807	0		
201263_at	0.705291260136426	0		TARS
213452_at	0.700628406937312	0		ZNF184
225344_at	0.690845684896899	0		
203133_at	0.686789233495541	0		SEC61B
203818_s_at	0.685434479377027	0		SF3A3
202413_s_at	0.684073197719258	0		USP1

AML complex vs. AML normal	samples: 36 / 62			
accuracy	0.959183673469388			
confidence	0.827538830649198			
failed:	4,17,26,95			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
222229_x_at	-1.15282283406825	0		
227056_at	-1.01959539261157	0		KIAA0141
200093_s_at - HG-U133B	-0.981168516451417	0*	3052.25	HINT1
201922_at	-0.946723517280923	0*	3970.8	YR-29
239791_at	-0.927299942476145	0*	54	HOXB6
200608_s_at	0.881421230727578	0*	1566.2	RAD21
235502_at	-0.858356821521878	0		
200093_s_at - HG-U133A	-0.84958486306905	0		HINT1
205436_s_at	0.848914256281541	0		H2AFX
223318_s_at	-0.843205304716435	0		MGC10974
200023_s_at - HG-U133B	-0.834951347999649	0		EIF3S5
201164_s_at	0.825610572112667	0		PUM1
203345_s_at	0.823373110066695	0		M96
212251_at	0.821052485124022	0		
218645_at	-0.816440269243142	0		ZNF277
236728_at	-0.815324685029762	0		
214911_s_at	0.812703140158658	0		
236892_s_at	-0.810032594833065	0		HOXB6
211950_at	0.809875752517154	0*	1367.5	RBAF600
207983_s_at	0.808929428489603	0		STAG2

AML complex vs. AML t(8;21)	samples: 36 / 13			
accuracy	1			
confidence	0.956366908409342			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201851_at	1.64654123030477	0		SH3GL1
228827_at	-1.63837794328364	0*	277.15	
214651_s_at	1.52618371146822	0		HOXA9
235521_at	1.52417126144756	0		HOXA3
204249_s_at	1.52365997713542	0*	1581.95	LMO2
203904_x_at	1.49494399498725	0		KAI1
206940_s_at	-1.48076766016125	0		POU4F1
211341_at	-1.47540487159533	0		POU4F1
209259_s_at	1.45032016623088	0		CSPG6
212058_at	1.43907164424644	0		KIAA0332
218577_at	1.42304726090167	0		FLJ20331
217963_s_at	1.41730181206619	0		HCS
206622_at	-1.41476408655437	0		TRH
200071_at - HG-U133A	1.4105258517176	0		SPF30
218933_at	1.38255573216414	0		MGC5347
205528_s_at	-1.38150242627303	0		CBFA2T1
218331_s_at	1.3810903886183	0		FLJ20360
202406_s_at	1.3795610685034	0		TIAL1
220796_x_at	1.36377544613334	0		FLJ14251
218582_at	1.35888148459997	0		FLJ20445

AML normal vs. all other	samples: 62 / 207			
accuracy	0.895910780669145			
confidence	0.964449931704009			
failed:	5,14,20,27,30,32,35,37,38,39,42,43,45,48,50,52,53,55,56,57,61,213,215,217,219,227,230,254			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
236892_s_at	0.883816204836633	0*	60.95	HOXB6
228904_at	0.842467327362967	0		
239791_at	0.82014114184115	0		HOXB6
205601_s_at	0.78108191394345	0		HOXB5
205600_x_at	0.763742762546178	0		HOXB5
205366_s_at	0.755814747220724	0*	322.65	HOXB6
230743_at	0.685019971063637	0		
205453_at	0.673160741612025	0		HOXB2
214651_s_at	0.668311761484385	0		HOXA9
200679_x_at	-0.662124332081048	0		HMG1
225406_at	0.660717097117062	0		TSG
200093_s_at - HG-U133B	0.660005840449192	0		HINT1
206295_at	0.640927517926634	0		IL18
235753_at	0.637566839566103	0		
217768_at	0.632918049830813	0		LOC51637
225553_at	0.62830766714963	0		
225175_s_at	-0.624292365035176	0		CTL2
200093_s_at - HG-U133A	0.621189010096421	0		HINT1
214911_s_at	-0.615055858265367	0		
241464_s_at	0.611746504394311	0		

AML normal vs. AML t(8;21)	samples: 62 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228827_at	-2.03460798747208	0*	162.15	
214651_s_at	1.87986749903764	0		HOXA9
205528_s_at	-1.64467496425566	0		CBFA2T1
235753_at	1.56101146788885	0		
205529_s_at	-1.4994140185132	0		CBFA2T1
211341_at	-1.4972813333234	0		POU4F1
206940_s_at	-1.48355335484551	0		POU4F1
209905_at	1.46906077761321	0		HOXA9
213150_at	1.46604197311664	0		HOXA10
217816_s_at	1.45253445141557	0		pcnp
219598_s_at	1.41726065845379	0		
205453_at	1.38558116676561	0		HOXB2
223498_at	1.33655832782001	0		
214000_s_at	-1.2765364955951	0		RGS10
235818_at	-1.27371437711255	0		
213844_at	1.25995066545668	0		HOXA5
235521_at	1.2540451261169	0		HOXA3
227279_at	1.2513845109424	0		MGC15737
222448_s_at	1.24728565933231	0		UMP-CMPK
213147_at	1.24192806323509	0		HOXA10

AML t(8;21) vs. all other	samples: 13 / 256			
accuracy	0.996282527881041			
confidence	1			
failed:	190			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228827_at	1.85657763737458	0		
205528_s_at	1.5282463620506	0		CBFA2T1
205529_s_at	1.44069436893782	0*	157.8	CBFA2T1
206622_at	1.31883260079515	0		TRH
206940_s_at	1.30418339343959	0		POU4F1
211341_at	1.2136561137121	0		POU4F1
212828_at	-1.0700055152284	0		SYNJ2
212480_at	-1.05079328033116	0		KIAA0376
219478_at	1.04231267665759	0		WFDC1
219598_s_at	-1.04225165555028	0		
204811_s_at	1.03799840690676	0		CACNA2D2
214000_s_at	1.01734079918989	0		RGS10
221581_s_at	-0.964830298373625	0		WBSCR5
224764_at	-0.954444787821262	0		ARHGAP10
34689_at	-0.942804241091645	0		TREX1
227279_at	-0.942193016486907	0		MGC15737
217816_s_at	-0.934103105967049	0		pcnp
207760_s_at	-0.925434637488157	0		NCOR2
238012_at	-0.924942905482366	0		
AFFX-r2-Hs28SrRNA-3_at	-			
HG-U133B	0.833222345890935	0		

Table 30: Analysis of 14 leukemia subgroups and normal bone marrow according to the method described by Westfall & Young. The 500 most significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

geneID	Golub	rawp	adjp	Gene symbol
201497_x_at	*	0.0001	**0.0001**	MYH11
201998_at	+	0.0001	**0.0001**	SIAT1
204150_at	+	0.0001	**0.0001**	STAB1
204511_at		0.0001	**0.0001**	KIAA0793
205805_s_at	+	0.0001	**0.0001**	ROR1
206255_at	+	0.0001	**0.0001**	BLK
206337_at		0.0001	**0.0001**	CCR7
207802_at	+	0.0001	**0.0001**	SGP28
207819_s_at		0.0001	**0.0001**	ABCB4
208091_s_at	+	0.0001	**0.0001**	DKFZP564K0822
208456_s_at	+	0.0001	**0.0001**	RRAS2
209061_at		0.0001	**0.0001**	NCOA3
209374_s_at	+	0.0001	**0.0001**	IGHM
210244_at	+	0.0001	**0.0001**	CAMP
212313_at		0.0001	**0.0001**	
212531_at	*	0.0001	**0.0001**	LCN2
212590_at	+	0.0001	**0.0001**	
212827_at	+	0.0001	**0.0001**	IGHM
212953_x_at	*	0.0001	**0.0001**	CALR
214450_at	*	0.0001	**0.0001**	CTSW
214615_at	+	0.0001	**0.0001**	P2Y10
215925_s_at	+	0.0001	**0.0001**	
219471_at	+	0.0001	**0.0001**	FLJ21562
219837_s_at	+	0.0001	**0.0001**	C17
221268_s_at		0.0001	**0.0001**	LOC81537
221601_s_at		0.0001	**0.0001**	TOSO
221969_at	*	0.0001	**0.0001**	PAX5
223287_s_at	+	0.0001	**0.0001**	FOXP1
223391_at	+	0.0001	**0.0001**	LOC81537
223514_at	+	0.0001	**0.0001**	CARD11
224794_s_at	+	0.0001	**0.0001**	LOC51148
224837_at	+	0.0001	**0.0001**	FOXP1
224838_at	*	0.0001	**0.0001**	
227224_at		0.0001	**0.0001**	
228390_at	+	0.0001	**0.0001**	
228827_at	*	0.0001	**0.0001**	

229070_at		0.0001	**0.0001** MGC12335
229072_at	+	0.0001	**0.0001**
229844_at	+	0.0001	**0.0001**
230768_at	+	0.0001	**0.0001**
232060_at		0.0001	**0.0001**
234725_s_at		0.0001	**0.0001** SEMA4B
236226_at		0.0001	**0.0001**
236280_at	+	0.0001	**0.0001**
236854_at	+	0.0001	**0.0001**
239214_at	*	0.0001	**0.0001**
239287_at	*	0.0001	**0.0001**
243780_at	+	0.0001	**0.0001**
38487_at	*	0.0001	**0.0001** FLJ12442
41660_at		0.0001	**0.0001** CELSR1
44790_s_at	+	0.0001	**0.0001** FLJ21562
202761_s_at		0.0001	**0.0002** SYNE-2
203074_at	+	0.0001	**0.0002** ANXA8
203936_s_at	+	0.0001	**0.0002** MMP9
203948_s_at	*	0.0001	**0.0002** MPO
204192_at	+	0.0001	**0.0002** CD37
204215_at	*	0.0001	**0.0002** MGC4175
205049_s_at	+	0.0001	**0.0002** CD79A
205192_at	*	0.0001	**0.0002** MAP3K14
205267_at		0.0001	**0.0002** POU2AF1
205528_s_at	+	0.0001	**0.0002** CBFA2T1
205901_at		0.0001	**0.0002** PNOC
207700_s_at		0.0001	**0.0002** NCOA3
207777_s_at		0.0001	**0.0002** SP140
208195_at		0.0001	**0.0002** TTN
209344_at	+	0.0001	**0.0002** TPM4
211352_s_at		0.0001	**0.0002** NCOA3
212386_at		0.0001	**0.0002**
212589_at	+	0.0001	**0.0002** RRAS2
212914_at		0.0001	**0.0002** PKP4
213142_x_at		0.0001	**0.0002** LOC54103
213309_at		0.0001	**0.0002** PLCL2
213689_x_at		0.0001	**0.0002** RPL5
213927_at	+	0.0001	**0.0002**
218469_at	+	0.0001	**0.0002** CKTSF1B1
219073_s_at		0.0001	**0.0002** OSBPL10
221586_s_at		0.0001	**0.0002** E2F5
225927_at	*	0.0001	**0.0002** MAP3K1

226122_at		0.0001	0.0002
226147_s_at		0.0001	0.0002
226496_at	+	0.0001	0.0002
226713_at	+	0.0001	0.0002
226989_at	+	0.0001	0.0002
227030_at		0.0001	0.0002
227173_s_at	*	0.0001	0.0002 BACH2
227670_at		0.0001	0.0002
238604_at		0.0001	0.0002
239393_at	+	0.0001	0.0002
242458_at		0.0001	0.0002
202524_s_at		0.0001	0.0004 KIAA0275
203949_at	*	0.0001	0.0004 MPO
205382_s_at	*	0.0001	0.0004 DF
205529_s_at	*	0.0001	0.0004 CBFA2T1
206126_at		0.0001	0.0004 BLR1
206676_at	+	0.0001	0.0004 CEACAM8
207000_s_at	+	0.0001	0.0004 PPP3CC
209168_at	+	0.0001	0.0004 GPM6B
210997_at		0.0001	0.0004 HGF
212387_at		0.0001	0.0004
212956_at		0.0001	0.0004 KIAA0882
218090_s_at		0.0001	0.0004
218468_s_at		0.0001	0.0004 CKTSF1B1
219820_at		0.0001	0.0004 NTT5
226326_at	+	0.0001	0.0004
226454_at		0.0001	0.0004 LOC92979
227414_at		0.0001	0.0004 DKFZp547E052
229487_at	*	0.0001	0.0004
229659_s_at		0.0001	0.0004
230245_s_at		0.0001	0.0004
236301_at		0.0001	0.0004
41220_at	+	0.0001	0.0004 MSF
203373_at	+	0.0001	0.0005 STATI2
203753_at		0.0001	0.0005 TCF4
209060_x_at		0.0001	0.0005 NCOA3
210755_at		0.0001	0.0005 HGF
213891_s_at		0.0001	0.0005
216044_x_at		0.0001	0.0005
235674_at	+	0.0001	0.0005
236458_at		0.0001	0.0005
242104_at		0.0001	0.0005

200654_at	+	0.0001	**0.0006** P4HB
203372_s_at	+	0.0001	**0.0006** STATI2
204604_at		0.0001	**0.0006** PFTK1
204951_at	*	0.0001	**0.0006** ARHH
205933_at	+	0.0001	**0.0006** SETBP1
206398_s_at	+	0.0001	**0.0006** CD19
210356_x_at	+	0.0001	**0.0006** MS4A2
217478_s_at	+	0.0001	**0.0006**
217504_at		0.0001	**0.0006** ABCA6
221030_s_at		0.0001	**0.0006** DKFZP564B1162
222146_s_at		0.0001	**0.0006**
222150_s_at		0.0001	**0.0006**
223422_s_at		0.0001	**0.0006** DKFZP564B1162
225144_at		0.0001	**0.0006**
227198_at	*	0.0001	**0.0006**
228377_at	+	0.0001	**0.0006** KIAA1384
228592_at		0.0001	**0.0006**
229194_at		0.0001	**0.0006**
230110_at		0.0001	**0.0006**
230648_at		0.0001	**0.0006**
232112_at		0.0001	**0.0006**
234140_s_at		0.0001	**0.0006** STIM2
235444_at		0.0001	**0.0006**
243798_at		0.0001	**0.0006**
203217_s_at		0.0001	**0.0007** SIAT9
204512_at		0.0001	**0.0007** HIVEP1
205557_at	*	0.0001	**0.0007** BPI
205997_at	+	0.0001	**0.0007** ADAM28
206177_s_at		0.0001	**0.0007** ARG1
206940_s_at	+	0.0001	**0.0007** POU4F1
208914_at		0.0001	**0.0007** GGA2
209101_at		0.0001	**0.0007** CTGF
209169_at		0.0001	**0.0007** GPM6B
209170_s_at	+	0.0001	**0.0007** GPM6B
209765_at	+	0.0001	**0.0007** ADAM19
212481_s_at		0.0001	**0.0007** TPM4
213772_s_at	*	0.0001	**0.0007** GGA2
214238_at		0.0001	**0.0007**
214315_x_at		0.0001	**0.0007** CALR
217418_x_at		0.0001	**0.0007** MS4A2
221004_s_at	+	0.0001	**0.0007** ITM3
223828_s_at		0.0001	**0.0007** LGALS12

224735_at		0.0001	0.0007
225246_at	+	0.0001	0.0007 STIM2
225563_at	+	0.0001	0.0007
226508_at		0.0001	0.0007
226635_at		0.0001	0.0007
227146_at		0.0001	0.0007
227243_s_at		0.0001	0.0007
227407_at	*	0.0001	0.0007
228555_at		0.0001	0.0007
229383_at		0.0001	0.0007
232950_s_at		0.0001	0.0007 NIR3
233955_x_at		0.0001	0.0007 HSPC195
235372_at		0.0001	0.0007 FREB
240572_s_at		0.0001	0.0007
34210_at	+	0.0001	0.0007 CDW52
AFFX-HUMGAPDH/M33197_3_at - HG-U133B	+	0.0001	0.0007 GAPD
203233_at		0.0001	0.0008 IL4R
204882_at		0.0001	0.0008 KIAA0053
206760_s_at		0.0001	0.0008 FCER2
209619_at	*	0.0001	0.0008 CD74
212285_s_at		0.0001	0.0008 AGRN
216095_x_at		0.0001	0.0008 MTMR1
221558_s_at	+	0.0001	0.0008 LEF1
222996_s_at		0.0001	0.0008 HSPC195
226538_at		0.0001	0.0008 MAN2A1
227152_at		0.0001	0.0008
230983_at		0.0001	0.0008
244261_at	+	0.0001	0.0008
64942_at	+	0.0001	0.0008
236787_at	+	0.0001	0.0009
205308_at		0.0001	0.001 LOC51101
208657_s_at		0.0001	0.001 MSF
209772_s_at	*	0.0001	0.001 CD24
209780_at		0.0001	0.001 DKFZP564F013
211126_s_at		0.0001	0.001 CSRP2
213511_s_at		0.0001	0.001
213539_at	+	0.0001	0.001 CD3D
213674_x_at		0.0001	0.001 IGHG3
214651_s_at	*	0.0001	0.001 HOXA9
214686_at		0.0001	0.001 ZNF266

214924_s_at		0.0001	0.001
216379_x_at	+	0.0001	0.001
218354_at		0.0001	0.001 LOC51693
224482_s_at		0.0001	0.001 MGC11316
224772_at	+	0.0001	0.001 MGC14961
227478_at		0.0001	0.001
227767_at		0.0001	0.001 CSNK1G3
228007_at	+	0.0001	0.001
228693_at		0.0001	0.001
230753_at		0.0001	0.001
230802_at		0.0001	0.001 DKFZP564B1162
231656_x_at		0.0001	0.001 OSBPL10
236341_at		0.0001	0.001 CTLA4
239122_at		0.0001	0.001 IL24
38149_at		0.0001	0.001 KIAA0053
200656_s_at	+	0.0001	0.0011 P4HB
204000_at		0.0001	0.0011 GNB5
208623_s_at		0.0001	0.0011 VIL2
210487_at	+	0.0001	0.0011 DNTT
201012_at		0.0001	0.0012 ANXA1
201069_at		0.0001	0.0012 MMP2
201200_at	+	0.0001	0.0012 CREG
201496_x_at	+	0.0001	0.0012 MYH11
201540_at	+	0.0001	0.0012 FHL1
201889_at		0.0001	0.0012 GS3786
202018_s_at	+	0.0001	0.0012 LTF
202709_at		0.0001	0.0012 FMOD
202880_s_at	+	0.0001	0.0012 PSCD1
203020_at		0.0001	0.0012 KIAA0471
203385_at		0.0001	0.0012 DGKA
203556_at		0.0001	0.0012 KIAA0854
203607_at		0.0001	0.0012 SAC2
203757_s_at	+	0.0001	0.0012 CEACAM6
203795_s_at	+	0.0001	0.0012 BCL7A
204199_at		0.0001	0.0012 RALGPS1A
204401_at		0.0001	0.0012 KCNN4
204661_at	*	0.0001	0.0012 CDW52
204674_at		0.0001	0.0012 LRMP
205383_s_at		0.0001	0.0012 ZNF288
205671_s_at		0.0001	0.0012 HLA-DOB
205790_at		0.0001	0.0012 SCAP1
206150_at		0.0001	0.0012 TNFRSF7

206515_at		0.0001	**0.0012** CYP4F3
206759_at		0.0001	**0.0012** FCER2
206871_at	+	0.0001	**0.0012** ELA2
207030_s_at		0.0001	**0.0012** CSRP2
207384_at		0.0001	**0.0012** PGLYRP
207641_at		0.0001	**0.0012** TACI
207957_s_at		0.0001	**0.0012** PRKCB1
208852_s_at	+	0.0001	**0.0012** CANX
209307_at		0.0001	**0.0012** SWAP70
209686_at		0.0001	**0.0012** S100B
209771_x_at	*	0.0001	**0.0012** CD24
210279_at		0.0001	**0.0012** GPR18
210788_s_at	+	0.0001	**0.0012** LOC51635
211105_s_at		0.0001	**0.0012** NFATC1
211341_at	+	0.0001	**0.0012** POU4F1
211657_at	+	0.0001	**0.0012**
212074_at		0.0001	**0.0012** KIAA0810
212314_at		0.0001	**0.0012** KIAA0746
212400_at	*	0.0001	**0.0012**
212509_s_at	+	0.0001	**0.0012**
212614_at		0.0001	**0.0012**
212838_at		0.0001	**0.0012** KIAA1010
214203_s_at		0.0001	**0.0012** PRODH
214786_at	+	0.0001	**0.0012** MAP3K1
215785_s_at	+	0.0001	**0.0012** CYFIP2
216320_x_at	+	0.0001	**0.0012**
217838_s_at		0.0001	**0.0012** RNB6
217979_at	*	0.0001	**0.0012** NET-6
219574_at		0.0001	**0.0012** FLJ20668
220001_at		0.0001	**0.0012** PADI5
220118_at		0.0001	**0.0012** TZFP
220999_s_at		0.0001	**0.0012** PRO1331
221602_s_at		0.0001	**0.0012** TOSO
223522_at		0.0001	**0.0012** GL012
224406_s_at	+	0.0001	**0.0012** IRTA2
224516_s_at		0.0001	**0.0012** HSPC195
224833_at	+	0.0001	**0.0012** ETS1
224918_x_at	+	0.0001	**0.0012** MGST1
224994_at		0.0001	**0.0012** CAMK2D
225230_at		0.0001	**0.0012** CEPT1
225327_at		0.0001	**0.0012** FLJ10980
225512_at		0.0001	**0.0012**

225592_at	+	0.0001	0.0012 NRM
225629_s_at		0.0001	0.0012 KIAA1538
226008_at		0.0001	0.0012 HCA4
226244_at	+	0.0001	0.0012
226408_at		0.0001	0.0012 TEAD2
226550_at		0.0001	0.0012
226878_at	+	0.0001	0.0012
226905_at		0.0001	0.0012
227046_at		0.0001	0.0012 C17orf26
227167_s_at		0.0001	0.0012
227189_at		0.0001	0.0012 KIAA1599
227261_at		0.0001	0.0012 KLF12
227408_s_at		0.0001	0.0012 MSTP043
227533_at		0.0001	0.0012
227607_at		0.0001	0.0012 KIAA1373
227646_at		0.0001	0.0012 EBF
228471_at		0.0001	0.0012
229513_at		0.0001	0.0012
229934_at	+	0.0001	0.0012
231736_x_at	+	0.0001	0.0012 MGST1
231873_at		0.0001	0.0012
232204_at		0.0001	0.0012 EBF
232210_at		0.0001	0.0012
232614_at		0.0001	0.0012
233072_at	+	0.0001	0.0012 KIAA1857
233261_at		0.0001	0.0012
234032_at		0.0001	0.0012
235061_at		0.0001	0.0012
235278_at		0.0001	0.0012
235385_at		0.0001	0.0012 FLJ20668
236190_at		0.0001	0.0012
236265_at		0.0001	0.0012
238057_at		0.0001	0.0012
238376_at		0.0001	0.0012
238587_at		0.0001	0.0012 MGC15437
238790_at		0.0001	0.0012
239231_at		0.0001	0.0012
239278_at	+	0.0001	0.0012
239442_at		0.0001	0.0012
241383_at	+	0.0001	0.0012
241525_at	+	0.0001	0.0012
32541_at		0.0001	0.0012 PPP3CC

74694_s_at		0.0001	**0.0012** FLJ23282
AFFX-HUMGAPDH/M33197_3_at HG-U133A	-	0.0001	**0.0012** GAPD
AFFX-HUMGAPDH/M33197_M_at HG-U133A	-	0.0001	**0.0012** GAPD
201189_s_at		0.0001	**0.0013** ITPR3
201811_x_at	+	0.0001	**0.0013** SH3BP5
201853_s_at		0.0001	**0.0013** CDC25B
202822_at		0.0001	**0.0013** LPP
203288_at		0.0001	**0.0013** KIAA0355
203685_at		0.0001	**0.0013** BCL2
203932_at	+	0.0001	**0.0013** HLA-DMB
205513_at	+	0.0001	**0.0013** TCN1
205614_x_at	+	0.0001	**0.0013** MST1
205863_at	+	0.0001	**0.0013** S100A12
208268_at		0.0001	**0.0013** ADAM28
208306_x_at	+	0.0001	**0.0013** HLA-DRB4
209075_s_at		0.0001	**0.0013** NIFU
209167_at	+	0.0001	**0.0013** GPM6B
209306_s_at		0.0001	**0.0013** SWAP70
210004_at	+	0.0001	**0.0013** OLR1
210448_s_at		0.0001	**0.0013** P2RX5
210658_s_at		0.0001	**0.0013** GGA2
210982_s_at	+	0.0001	**0.0013** HLA-DRA
212382_at		0.0001	**0.0013**
212385_at		0.0001	**0.0013**
212579_at		0.0001	**0.0013** KIAA0650
212970_at		0.0001	**0.0013**
212985_at	+	0.0001	**0.0013**
213353_at	+	0.0001	**0.0013** ABCA5
213453_x_at	+	0.0001	**0.0013** GAPD
215346_at		0.0001	**0.0013** TNFRSF5
216218_s_at		0.0001	**0.0013** PLCL2
218100_s_at		0.0001	**0.0013** ESRRBL1
219734_at		0.0001	**0.0013** FLJ20174
225065_x_at	+	0.0001	**0.0013**
225635_s_at		0.0001	**0.0013**
225640_at		0.0001	**0.0013**
226641_at		0.0001	**0.0013**
227817_at		0.0001	**0.0013**
228029_at		0.0001	**0.0013** KIAA1982
229681_at		0.0001	**0.0013**

230803_s_at		0.0001	**0.0013** DKFZP564B1162
230917_at		0.0001	**0.0013**
231793_s_at		0.0001	**0.0013** CAMK2D
232739_at		0.0001	**0.0013**
235401_s_at		0.0001	**0.0013** FREB
235753_at	+	0.0001	**0.0013**
237411_at		0.0001	**0.0013** LOC153516
238516_at		0.0001	**0.0013** BMPR2
242866_x_at		0.0001	**0.0013**
243030_at		0.0001	**0.0013**
266_s_at	+	0.0001	**0.0013** CD24
35974_at	+	0.0001	**0.0013** LRMP
203057_s_at		0.0001	**0.0014** PRDM2
205105_at		0.0001	**0.0014** MAN2A1
210763_x_at		0.0001	**0.0014** LY117
212569_at		0.0001	**0.0014** KIAA0650
212886_at		0.0001	**0.0014** DKFZP434C171
221331_x_at		0.0001	**0.0014** CTLA4
239292_at		0.0001	**0.0014**
202052_s_at	+	0.0001	**0.0015** RAI14
207734_at		0.0001	**0.0015** FLJ20340
209822_s_at		0.0001	**0.0015** VLDLR
210299_s_at	+	0.0001	**0.0015** FHL1
211771_s_at		0.0001	**0.0015** POU2F2
219090_at		0.0001	**0.0015** SLC24A3
219667_s_at		0.0001	**0.0015** BANK
226258_at		0.0001	**0.0015**
227584_at	+	0.0001	**0.0015**
201061_s_at		0.0001	**0.0017** EPB72
202863_at	+	0.0001	**0.0017** SP100
204069_at	*	0.0001	**0.0017** MEIS1
204118_at		0.0001	**0.0017** CD48
204163_at		0.0001	**0.0017** EMILIN
206245_s_at		0.0001	**0.0017** NS1-BP
208651_x_at	+	0.0001	**0.0017** CD24
209236_at		0.0001	**0.0017**
211796_s_at		0.0001	**0.0017** TRB
212231_at		0.0001	**0.0017** FBXO21
213600_at		0.0001	**0.0017** KIAA0545
218237_s_at	+	0.0001	**0.0017** SLC38A1
218614_at		0.0001	**0.0017** FLJ10652
227606_s_at		0.0001	**0.0017** KIAA1373

230877_at		0.0001	**0.0017** IGHG3
231794_at		0.0001	**0.0017** CTLA4
200068_s_at - HG-U133B		0.0001	**0.0018** CANX
200953_s_at	+	0.0001	**0.0018** CCND2
201810_s_at		0.0001	**0.0018** SH3BP5
202421_at		0.0001	**0.0018** IGSF3
203143_s_at		0.0001	**0.0018** KIAA0040
203355_s_at	+	0.0001	**0.0018** KIAA0942
203796_s_at	+	0.0001	**0.0018** BCL7A
204670_x_at	+	0.0001	**0.0018** HLA-DRB5
204891_s_at		0.0001	**0.0018** LCK
207168_s_at	+	0.0001	**0.0018** H2AFY
207269_at	+	0.0001	**0.0018** DEFA4
208894_at	+	0.0001	**0.0018** HLA-DRA
209827_s_at		0.0001	**0.0018** IL16
211138_s_at		0.0001	**0.0018** KMO
212311_at		0.0001	**0.0018** KIAA0746
214575_s_at	+	0.0001	**0.0018** AZU1
220059_at		0.0001	**0.0018** BRDG1
221234_s_at		0.0001	**0.0018** BACH2
221778_at		0.0001	**0.0018** KIAA1718
221865_at		0.0001	**0.0018**
222477_s_at		0.0001	**0.0018** TM7SF3
224609_at		0.0001	**0.0018** CTL2
225136_at		0.0001	**0.0018**
227242_s_at		0.0001	**0.0018**
228083_at	+	0.0001	**0.0018**
228343_at		0.0001	**0.0018** POU2F2
228551_at		0.0001	**0.0018**
229168_at		0.0001	**0.0018**
230551_at		0.0001	**0.0018**
231332_at		0.0001	**0.0018**
242774_at	+	0.0001	**0.0018** SYNE-2
243154_at	+	0.0001	**0.0018**
243932_at		0.0001	**0.0018**
38269_at	+	0.0001	**0.0018** PKD2
200650_s_at		0.0001	**0.0019** LDHA
201825_s_at		0.0001	**0.0019** LOC51097
205599_at		0.0001	**0.0019** TRAF1
212660_at		0.0001	**0.0019** KIAA0239
219029_at		0.0001	**0.0019** FLJ21657
222520_s_at		0.0001	**0.0019** ESRRBL1

222915_s_at	+	0.0001	**0.0019**	BANK
224520_s_at		0.0001	**0.0019**	MGC13168
227900_at	+	0.0001	**0.0019**	
236796_at		0.0001	**0.0019**	
236979_at	+	0.0001	**0.0019**	
242388_x_at		0.0001	**0.0019**	
242520_s_at		0.0001	**0.0019**	
37831_at		0.0001	**0.0019**	KIAA0545
AFFX-HUMGAPDH/M33197_M_at	-	0.0001	**0.0019**	GAPD
HG-U133B				
205624_at	*	0.0001	**0.002**	CPA3
209369_at		0.0001	**0.002**	ANXA3
214761_at	+	0.0001	**0.002**	OAZ
218531_at		0.0001	**0.002**	FLJ21749
227568_at		0.0001	**0.002**	
230834_at		0.0001	**0.002**	
230986_at		0.0001	**0.002**	
235023_at		0.0001	**0.002**	
235982_at		0.0001	**0.002**	FCRH1
201362_at		0.0001	**0.0021**	NS1-BP
202080_s_at	+	0.0001	**0.0021**	KIAA1042
202606_s_at		0.0001	**0.0021**	TLK1
204205_at		0.0001	**0.0021**	MDS019
204351_at	+	0.0001	**0.0021**	S100P
205223_at		0.0001	**0.0021**	KIAA0645
205414_s_at		0.0001	**0.0021**	KIAA0672
208302_at		0.0001	**0.0021**	HB-1
209365_s_at	*	0.0001	**0.0021**	ECM1
211502_s_at		0.0001	**0.0021**	PFTK1
211883_x_at		0.0001	**0.0021**	CEACAM1
211889_x_at		0.0001	**0.0021**	CEACAM1
212012_at	+	0.0001	**0.0021**	D2S448
213370_s_at		0.0001	**0.0021**	DKFZP434L243
218589_at	+	0.0001	**0.0021**	P2Y5
219221_at		0.0001	**0.0021**	FLJ22332
223321_s_at		0.0001	**0.0021**	FGFRL1
223894_s_at	+	0.0001	**0.0021**	FTS
224811_at		0.0001	**0.0021**	
225019_at		0.0001	**0.0021**	CAMK2D
225917_at		0.0001	**0.0021**	DKFZp762B226
226043_at	+	0.0001	**0.0021**	AGS3
226252_at		0.0001	**0.0021**	

226560_at		0.0001	**0.0021**
227998_at	*	0.0001	**0.0021** MGC17528
229001_at		0.0001	**0.0021**
230689_at		0.0001	**0.0021**
231418_at		0.0001	**0.0021** MS4A2
239054_at		0.0001	**0.0021**
243362_s_at	+	0.0001	**0.0021** LEF1

Table 31a: In total 46 cases of ALL were analyzed. 44 of 46 cases (95.7%) were assigned to the correct ALL subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL t(4;11)	ALL t(8;14)	ALL B not Ph	ALL Ph	T-ALL	total	sensitivity %	specificity %
ALL t(4;11)	9					9	100.00	100.00
ALL t(8;14)		4				4	100.00	100.00
ALL B not Ph			8	1		9	88.89	88.89
ALL Ph			1	14		15	93.33	93.33
T-ALL					9	9	100.00	100.00
total	9	4	9	15	9	46		

Table 31b: In total 184 individual assignments of ALL were analyzed. 182 of 184 assignments (98.9%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL t(4;11)	ALL t(8;14)	ALL B Ph	not ALL Ph	T-ALL	total	sensitivity %	Specificity %
ALL t(4;11)	36					36	100.00	100.00
ALL t(8;14)		16				16	100.00	100.00
ALL B not Ph			35	1		36	97.22	97.22
ALL Ph			1	59		60	98.33	98.33
T-ALL					36	36	100.00	100.00
total	36	16	36	60	36	184		

Table 32: Analysis of 5 ALL subtypes according to the method described by Golub et al.

ALL

	n
ALL t(4;11)	9
ALL t(8;14)	4
ALL B not Ph	9
ALL Ph	15
T-ALL	9

ALL t(4;11) vs. all other	samples: 9 / 37			
Accuracy	1			
Confidence	1			
Gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
219033_at	3.20704240055607	0*	2553.55	FLJ21308
219463_at	2.92935553285382	0		C20orf103
204069_at	2.82114201903624	0		MEIS1
237431_at	2.55145965416011	0		
205899_at	2.08001706361176	0		CCNA1
221969_at	2.05226504657001	0		PAX5
225592_at	1.98551092155834	0		NRM
242414_at	1.90103345468382	0		
225563_at	1.85734510779608	0		
201105_at	1.84845429911833	0		LGALS1
243756_at	1.82938790694615	0		
213894_at	1.79258061939732	0		KIAA0960
215925_s_at	1.74909667158721	0		
228083_at	1.74681828228852	0		
204044_at	1.72555848313614	0		QPRT
209170_s_at	1.69865585409382	0		GPM6B
209168_at	1.67497314565832	0		GPM6B
210934_at	1.66143224232084	0		BLK
238750_at	1.59639718466905	0		
224681_at	1.58202928459614	0		GNA12

ALL t(4;11) vs. ALL t(8;14)	samples: 9 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210045_at	6.76734853184964	0*	142.15	IDH2
240106_at	6.10571301118426	0		
202853_s_at	-5.88804457870992	0		RYK
242434_at	-5.60754470569171	0		
237431_at	5.31661820706767	0		
201540_at	4.94655082712075	0		FHL1
215855_s_at	4.71299810202736	0		
212357_at	4.18767818184794	0		KIAA0280
204798_at	4.12313508850913	0		MYB
226795_at	4.12248256776444	0		
77508_r_at	4.0317985345148	0		FLJ23282
46142_at	3.95748459279267	0		FLJ12681
225277_at	3.7552029934786	0		
210934_at	3.72127171897839	0		BLK
215537_x_at	3.53324247477066	0		
232201_at	3.50091671488931	0		NKD2
214505_s_at	3.42260996379197	0		FHL1
244261_at	3.40910490910101	0		
208614_s_at	3.34565043119022	0		FLNB
210298_x_at	3.30171221592859	0		FHL1

ALL t(4;11) vs. ALL B not Ph	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
237431_at	5.31661820706767	0*	49	
219033_at	3.19032095561144	0		FLJ21308
219463_at	2.69567768562793	0		C20orf103
204069_at	2.54127866831197	0		MEIS1
201105_at	2.30596776500018	0		LGALS1
200907_s_at	2.19034049161844	0		KIAA0992
242414_at	2.08870062415486	0		
222492_at	-2.04226084466602	0		FLJ21324
230441_at	-2.03717805375485	0		
235291_s_at	2.0210425168076	0		
225592_at	2.01329642963674	0		NRM
200906_s_at	1.9632986862999	0		
201153_s_at	1.93254941630797	0		MBNL
201152_s_at	1.93227192981893	0		MBNL
241985_at	-1.91875000661653	0		
213894_at	1.89533012552966	0		KIAA0960
243756_at	1.82938790694615	0		
225563_at	1.82046495626766	0		
232231_at	1.8138577510169	0		
240581_at	1.80942575017411	0		

ALL t(4;11) vs. ALL Ph	samples: 9 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204069_at	3.31118886883646	0*	482.55	MEIS1
219033_at	3.24786485857293	0		FLJ21308
219463_at	2.78353259146178	0		C20orf103
221969_at	2.4416835946504	0		PAX5
201874_at	2.38057857279198	0		FLJ21047
209170_s_at	2.31526351178702	0		GPM6B
233500_x_at	2.23629715560156	0		LLT1
205899_at	2.23375311954146	0		CCNA1
242414_at	2.21567202901383	0		
205821_at	2.10144186601662	0		D12S2489E
205055_at	2.04951650013049	0		ITGAE
209168_at	2.02899949049115	0		GPM6B
226939_at	1.99568402107224	0		
209354_at	-1.9938191217443	0		TNFRSF14
200906_s_at	1.9632986862999	0		
225563_at	1.88712595721941	0		
237431_at	1.87880985981148	0		
34210_at	-1.86187594200254	0		CDW52
202853_s_at	-1.84984316383277	0		RYK
209167_at	1.84829764568262	0		GPM6B

ALL t(4;11) vs. T-ALL	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221969_at	5.83664657385464	0*	1301	PAX5
237431_at	5.31661820706767	0		
213772_s_at	4.80540935532116	0		GGA2
219463_at	3.9253737114322	0		C20orf103
210934_at	3.72127171897839	0		BLK
242292_at	-3.53231266693437	0		
226496_at	3.49024496949904	0		
244261_at	3.40910490910101	0		
205640_at	3.04306419050975	0		ALDH3B1
219033_at	3.03434195473282	0		FLJ21308
209168_at	3.02932118514235	0		GPM6B
205821_at	2.9956567374574	0		D12S2489E
235706_at	2.99518505957364	0		CPM
225592_at	2.98114633774562	0		NRM
225314_at	-2.87525509857994	0		
209170_s_at	2.832580891342	0		GPM6B
215925_s_at	2.79328349720245	0		
204069_at	2.67025815490556	0		MEIS1
210192_at	2.63764031456982	0		ATP8A1
217080_s_at	2.60699026264913	0		HOMER-2B

ALL t(8;14) vs. all other	samples: 4 / 42			
accuracy	1			
confidence	0.920758831240362			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225277_at	-2.57998811180236	0		
228211_at	-2.14623380341388	0*	20.8	
202249_s_at	-1.96332308011424	0*	1	H326
221834_at	-1.9031437121116	0		
202262_x_at	-1.89325979398387	0		DDAH2
215537_x_at	-1.86843810729553	0		
209253_at	-1.83062488265555	0		SCAM-1
218836_at	1.75015142111032	0*	431.25	FLJ22638
201540_at	-1.7433648326086	0		FHL1
203373_at	-1.73135591115253	0		STATI2
212357_at	-1.70867340748188	0		KIAA0280
229061_s_at	1.637709601518	0		SLC25A13
211540_s_at	-1.62480264702951	0		RB1
213639_s_at	-1.6005915843515	0		KIAA0557
207971_s_at	-1.60022833182646	0		KIAA0582
202328_s_at	-1.58949139934067	0		PKD1
236019_at	-1.57756633888103	0		
36612_at	-1.57219062906198	0		KIAA0280
211031_s_at	-1.56936126526028	0		CYLN2

ALL t(8;14) vs. ALL B not Ph	samples: 4 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
231567_s_at	-2.72106559758946	0*	34.3	TSP-NY
225277_at	-2.51129165288142	0		
236019_at	-2.39137207272003	0		
239835_at	2.1931044914088	0		KIAA1842
235287_at	-2.11679606735121	0.01		
221834_at	-2.07908926017389	0.01		
224221_s_at	-2.01560021968657	0.01		VAV3
202249_s_at	-2.00760725399781	0		H326
222275_at	-1.99241461922196	0.01		
231181_at	1.9495774287402	0		
202137_s_at	-1.92788330147706	0.01		BS69
212535_at	-1.92074458469524	0.01		
244230_at	-1.90852603079528	0		
215622_x_at	1.89164878686732	0.01		HSPC226
233813_at	-1.8799760260639	0.01		
209891_at	1.87886429835728	0		AD024
203373_at	-1.86193326506748	0		STATI2
213504_at	1.8188709452285	0		MOV34-34KD
237006_at	-1.7948046900018	0.02		
AFFX-r2-Hs18SrRNA-M_x_at - HG-U133B	1.2766621379286	0.01		

ALL t(8;14) vs. ALL Ph	samples: 4 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204663_at	-3.923285216392	0*	80.55	ME3
203373_at	-3.79361888147031	0		STATI2
207971_s_at	-3.75632756767036	0		KIAA0582
221834_at	-3.73210732395713	0		
212535_at	-3.35180803492209	0		
210487_at	-2.66400596339357	0		DNTT
226607_at	-2.65303285070543	0		L3MBTL
214505_s_at	-2.30002142127038	0		FHL1
226545_at	-2.26350222846019	0		
201540_at	-2.21889045310099	0		FHL1
209253_at	-2.17983750831107	0		SCAM-1
228496_s_at	-2.17784383479245	0		CRIM1
213854_at	-2.14963630962421	0		SYNGR1
228211_at	-2.14770747938169	0		
212012_at	-2.10857376713896	0		D2S448
208217_at	-2.10769716540219	0		GABRR2
202519_at	-2.05798709970069	0		MONDOA
218836_at	2.05747195088222	0		FLJ22638
211031_s_at	-2.05686503189171	0		CYLN2
50277_at	1.4804958933411	0		GGA1

ALL t(8;14) vs. T-ALL	samples: 4 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
213772_s_at	4.99941703918842	0*	105.35	GGA2
236019_at	-4.8835710129593	0.01		
225277_at	-4.63399536600695	0		
40148_at	3.56542456382539	0.01		APBB2
228211_at	-3.35861431980337	0.01		
201334_s_at	3.32612092220108	0		ARHGEF12
201417_at	-2.74359054965603	0		
206241_at	-2.66958809534806	0		KPNA5
208918_s_at	2.59071326340578	0		FLJ13052
210038_at	-2.55792113825771	0		
225735_at	-2.54773299400117	0		
209253_at	-2.33749346955264	0		SCAM-1
202262_x_at	-2.29867528817227	0		DDAH2
225129_at	2.29232308514395	0.01		MDS026
221969_at	2.278395672233	0		PAX5
225080_at	2.24115131588386	0.01		MYO1C
218338_at	-2.22116851483018	0.01		EDR1
208664_s_at	-2.20362132175544	0.01		TTC3
201029_s_at	-2.14618908100153	0		MIC2
56256_at	1.43796973813133	0		LOC51092

ALL B not Ph vs. all other	samples: 9 / 37			
accuracy	0.934782608695652			
confidence	0.902657186900126			
failed:	5,7,8			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
219358_s_at	-1.04393215326702	0.01*	1	CENTA2
220744_s_at	-1.00349163214942	0*	1	WDR10
203808_at	-0.907795727801968	0		AKT2
243228_at	0.879849065993121	0		
218517_at	-0.867959639957627	0		FLJ22479
226646_at	0.864565503015451	0*	490.45	KLF2
224739_at	0.839978529078003	0		MG61
219036_at	-0.833911794382181	0		BITE
218464_s_at	-0.832082954669612	0.01		FLJ10700
211953_s_at	-0.830459962940188	0		KPNB3
241383_at	-0.819553908934904	0		
207403_at	-0.812859958493534	0		IRS4
210519_s_at	-0.801666674223177	0		
214144_at	-0.796475066163317	0		POLR2D
209135_at	-0.787608359617365	0		ASPH
218543_s_at	0.773154455437408	0*	765.05	FLJ22693
34210_at	0.555729083194618	0		CDW52

ALL B not Ph vs. ALL Ph	samples: 9 / 15			
accuracy	0.916666666666667			
confidence	1			
failed:	3,18			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
219358_s_at	-1.52735607926994	0		CENTA2
241383_at	-1.07499870203752	0.01		
213895_at	-1.05505220750298	0		EMP1
202123_s_at	-1.02481061931947	0*	753.7	ABL1
205911_at	-1.0236634987836	0.01		PTHR1
242223_at	1.02343172223498	0.01		
211709_s_at	-1.01491744255679	0		SCGF
234839_at	-1.00185285072786	0		
212150_at	-0.996731200580515	0		KIAA0143
221991_at	-0.987741661696868	0		NXPH3
218543_s_at	0.973909033712243	0		FLJ22693
201874_at	0.966766364385792	0		FLJ21047
212188_at	-0.947998533949464	0		LOC115207
207520_at	-0.936622132674122	0		
213979_s_at	-0.935519171149617	0		CTBP1
229745_x_at	-0.93424475879621	0		
216680_s_at	-0.934196756237652	0.01		EPHB4
202572_s_at	0.924395823520243	0		KIAA0964
243228_at	0.916138491705783	0		

ALL B not Ph vs. T-ALL	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
242292_at	-3.53231266693437	0*	19.4	
36566_at	2.04687603382912	0		CTNS
230636_s_at	1.96129371358941	0		BTEB1
266_s_at	1.95685220231101	0		CD24
209771_x_at	1.95325312023269	0		CD24
219631_at	-1.90940390225071	0		FLJ12929
202113_s_at	1.86969444770264	0		SNX2
216379_x_at	1.84446878357139	0		
221969_at	1.82924887172424	0		PAX5
229487_at	1.78170685853126	0		
208650_s_at	1.77571318786079	0		CD24
218464_s_at	-1.71465707824422	0		FLJ10700
213944_x_at	1.69297405468728	0		
226496_at	1.65125933296341	0		
202206_at	-1.58502966518677	0		ARL7
205504_at	1.58481348793145	0		BTK
213539_at	-1.56405807954932	0		CD3D
211101_x_at	1.55958748994576	0		LILRA2
244876_at	1.55727218904507	0		
209772_s_at	1.54041193817483	0		CD24

ALL Ph vs. all other	samples: 15 / 31			
accuracy	0.934782608695652			
confidence	0.864155721068077			
failed:	5,11,37			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
202123_s_at	1.03184989278993	0		ABL1
201874_at	-0.922781388634418	0		FLJ21047
204501_at	0.896802057215648	0		NOV
212998_x_at	0.86615498180542	0		HLA-DQB1
224833_at	-0.858830478869203	0*	396.95	ETS1
222154_s_at	0.853355151564312	0		DKFZP564A2416
222237_s_at	0.842490839365056	0		
231887_s_at	0.818989313012035	0		KIAA1274
206995_x_at	0.814915994355934	0		SREC
206940_s_at	0.805187827741759	0		POU4F1
228737_at	-0.794850815744375	0		C20orf100
214321_at	0.787185980142624	0		NOV
212365_at	0.782772195022069	0		MYO1B
204030_s_at	0.779040391109499	0		SCHIP1
207971_s_at	0.777645713400436	0		KIAA0582
224772_at	0.777324945979331	0		MGC14961
230659_at	0.775582345606179	0		KIAA0212
214051_at	-0.763853883412362	0		TMSNB
231897_at	0.756283108145232	0		
206302_s_at	0.754443263514809	0		NUDT4

ALL Ph vs. T-ALL	samples: 15 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
218224_at	-2.4418494296856	0		PNMA1
213854_at	2.14963630962421	0		SYNGR1
221969_at	2.06978634038245	0*	152.35	PAX5
205101_at	1.84182814954198	0		MHC2TA
213539_at	-1.83994967875006	0		CD3D
228988_at	-1.79658055608971	0		ZNF6
208894_at	1.79489847703276	0		HLA-DRA
209604_s_at	-1.75648531255811	0		GATA3
209619_at	1.72743796589982	0		CD74
209771_x_at	1.69086499548436	0		CD24
210982_s_at	1.68104679025052	0		HLA-DRA
229487_at	1.66237077940113	0		
235706_at	1.65050775066494	0		CPM
226878_at	1.64629305544324	0		
219631_at	-1.6447182870532	0		FLJ12929
216379_x_at	1.61950446576807	0		
232234_at	-1.6009007845449	0		C20orf24
210116_at	-1.58593866198308	0		SH2D1A
224772_at	1.58464619249453	0		MGC14961
213944_x_at	1.58085800202538	0		

T-ALL vs. all other	samples: 9 / 37			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
218224_at	1.9746486763803	0		PNMA1
219631_at	1.74096689257481	0		FLJ12929
213539_at	1.72260640123424	0		CD3D
209771_x_at	-1.54682027770245	0		CD24
216379_x_at	-1.50086383881878	0		
208894_at	-1.4723749670674	0		HLA-DRA
206804_at	1.44192284369386	0		CD3G
266_s_at	-1.41281622043848	0		CD24
232234_at	1.4114153057648	0		C20orf24
210982_s_at	-1.40110964085237	0		HLA-DRA
213772_s_at	-1.38475219732458	0		GGA2
235706_at	-1.37948942896001	0		CPM
206398_s_at	-1.37387052076155	0		CD19
242292_at	1.3716037079612	0		
228988_at	1.36889729345744	0		ZNF6
221969_at	-1.35174546838558	0*	149.65	PAX5
202113_s_at	-1.32897344000246	0		SNX2
202746_at	1.32364323412114	0		
226496_at	-1.30740184360227	0		

Table 33: Analysis of 5 ALL subgroups according to the method described by Westfall & Young. The 23 significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

geneID	Golub	rawp	adjp	Gene symbol
219463_at	+	0.0001	**0.0042**	C20orf103
204069_at	*	0.0001	**0.0046**	MEIS1
219033_at	*	0.0001	**0.0051**	FLJ21308
221969_at	*	0.0001	**0.0071**	PAX5
205899_at	+	0.0001	**0.0081**	CCNA1
237431_at	*	0.0001	**0.0088**	
242414_at	+	0.0001	**0.0091**	
225563_at	+	0.0001	**0.0122**	
215925_s_at	+	0.0001	**0.0157**	
209168_at	+	0.0001	**0.0168**	GPM6B
204044_at	+	0.0001	**0.0170**	QPRT
225592_at	+	0.0001	**0.0174**	NRM
228083_at	+	0.0001	**0.0179**	
218224_at	+	0.0001	**0.0190**	PNMA1
213539_at	+	0.0001	**0.0195**	CD3D
213894_at	+	0.0001	**0.0197**	KIAA0960
201105_at	+	0.0001	**0.0199**	LGALS1
219631_at	+	0.0001	**0.0199**	FLJ12929
209170_s_at	+	0.0001	**0.0201**	GPM6B
243756_at	+	0.0001	**0.0214**	
209822_s_at		0.0001	**0.0254**	VLDLR
228988_at	+	0.0001	**0.0454**	ZNF6
235749_at		0.0002	**0.0477**	

Table 34a: In total 173 cases of AML were analyzed. 160 of 174 cases (92.5%) were assigned to the correct AML subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	+8	other	complex	normal	t(8;21)	t(15;17)	inv(16)	MLL	total	sensitivity %	specificity %
+8	6			4					10	60.00	100.00
other		3	1	1					5	60.00	100.00
complex			33	3					36	91.67	94.29
normal			1	59				2	62	95.16	85.51
t(8;21)					13				13	100.00	100.00
t(15;17)						20			20	100.00	100.00
inv(16)							12		12	100.00	100.00
MLL				2				13	15	86.67	86.67
total	6	3	35	69	13	20	12	15	173		

Table 34b: In total 1211 individual assignments of AML were analyzed. 1198 of 1211 assignments (98.9%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

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	+8	other	complex	normal	t(8;21)	t(15;17)	inv(16)	MLL	total	sensitivity %	specificity %
+8	66			4					70	94.29	100.00
other		33	1	1					35	94.29	100.00
complex			249	3					252	98.81	99.20
normal			1	432				2	434	99.54	97.74
t(8;21)					91				91	100.00	100.00
t(15;17)						140			140	100.00	100.00
inv(16)							84		84	100.00	100.00
MLL				2				103	105	98.10	98.10
total	66	33	251	442	91	140	84	105	1211		

Table 35: Analysis of 8 AML subtypes according to the method described by Golub et al.

AML subtype	n
trisomy 8	10
other aberrant	5
complex	36
normal	62
t(8;21)	13
t(15;17)	20
inv(16)	12
MLL	15

trisomy 8 vs. all other	samples: 10 / 163			
accuracy	0.959537572254335			
confidence	0.569726638054273			
failed:	1,2,9,10,32,44,50			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214394_x_at	1.01312549146188	0		FLJ20897
222166_at	-0.966941507782627	0		
242975_s_at	-0.84543459151348	0		GNAS
218549_s_at	0.837748897801293	0*	1095.85	LOC51115
218642_s_at	0.837443970437429	0		MGC2217
212250_at	0.837142769828465	0		
203110_at	0.812826558097073	0		PTK2B
219518_s_at	-0.798960392573077	0.01		FLJ22637
237068_at	-0.76378369742971	0		
206781_at	-0.759613817823006	0		DNAJC4
224804_s_at	-0.756694932705637	0.01		FLJ00005
235647_at	-0.746385695306755	0*	1	
203007_x_at	0.741371207542559	0		
212449_s_at	0.729872362915738	0		LYPLA1
231981_at	0.722528507843912	0*	199.8	
218482_at	0.71984358195818	0		DC6
224076_s_at	0.717538242394189	0		WHSC1L1
231101_at	-0.7149698250145	0		PPP2R5E

trisomy 8 vs. other aberrant	samples: 10 / 5			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
229848_at	-2.61497492874017	0*	36.7	ZNF10
239538_at	-2.22698957925109	0		
230713_at	-2.16807291296049	0		
209490_s_at	-2.08613392690798	0		PPT2
229362_at	-2.0821284659189	0		
225073_at	-2.06488846603302	0		HSPC232
239699_s_at	-2.02729155150144	0		
242363_at	-1.94643377690021	0		
201974_s_at	-1.88600099933531	0		LOC51622
219027_s_at	-1.86639067868364	0		MYO9A
234643_x_at	1.78480980429735	0		
236837_x_at	-1.7783166983573	0		
226783_at	-1.75409747751331	0		
238039_at	-1.74203897189399	0.01		
224044_at	-1.72117511206513	0.01		FLJ11040
226324_s_at	-1.71772128724622	0		SLB
227587_at	-1.71651011254536	0		MGC15906
229637_at	-1.71361022272893	0.01		
227744_s_at	-1.70786273052662	0		HNRPD
635_s_at	1.25062226167699	0		PPP2R5B

trisomy 8 vs. complex	samples: 10 / 36			
accuracy	1			
confidence	0.855027999708228			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
222229_x_at	1.23332137897808	0		
208697_s_at	1.15066098039301	0		EIF3S6
205849_s_at	1.14869307530221	0		UQCRB
212586_at	1.11153173777253	0*	1231.4	ARTS-1
208646_at	1.07422424644875	0		
230795_at	-1.06732853628123	0		H4F2
202746_at	-1.03422849717783	0		
226545_at	-1.00972156245463	0*	100.15	
222166_at	-0.999828982909011	0*	1	
210715_s_at	-0.978857795907469	0*	573.3	SPINT2
228652_at	-0.974511468277957	0		
217979_at	-0.973647566321829	0*	234.35	NET-6
201548_s_at	-0.970651188910704	0*	289.85	PLU-1
202747_s_at	-0.952100249128964	0		ITM2A
201602_s_at	-0.951073671804128	0		PPP1R12A
205674_x_at	-0.945871996779656	0		FXYD2
244740_at	-0.942099475768156	0		
219518_s_at	-0.938970502867646	0		FLJ22637
227249_at	-0.931085853722028	0		NUDE1

trisomy 8 vs. normal	samples: 10 / 62			
accuracy	0.944444444444444			
confidence	1			
failed:	1,2,3,5			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214394_x_at	1.16270137582694	0		FLJ20897
235124_at	-1.01432223685267	0		
203007_x_at	0.983414984588329	0		
206781_at	-0.970185909793454	0		DNAJC4
242975_s_at	-0.968085578079267	0		GNAS
203110_at	0.964568800558985	0		PTK2B
212251_at	0.940237396721025	0*	4073.8	
225406_at	-0.932943214378223	0		TSG
234726_s_at	-0.900642735364519	0		
218482_at	0.893526812115568	0		DC6
237291_at	-0.889981273455646	0		
235647_at	-0.884166779739501	0		
236837_x_at	-0.866101703732076	0.01		
222166_at	-0.864343877506541	0		
225889_at	-0.864142405574917	0		
217994_x_at	-0.85609014416877	0		
203602_s_at	-0.841071963439903	0		ZNF151
228092_at	-0.837138335753897	0		
224804_s_at	-0.83110664616695	0		FLJ00005
212250_at	0.827294640416809	0		

trisomy 8 vs. t(8;21)	samples: 10 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228827_at	-2.03460798747208	0*	162.15	
203188_at	1.98171895993959	0		B3GNT6
209522_s_at	1.87499941760774	0		CRAT
50221_at	1.77237042593137	0		
212586_at	1.70313290894867	0		ARTS-1
217816_s_at	1.69811663165145	0		pcnp
219084_at	1.68534097481951	0		NSD1
241370_at	1.66453119103938	0		
221581_s_at	1.64609943226078	0		WBSCR5
205528_s_at	-1.64467496425566	0		CBFA2T1
211341_at	-1.63310072579237	0		POU4F1
212250_at	1.62854737716103	0		
206940_s_at	-1.60737424398258	0		POU4F1
205529_s_at	-1.591491111654	0		CBFA2T1
213150_at	1.57881564631984	0		HOXA10
214394_x_at	1.57039311243451	0		FLJ20897
212895_s_at	1.56878968456679	0		ABR
218341_at	1.53928870336148	0		FLJ11838
204249_s_at	1.52597204656408	0		LMO2
214651_s_at	1.52240931149048	0		HOXA9

trisomy 8 vs. t(15;17)	samples: 10 / 20			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214450_at	-3.0865086945171	0*	1926.7	CTSW
212953_x_at	-2.71319553382926	0		CALR
236787_at	-2.4273500798775	0		
200952_s_at	-2.39696270141848	0		CCND2
205624_at	-2.38480346275743	0		CPA3
38487_at	-2.38251622694176	0		FLJ12442
205614_x_at	-2.24846130719191	0		MST1
206761_at	-2.20501899975366	0		TACTILE
216320_x_at	-2.16690689445934	0		
224794_s_at	-2.14479331910386	0		LOC51148
233072_at	-2.07721746169547	0		KIAA1857
221004_s_at	-2.05892662897696	0		ITM3
227326_at	-2.04924504239987	0		
221980_at	-2.01752809990056	0		
225547_at	1.98126007880124	0		
210145_at	1.95455412087558	0		PLA2G4A
212509_s_at	-1.92046303571342	0		
209344_at	-1.90906303754685	0		TPM4
201029_s_at	-1.87538506046111	0		MIC2

trisomy 8 vs. inv(16)	samples: 10 / 12			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233138_at	-3.4735123827114	0*	54.25	
209365_s_at	-3.00986865470169	0		ECM1
202283_at	-2.6160707896185	0		SERPINF1
218942_at	2.45751904192227	0		FLJ22055
201828_x_at	2.21365274281998	0		CXX1
200951_s_at	-2.02357943949022	0		CCND2
226120_at	2.01082485261142	0		LOC123016
203188_at	1.9379696222037	0		B3GNT6
202085_at	1.9147903697218	0		TJP2
206135_at	-1.90877055638373	0		KIAA0535
210024_s_at	1.90335978018863	0		UBE2E3
204661_at	-1.83776082826379	0		CDW52
241525_at	-1.83006374766269	0		
208710_s_at	1.80896001968559	0		AP3D1
34210_at	-1.75572696362264	0		CDW52
201497_x_at	-1.74852845185764	0		MYH11
212236_x_at	-1.74679406476776	0		
213810_s_at	-1.69077455623534	0		FLJ10342
212250_at	1.62885302351785	0		
202370_s_at	1.61951331078439	0		CBFB

trisomy 8 vs. MLL	samples: 10 / 15			
accuracy	1			
confidence	0.8689072208975			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
200056_s_at - HG-U133A	1.60303643777462	0		C1D
212250_at	1.47262825515036	0		
228024_at	1.43968630786794	0		PAK1
205355_at	1.39534301157978	0		ACADSB
225700_at	1.39419450937928	0		
234726_s_at	-1.36257922965513	0		
202619_s_at	1.34323877280623	0		PLOD2
205453_at	1.29520111839967	0		HOXB2
202823_at	1.28255326311509	0		TCEB1
210749_x_at	1.26893758929818	0		DDR1
227786_at	1.24020773870069	0		TRAP25
212479_s_at	1.23922427261637	0*	437.3	FLJ13910
219312_s_at	1.21983738431425	0		RINZF
218172_s_at	1.21403337241271	0*	285.95	PRO2577
200867_at	1.2110165320696	0*	531	
202956_at	1.21043821718201	0*	550.6	BIG1
213902_at	1.19710457307816	0		ASAH
239597_at	-1.19444081572455	0		
214789_x_at	1.19367799101574	0		SRP46
203053_at	1.18683041233911	0		BCAS2

other aberrant vs. all other	samples: 5 / 168			
accuracy	0.994219653179191			
confidence	0.899486235418654			
failed:	4			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233328_x_at	-1.52904798962408	0.01		
219156_at	1.27140814977495	0		FLJ11271
214310_s_at	-1.27139871979195	0		ZFPL1
229003_x_at	-1.20449873883071	0		
213725_x_at	1.1911680827765	0		
236648_at	1.15777539407154	0*	1	
226634_at	1.15695756502745	0		
224664_at	1.14829275512581	0		
219337_at	-1.09306764196133	0		FLJ20584
228660_x_at	1.09254562955252	0*	82	SEMA4F
217375_at	-1.08474018637782	0		
219027_s_at	1.0790791377144	0		MYO9A
239538_at	1.07873188809285	0		
203796_s_at	1.04936325547633	0		BCL7A
211918_x_at	-1.04651632950823	0.01		PLAC3
241795_at	-1.04488187252	0		
222147_s_at	-1.02048867081398	0.01		
227206_at	-1.01633702093738	0.01		
635_s_at	-1.01612668262432	0		PPP2R5B

other aberrant vs. complex	samples: 5 / 36			
accuracy	0.975609756097561			
confidence	0.990141898103344			
failed:	2			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225804_at	1.56382089574999	0		
211819_s_at	-1.45297162934509	0*	1	SH3D5
233328_x_at	-1.44097598487297	0*	1	
229003_x_at	-1.40901327014506	0*	1	
223712_at	1.36997409793585	0		DCOHM
635_s_at	-1.34942029903122	0		PPP2R5B
231002_s_at	1.3258291286036	0		NUP88
241734_at	1.32533459318655	0		
201530_x_at	1.3093371019822	0		EIF4A1
211918_x_at	-1.30264105037178	0.01		PLAC3
222229_x_at	1.214222183319	0		
231945_at	-1.2091074222176	0.01		KIAA1275
202150_s_at	-1.2052224977219	0		HEF1
212171_x_at	-1.20353762848401	0		VEGF
214310_s_at	-1.19546833367549	0		ZFPL1
219337_at	-1.19331909893746	0		FLJ20584
235263_at	1.19244840508646	0		DKFZP434A0131
233195_at	-1.19077762820993	0		
210817_s_at	1.17387606136153	0		NDP52

other aberrant vs. normal	samples: 5 / 62			
accuracy	0.985074626865672			
confidence	0.991986319540221			
failed:	4			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233328_x_at	-1.9106472582954	0*	1	
220924_s_at	1.36395677335271	0		SLC38A2
213725_x_at	1.33852421412964	0*	1096.35	
229003_x_at	-1.33766416205182	0		
207057_at	1.32428111403211	0		SLC16A7
239393_at	1.30248902092406	0		
218041_x_at	1.28800254801096	0		PRO1068
219156_at	1.27488096632736	0		FLJ11271
227206_at	-1.24583383572442	0		
217375_at	-1.22806408433652	0.01		
219337_at	-1.22223242666913	0.01		FLJ20584
214894_x_at	1.21435713598714	0		MACF1
225452_at	1.19358949672009	0		PPARBP
205316_at	1.18925500392873	0		SLC15A2
212469_at	1.17704907364629	0		IDN3
214310_s_at	-1.176580899867	0.01		ZFPL1
226634_at	1.15416325511173	0		
234132_at	-1.14588852496026	0.01		
215115_x_at	-1.14294381059057	0		NTRK3
45633_at	0.924726636126963	0		FLJ13912

other aberrant vs. t(8;21)	samples: 5 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221770_at	7.99150022255116	0*	55.8	RPE
205607_s_at	5.76670522441814	0		LOC57147
225670_at	3.48256305910835	0		
34689_at	3.47855359314813	0		TREX1
203796_s_at	3.25650613162099	0		BCL7A
226634_at	3.21064553321956	0		
232127_at	2.70698092772246	0.01		
200659_s_at	2.68716126436031	0		PHB
202288_at	2.6425819500005	0		FRAP1
234005_x_at	2.64219114616805	0		STK36
212309_at	2.52957598578167	0		CLASP2
221206_at	2.4774418396665	0		FLJ21459
222163_s_at	2.44259488401336	0		MGC5347
210128_s_at	2.40486023166818	0		LTB4R
242448_at	2.40485463677367	0		
212895_s_at	2.38453513890117	0		ABR
213313_at	2.35617502073221	0		GAPCENA
220796_x_at	2.33914050862301	0		FLJ14251
242363_at	2.29793881298951	0		
225902_at	2.28202551140514	0		

other aberrant vs. t(15;17)	samples: 5 / 20			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
213716_s_at	5.68177086653034	0*	124.75	SECTM1
235483_at	3.71724867723655	0		
224664_at	3.45875495264879	0		
214310_s_at	-3.345175974803	0		ZFPL1
38487_at	-3.26848789132101	0		FLJ12442
210128_s_at	3.21387420114625	0		LTB4R
214450_at	-3.16199946091496	0		CTSW
209428_s_at	-2.91976796793381	0		ZFPL1
233328_x_at	-2.90760586187832	0		
201034_at	2.88463519708491	0		ADD3
212953_x_at	-2.71444362815032	0		CALR
201753_s_at	2.7070306360752	0		ADD3
208629_s_at	-2.67288815920275	0		HADHA
205668_at	2.67287531876386	0		LY75
229937_x_at	2.57076096076482	0		
227701_at	2.49972617912329	0		
203948_s_at	-2.49051133555807	0		MPO
219280_at	2.49000744284001	0		WDR9
227999_at	2.46891417509171	0		LOC170394

other aberrant vs. inv(16)	samples: 5 / 12			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
227224_at	4.52730002135185	0*	67.25	
212469_at	4.42589960567721	0		IDN3
229003_x_at	-3.90005268853897	0		
239538_at	3.74361173339624	0		
216399_s_at	3.5206821287331	0		
223471_at	3.22276962259045	0		
201338_x_at	3.16855282128268	0		GTF3A
231926_at	3.15052042879849	0		
202370_s_at	3.09376701617797	0		CBFB
224664_at	3.04111626168471	0		
204858_s_at	-2.96720397750981	0		ECGF1
227701_at	2.92458695035083	0		
212686_at	2.82379160235424	0		KIAA1157
242525_at	2.80598603189029	0		
211824_x_at	-2.77113099215966	0		DEFCAP
218259_at	2.6673432505011	0		KIAA1243
229848_at	2.61497492874017	0		ZNF10
238791_at	2.55305211995074	0		
212287_at	2.52556127587716	0		JJAZ1
205055_at	2.49589801203404	0		ITGAE

other aberrant vs. MLL	samples: 5 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
232125_at	2.83634822109321	0*	10.45	
222335_at	2.80079072544706	0		
203593_at	2.50443810972067	0		CD2AP
220924_s_at	2.44940338874045	0		SLC38A2
234584_s_at	2.36473818619324	0		ATE1
228328_at	2.2823093126082	0		
203177_x_at	2.20405255989013	0		TFAM
218041_x_at	2.19960407203391	0		PRO1068
222982_x_at	2.1705009156018	0		SLC38A2
240201_at	2.17038421694015	0		
223401_at	2.1574569971375	0		MDS006
207057_at	2.10339239461692	0		SLC16A7
218499_at	2.08679728034545	0		MST4
231926_at	2.03322303603834	0		
202926_at	2.01182753157743	0		NAG
216399_s_at	1.98784990984825	0		
212549_at	1.98266739917742	0		
203897_at	1.95412833774499	0		LOC57149
226741_at	1.94025028754913	0		LOC51234
243154_at	1.93816368688103	0		

complex vs. all other	samples: 36 / 137			
accuracy	0.936416184971098			
confidence	0.914058016154132			
failed:	2,5,9,12,14,19,23,26,30,32,36			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
222229_x_at	-0.977113333847485	0		
223318_s_at	-0.871134323886282	0		MGC10974
200608_s_at	0.859861630456657	0*	1754.85	RAD21
209085_x_at	0.827754504723174	0*	543.85	RFC1
201377_at	0.821542753098708	0		KIAA0144
214700_x_at	0.816898518764863	0		
227056_at	-0.808158632738399	0		KIAA0141
201164_s_at	0.805491372224207	0		PUM1
202413_s_at	0.794856444512317	0		USP1
209523_at	0.794733968085209	0		
205382_s_at	-0.786501229240988	0		DF
213452_at	0.763286023547173	0		ZNF184
203904_x_at	0.761563303490256	0		KAI1
212629_s_at	0.758597736815579	0		PRKCL2
219793_at	0.753945856377937	0		SNX16
200093_s_at - HG-U133B	-0.7505050474584	0		HINT1
225065_x_at	-0.740661805635393	0		
210053_at	0.737429178254302	0		TAF5
209259_s_at	0.734770265079843	0		CSPG6
209023_s_at	0.732408586508097	0		STAG2

complex vs. normal	samples: 36 / 62			
accuracy	0.959183673469388			
confidence	0.816646490079598			
failed:	9,23,36,88			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
222229_x_at	-1.12052810135302	0		
227056_at	-1.02600466720905	0		KIAA0141
201922_at	-0.972449400267713	0*	3970.8	YR-29
200093_s_at - HG-U133B	-0.968640220043115	0		HINT1
239791_at	-0.927299942476145	0*	54	HOXB6
200608_s_at	0.882207986996843	0*	1566.2	RAD21
235502_at	-0.870929654024877	0		
223318_s_at	-0.867424298137502	0		MGC10974
200023_s_at - HG-U133B	-0.86661263717398	0		EIF3S5
200093_s_at - HG-U133A	-0.86073091922176	0		HINT1
218645_at	-0.842132977275412	0		ZNF277
213846_at	-0.824280554924366	0		COX7C
236728_at	-0.819459743485574	0		
236892_s_at	-0.810032594833065	0		HOXB6
241395_at	-0.806502754696553	0		
211950_at	0.803157394705844	0*	1367.5	RBAF600
203345_s_at	0.79268995247901	0		M96
231277_x_at	-0.79165327189793	0		
212251_at	0.787798207070077	0		

complex vs. t(8;21)	samples: 36 / 13			
accuracy	1			
confidence	0.956366908409342			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201851_at	1.64654123030477	0		SH3GL1
228827_at	-1.63837794328364	0*	277.15	
214651_s_at	1.52618371146822	0		HOXA9
235521_at	1.52417126144756	0		HOXA3
204249_s_at	1.52365997713542	0*	1581.95	LMO2
203904_x_at	1.49494399498725	0		KAI1
206940_s_at	-1.48076766016125	0		POU4F1
211341_at	-1.47540487159533	0		POU4F1
209259_s_at	1.45032016623088	0		CSPG6
212058_at	1.43907164424644	0		KIAA0332
218577_at	1.42304726090167	0		FLJ20331
217963_s_at	1.41730181206619	0		HCS
206622_at	-1.41476408655437	0		TRH
200071_at - HG-U133A	1.4105258517176	0		SPF30
218933_at	1.38255573216414	0		MGC5347
205528_s_at	-1.38150242627303	0		CBFA2T1
218331_s_at	1.3810903886183	0		FLJ20360
202406_s_at	1.3795610685034	0		TIAL1
220796_x_at	1.36377544613334	0		FLJ14251
218582_at	1.35888148459997	0		FLJ20445

complex vs. t(15;17)	samples: 36 / 20			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205382_s_at	-2.47024872277389	0		DF
212953_x_at	-2.44599456599903	0*	4652.35	CALR
64942_at	-2.28304127550384	0		
214450_at	-2.2627370518124	0		CTSW
38487_at	-2.15395063071356	0		FLJ12442
224794_s_at	-2.14479331910386	0		LOC51148
220798_x_at	-2.06303065394458	0		FLJ11535
216032_s_at	-2.05259440043708	0		SDBCAG84
203948_s_at	-2.04245448483567	0		MPO
209732_at	1.90630142681759	0		CLECSF2
230526_at	1.90204644112897	0		FLJ20015
238022_at	-1.89121106100583	0		
200654_at	-1.73209407132843	0		P4HB
204150_at	-1.72000809746397	0		STAB1
213447_at	1.71480861978241	0		IPW
206847_s_at	1.68023930751716	0		HOXA7
203074_at	-1.65576107663154	0		ANXA8
219837_s_at	-1.65191807395586	0		C17
200931_s_at	1.6356222023809	0		VCL
201923_at	1.60784567114272	0		PRDX4

complex vs. inv(16)	samples: 36 / 12			
accuracy	1			
confidence	0.957308305034528			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203092_at	1.77664454556306	0		TIMM44
209190_s_at	-1.75723541848141	0*	1593.8	DIAPH1
201497_x_at	-1.74852845185764	0*	134.75	MYH11
205076_s_at	-1.73951655525411	0		CRA
241525_at	-1.71682483225979	0		
213779_at	1.71354352282537	0		
210982_s_at	-1.70318998731519	0		HLA-DRA
200985_s_at	1.64643993864436	0		CD59
212463_at	1.6457941052799	0		
200675_at	1.61546783522649	0*	707.85	CD81
218942_at	1.59347299102441	0		FLJ22055
200984_s_at	1.56833724351535	0		CD59
208894_at	-1.54975491884609	0		HLA-DRA
202265_at	1.53139324627965	0		BMI1
224724_at	-1.5143785002027	0		KIAA1247
210715_s_at	1.49004107536748	0		SPINT2
213452_at	1.48522101377482	0		ZNF184
205382_s_at	-1.45942422076027	0		DF
201360_at	-1.45905524413008	0		CST3

complex vs. MLL	samples: 36 / 15			
accuracy	1			
confidence	0.928537448772464			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228083_at	-1.83691594955677	0		
201105_at	-1.56013660814198	0		LGALS1
201377_at	1.5390279619994	0		KIAA0144
201358_s_at	1.46121373620596	0		COPB
203387_s_at	1.43200690176451	0		KIAA0603
201585_s_at	1.42612880048733	0		SFPQ
222982_x_at	1.4232823410753	0		SLC38A2
202746_at	1.40541613814493	0*	277.15	
204951_at	1.38290450200254	0*	224.05	ARHH
203725_at	1.35090921185734	0		GADD45A
203544_s_at	1.33195316834084	0		STAM
225804_at	-1.31098146845679	0		
203386_at	1.30903268579411	0		KIAA0603
201359_at	1.3066438308133	0		COPB
201830_s_at	1.29170882160348	0		NET1
218041_x_at	1.27263528593652	0		PRO1068
223318_s_at	-1.27042416454958	0		MGC10974
212222_at	1.26786775770503	0		KIAA0077
201829_at	1.26235979300155	0		NET1
200608_s_at	1.25213416895148	0		RAD21

normal vs. all other	samples: 62 / 111			
accuracy	0.895953757225434			
confidence	0.738387670770008			
failed:	5,17,21,25,32,39,45,50,51,52,54,58,64,70,76,77,86,113			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
200023_s_at - HG-U133B	0.848290349062723	0		EIF3S5
236892_s_at	0.786541449606513	0*	60.95	HOXB6
201922_at	0.746117686034684	0		YR-29
239791_at	0.744707047378434	0		HOXB6
209055_s_at	-0.714503324187594	0		CDC5L
228904_at	0.707817878234848	0*	407.75	
224935_at	0.678011793604072	0		EIF2S3
236728_at	0.65220413902298	0		
238026_at	0.649420462340497	0		RPL35A
200679_x_at	-0.648886126347934	0*	782.25	HMG1
205366_s_at	0.642743252402536	0		HOXB6
225326_at	0.638282205886151	0*	835.95	KIAA1311
205601_s_at	0.638114898511556	0		HOXB5
205600_x_at	0.637054089932379	0		HOXB5
230743_at	0.631769166997722	0		
218645_at	0.629514230580722	0		ZNF277
226236_at	0.621355082335747	0		
200023_s_at - HG-U133A	0.620074058363248	0		EIF3S5
222976_s_at	-0.616559773343974	0		NTRK1

normal vs. t(8;21)	samples: 62 / 13			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228827_at	-2.03460798747208	0*	162.15	
214651_s_at	1.91662233809597	0		HOXA9
205528_s_at	-1.64467496425566	0		CBFA2T1
235753_at	1.61885010435257	0		
213150_at	1.50131650688172	0		HOXA10
205529_s_at	-1.4994140185132	0		CBFA2T1
211341_at	-1.4972813333234	0		POU4F1
209905_at	1.49669514190498	0		HOXA9
217816_s_at	1.49149650897312	0		pcnp
206940_s_at	-1.48516417693355	0		POU4F1
219598_s_at	1.43454923845259	0		
205453_at	1.38558116676561	0		HOXB2
223498_at	1.34625406703267	0		
213844_at	1.29651280723136	0		HOXA5
213147_at	1.27938232308768	0		HOXA10
222448_s_at	1.27922181680816	0		UMP-CMPK
214000_s_at	-1.2765364955951	0		RGS10
235521_at	1.27567444648757	0		HOXA3
235818_at	-1.27371437711255	0		
217963_s_at	1.27141827915888	0		HCS

normal vs. t(15;17)	samples: 62 / 20			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212953_x_at	-2.64495441949702	0*	4541.1	CALR
203948_s_at	-2.28625389247329	0		MPO
214450_at	-2.28053432941651	0		CTSW
38487_at	-2.27507979049885	0		FLJ12442
224794_s_at	-2.14479331910386	0		LOC51148
233072_at	-2.02319157581908	0		KIAA1857
236787_at	-1.97410536661333	0		
221004_s_at	-1.94014484972668	0		ITM3
209732_at	1.93197336691263	0		CLECSF2
214651_s_at	1.91723603396294	0		HOXA9
216032_s_at	-1.83899991398145	0		SDBCAG84
200952_s_at	-1.79422847402715	0		CCND2
208852_s_at	-1.77756000185084	0		CANX
200654_at	-1.77272215049273	0		P4HB
204150_at	-1.76741205974851	0		STAB1
235753_at	1.73443643867114	0		
64942_at	-1.71976456537364	0		
203949_at	-1.70342423200997	0		MPO
205614_x_at	-1.65262473388504	0		MST1

normal vs. inv(16)	samples: 62 / 12			
accuracy	1			
confidence	0.955620690178973			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214651_s_at	1.8118390923002	0		HOXA9
209365_s_at	-1.79092214915991	0*	390.9	ECM1
200951_s_at	-1.75939101209319	0		CCND2
201497_x_at	-1.74852845185764	0		MYH11
231310_at	-1.60730854736648	0*	167.8	
235753_at	1.60402701006007	0		
223385_at	-1.57142154491015	0		CYP2S1
231259_s_at	-1.49428776750791	0		CCND2
213353_at	1.47632425092475	0		ABCA5
202370_s_at	1.47587674217457	0*	942.4	CBFB
209905_at	1.44874209939309	0		HOXA9
204661_at	-1.44586168569344	0		CDW52
200675_at	1.39363453223823	0		CD81
207194_s_at	-1.38591797740996	0		ICAM4
213150_at	1.36428212315189	0		HOXA10
235818_at	-1.35992709972839	0		
228834_at	-1.35025928739893	0		TOB1
201324_at	-1.34841230643998	0		EMP1
218942_at	1.34162679981249	0		FLJ22055

normal vs. MLL	samples: 62 / 15			
accuracy	0.948051948051948			
confidence	0.898189333713789			
failed:	50,54,68,69			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205453_at	1.38558116676561	0*	203.25	HOXB2
225406_at	1.3008944013052	0*	191.3	TSG
222465_at	1.26538127373241	0*	1271.25	C15orf15
225326_at	1.13719416264236	0		KIAA1311
200829_x_at	1.1359357025281	0		ZNF207
227786_at	1.1032082540668	0		TRAP25
200056_s_at - HG-U133B	1.0989163336081	0		C1D
238856_s_at	1.093395457322	0		
200673_at	1.0918171848605	0		LAPTM4A
226250_at	1.0869927098714	0		
233559_s_at	-1.08564709559314	0		FENS-1
227680_at	1.0800659307262	0		
228904_at	1.06689615547167	0		
225700_at	1.0577778855845	0		
202377_at	1.05091847162674	0		HSOBRGRP
229232_at	1.04560760831211	0		
231870_s_at	1.04167487270266	0		LOC51068
222982_x_at	1.04035495200911	0		SLC38A2
209160_at	1.03517022790078	0		AKR1C3
223982_s_at	1.03308565481985	0		IPLA2

t(8;21) vs. all other	samples: 13 / 160			
accuracy	0.994219653179191			
confidence	1			
failed:	30			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228827_at	1.83673626836317	0		
211341_at	1.52047414341304	0		POU4F1
205528_s_at	1.51763257492904	0		CBFA2T1
206940_s_at	1.51745205298829	0		POU4F1
205529_s_at	1.43922881664177	0*	157.65	CBFA2T1
206622_at	1.22745062154907	0		TRH
219598_s_at	-1.21843492013845	0		
214651_s_at	-1.19784094554498	0		HOXA9
221581_s_at	-1.18072565374051	0		WBSCR5
227279_at	-1.10206247133481	0		MGC15737
204811_s_at	1.07742972237323	0		CACNA2D2
213150_at	-1.06934246090682	0		HOXA10
223498_at	-1.06722279372155	0		
215087_at	-1.06292558713408	0		
209522_s_at	-1.05686457779708	0		CRAT
204495_s_at	-1.05020858389696	0		DKFZP434H132
34689_at	-1.04236110585044	0		TREX1
201425_at	-1.04073518265119	0		ALDH2
225010_at	-1.0307918013289	0		

t(8;21) vs. t(15;17)	samples: 13 / 20			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214450_at	-3.53862069365814	0*	1809.95	CTSW
38487_at	-3.30334484935728	0		FLJ12442
209732_at	3.18277220746091	0		CLECSF2
204150_at	-2.73329912927614	0		STAB1
201596_x_at	-2.73162867034962	0		KRT18
213944_x_at	-2.5862372690463	0		
230526_at	2.42276930706474	0		FLJ20015
212509_s_at	-2.33481477262277	0		
211990_at	2.3270695509372	0		HLA-DPA1
204319_s_at	2.25060861801642	0		RGS10
205614_x_at	-2.24846130719191	0		MST1
216320_x_at	-2.16690689445934	0		
224794_s_at	-2.14479331910386	0		LOC51148
224839_s_at	-2.07810412712239	0		GPT2
227326_at	-2.04924504239987	0		
238365_s_at	-2.03674279873081	0		
228827_at	2.03460798747208	0		
228570_at	-2.03169244854036	0		
205349_at	-2.02142471684527	0		GNA15
AFFX-HUMRGE/M10098_3_at - HG-U133B	0.424247547600803	0.01		

t(8;21) vs. inv(16)	samples: 13 / 12			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233138_at	-3.4735123827114	0*	54.25	
202283_at	-2.6160707896185	0		SERPINF1
201596_x_at	-2.55517188589615	0		KRT18
233555_s_at	-2.48943541958708	0		
226818_at	-2.3621676751726	0		
212828_at	-2.33130605042964	0		SYNJ2
227276_at	-2.31171718422321	0		TEM7R
224724_at	-2.30850265580909	0		KIAA1247
224764_at	-2.25934489179779	0		ARHGAP10
224049_at	-2.25244855640038	0		KCNK17
205453_at	-2.23059959679219	0		HOXB2
226841_at	-2.21329419316194	0		
209975_at	-2.21237181448127	0		CYP2E
205076_s_at	-2.21083117233863	0		CRA
202340_x_at	-2.18671963481275	0		NR4A1
210314_x_at	-2.17138407196792	0		TNFSF13
34689_at	-2.16463995293403	0		TREX1
235359_at	-2.12423469465025	0		
212188_at	-2.11590883979512	0		LOC115207

t(8;21) vs. MLL	samples: 13 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214651_s_at	-2.42114497347366	0		HOXA9
201105_at	-2.17374439391796	0*	3881.25	LGALS1
228827_at	2.03460798747208	0		
206009_at	2.02655766969028	0		ITGA9
228083_at	-1.99768244710951	0		
213150_at	-1.98436589229381	0		HOXA10
50221_at	-1.94810783752319	0		
221581_s_at	-1.89677192380517	0		WBSCR5
235753_at	-1.88396584115232	0		
206622_at	1.79659162526109	0		TRH
209905_at	-1.76718971964498	0		HOXA9
204069_at	-1.75588643276789	0		MEIS1
209160_at	1.75500319419551	0		AKR1C3
235818_at	1.70111545046162	0		
223498_at	-1.67798456165549	0		
211404_s_at	-1.67488607654784	0		APLP2
209500_x_at	-1.66210516483391	0		TNFSF13
203949_at	1.65967693892027	0		MPO
214875_x_at	-1.65852470588382	0		APLP2
206576_s_at	1.65525942936471	0		CEACAM1

t(15;17) vs. all other	samples: 20 / 153			
accuracy	1			
confidence	0.974825330584744			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
214450_at	2.37884420275909	0		CTSW
38487_at	2.3638580246371	0		FLJ12442
212953_x_at	2.2214455881427	0		CALR
224794_s_at	2.14479331910386	0		LOC51148
204150_at	1.86162641245742	0		STAB1
221004_s_at	1.76116204864653	0		ITM3
64942_at	1.69621465377368	0		
203948_s_at	1.69389165333818	0*	12531.95	MPO
219837_s_at	1.66274419263843	0		C17
209732_at	-1.62000854961475	0		CLECSF2
200654_at	1.60816308060741	0		P4HB
216032_s_at	1.56292593677518	0		SDBCAG84
203074_at	1.56165682129626	0		ANXA8
241383_at	1.55580639460104	0		
233072_at	1.55533732715567	0		KIAA1857
211990_at	-1.55075101261749	0		HLA-DPA1
236787_at	1.54395725173734	0		
210755_at	1.52750902206113	0		HGF
209344_at	1.52382095011605	0		TPM4
210788_s_at	1.50209974954928	0		LOC51635

t(15;17) vs. inv(16)	samples: 20 / 12			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204661_at	-3.70847055085953	0*	1899.15	CDW52
209732_at	-3.23538966029247	0		CLECSF2
241742_at	-3.11768531834572	0		PRAM-1
38487_at	3.08138549900179	0		FLJ12442
238022_at	3.0278549438122	0		
204563_at	-2.99471501611954	0		SELL
34210_at	-2.99398735377828	0		CDW52
203535_at	-2.97123029136408	0		S100A9
217478_s_at	-2.93655072055469	0		
214450_at	2.92945546081029	0		CTSW
211991_s_at	-2.91096104465505	0		HLA-DPA1
208306_x_at	-2.87060964824031	0		HLA-DRB4
213779_at	2.84856846381654	0		
211990_at	-2.76844422327205	0		HLA-DPA1
221004_s_at	2.72545702224706	0		ITM3
209312_x_at	-2.66880572066538	0		HLA-DRB1
219789_at	-2.64334906817191	0		NPR3
204425_at	-2.62831954360607	0		ARHGAP4
205076_s_at	-2.59502309617401	0		CRA
64942_at	2.28304127550384	0		

t(15;17) vs. MLL	samples: 20 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205624_at	3.0741697102978	0*	2052.6	CPA3
38487_at	2.78111206643545	0		FLJ12442
203948_s_at	2.68497999695567	0		MPO
221004_s_at	2.64526084301972	0		ITM3
200951_s_at	2.52924582612911	0		CCND2
206761_at	2.52586949939666	0		TACTILE
203949_at	2.44678680592607	0		MPO
214651_s_at	-2.42192013365627	0		HOXA9
200952_s_at	2.39696270141848	0		CCND2
64942_at	2.28304127550384	0		
200953_s_at	2.24845652213108	0		CCND2
204150_at	2.2435902165197	0		STAB1
212953_x_at	2.22414089725316	0		CALR
233072_at	2.22380780245301	0		KIAA1857
214450_at	2.16984309325722	0		CTSW
224794_s_at	2.14479331910386	0		LOC51148
205349_at	2.12589700684588	0		GNA15
212509_s_at	2.11142192746438	0		
224839_s_at	2.07810412712239	0		GPT2
210788_s_at	2.07490438621852	0		LOC51635

inv(16) vs. all other	samples: 12 / 161			
accuracy	0.988439306358382			
confidence	1			
failed:	4,5			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
201497_x_at	1.74852845185764	0*	134.75	MYH11
200675_at	-1.37014908718923	0		CD81
233555_s_at	1.33083128494836	0		
224724_at	1.3278495786994	0		KIAA1247
241525_at	1.30966026882784	0		
202370_s_at	-1.24406045913745	0		CBFB
218942_at	-1.21682758933894	0		FLJ22055
201496_x_at	1.21510481759962	0		MYH11
204661_at	1.21332222789748	0		CDW52
222862_s_at	1.21194822636852	0		AK5
200665_s_at	1.20473287395901	0		SPARC
225330_at	-1.17881556984529	0		
34210_at	1.14323693974495	0		CDW52
223471_at	-1.13566677236541	0		
213779_at	-1.12982358521787	0		
214651_s_at	-1.12057321021092	0		HOXA9
201324_at	1.11862902082417	0		EMP1
213737_x_at	-1.10994603608752	0		
225055_at	-1.10931729132663	0		FLJ10120
201506_at	1.1081095188939	0		TGFBI

inv(16) vs. MLL	samples: 12 / 15			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
200951_s_at	4.24994685464806	0*	75.6	CCND2
228058_at	3.25212044058077	0		
219271_at	2.57049778814556	0		FLJ12691
231259_s_at	2.43255056573718	0		CCND2
214651_s_at	-2.30388406553935	0		HOXA9
202551_s_at	2.25890379783091	0		CRIM1
205453_at	2.23059959679219	0		HOXB2
200953_s_at	2.19700687874039	0		CCND2
213737_x_at	-2.16186095833837	0		
235818_at	2.13054793207832	0		
225653_at	2.10834669134201	0		
232636_at	-2.07022186491858	0		
202746_at	2.06211630393441	0		
200665_s_at	2.03751489015447	0		SPARC
203949_at	2.01364277991339	0		MPO
202552_s_at	1.96670486082105	0		CRIM1
223471_at	-1.96529988161274	0		
201828_x_at	-1.9593150488894	0		CXX1
235359_at	1.95403665761428	0		
202747_s_at	1.9384101680124	0		ITM2A

MLL vs. all other	samples: 15 / 158			
accuracy	0.947976878612717			
confidence	1			
failed:	1,6,7,10,12,14,25,102,114			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
228083_at	1.19088467978442	0*	2180.6	
222982_x_at	-1.10285933642875	0		SLC38A2
201105_at	1.03478994002288	0		LGALS1
209160_at	-1.02713455370792	0		AKR1C3
204951_at	-0.985909332656785	0		ARHH
218041_x_at	-0.943257946797628	0		PRO1068
225776_at	-0.938314906907134	0		BAZ2A
202746_at	-0.936926874759212	0		
205472_s_at	0.936018216120354	0		DACH
205453_at	-0.935915983498264	0		HOXB2
203380_x_at	-0.926524173527231	0		SFRS5
203372_s_at	0.926509074446515	0		STATI2
225285_at	-0.922143795249267	0		
203373_at	0.921657224293489	0		STATI2
201830_s_at	-0.917500470432308	0		NET1
236378_at	-0.911274344991347	0		
209616_s_at	0.911180477081636	0		CES1
218718_at	-0.905113907165327	0		PDGFC
225406_at	-0.898505260085313	0		TSG
49306_at	0.646783585229759	0		AD037

Table 36: Analysis of 8 AML subgroups according to the method described by Westfall & Young. The 226 significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

geneID	Golub	rawp	Adjp	
201497_x_at	*	0.0001	**0.0001**	MYH11
212953_x_at	*	0.0001	**0.0001**	CALR
214450_at	*	0.0001	**0.0001**	CTSW
224794_s_at	+	0.0001	**0.0001**	LOC51148
228827_at	*	0.0001	**0.0001**	
38487_at	+	0.0001	**0.0001**	FLJ12442
203074_at	+	0.0001	**0.0002**	ANXA8
204150_at	+	0.0001	**0.0002**	STAB1
219837_s_at	+	0.0001	**0.0002**	C17
64942_at	+	0.0001	**0.0002**	
203948_s_at	*	0.0001	**0.0003**	MPO
205528_s_at	+	0.0001	**0.0003**	CBFA2T1
205529_s_at	*	0.0001	**0.0003**	CBFA2T1
206940_s_at	+	0.0001	**0.0003**	POU4F1
209344_at	+	0.0001	**0.0003**	TPM4
210755_at	+	0.0001	**0.0003**	HGF
210997_at		0.0001	**0.0003**	HGF
211341_at	+	0.0001	**0.0003**	POU4F1
212285_s_at		0.0001	**0.0003**	AGRN
212481_s_at		0.0001	**0.0003**	TPM4
216320_x_at	+	0.0001	**0.0003**	
223828_s_at		0.0001	**0.0003**	LGALS12
227243_s_at		0.0001	**0.0003**	
233072_at	+	0.0001	**0.0003**	KIAA1857
236787_at	+	0.0001	**0.0003**	
200952_s_at	+	0.0001	**0.0004**	CCND2
205614_x_at	+	0.0001	**0.0004**	MST1
212509_s_at	+	0.0001	**0.0004**	
216032_s_at	+	0.0001	**0.0004**	SDBCAG84
221004_s_at	+	0.0001	**0.0004**	ITM3
241383_at	+	0.0001	**0.0004**	
200656_s_at		0.0001	**0.0005**	P4HB
200953_s_at	+	0.0001	**0.0005**	CCND2
201496_x_at	+	0.0001	**0.0005**	MYH11
214203_s_at		0.0001	**0.0005**	PRODH

214315_x_at		0.0001	**0.0005** CALR
219090_at		0.0001	**0.0005** SLC24A3
227046_at		0.0001	**0.0005** C17orf26
227242_s_at		0.0001	**0.0005**
209686_at		0.0001	**0.0007** S100B
228660_x_at	*	0.0001	**0.0007** SEMA4F
241525_at	+	0.0001	**0.0011**
210788_s_at	+	0.0001	**0.0017** LOC51635
227326_at	+	0.0001	**0.0023**
208852_s_at	+	0.0001	**0.0027** CANX
229168_at		0.0001	**0.0031**
242520_s_at		0.0001	**0.0031**
200951_s_at	*	0.0001	**0.0033** CCND2
203949_at	+	0.0001	**0.0033** MPO
204163_at		0.0001	**0.0033** EMILIN
205663_at		0.0001	**0.004** PCBP3
204116_at		0.0001	**0.005** IL2RG
221253_s_at		0.0001	**0.005** MGC3178
238365_s_at	+	0.0001	**0.0058**
200654_at	+	0.0001	**0.0072** P4HB
201069_at		0.0001	**0.0072** MMP2
200608_s_at	*	0.0001	**0.0074** RAD21
210998_s_at		0.0001	**0.0077** HGF
211668_s_at		0.0001	**0.0077** PLAU
212259_s_at		0.0001	**0.0077** HPIP
224839_s_at	+	0.0001	**0.0077** GPT2
223321_s_at		0.0001	**0.0083** FGFRL1
225065_x_at	+	0.0001	**0.0085**
206622_at	+	0.0001	**0.0086** TRH
205076_s_at	+	0.0001	**0.009** CRA
231050_at		0.0001	**0.009** HRLP5
235753_at	+	0.0001	**0.009**
214000_s_at	+	0.0001	**0.0093** RGS10
231259_s_at	+	0.0001	**0.0095** CCND2
200047_s_at - HG-U133A		0.0001	**0.0096** YY1
204811_s_at	+	0.0001	**0.0101** CACNA2D2
229621_x_at		0.0001	**0.0102**
205382_s_at	+	0.0001	**0.0103** DF
213514_s_at		0.0001	**0.0105** DIAPH1
200986_at		0.0001	**0.0107** SERPING1
217419_x_at		0.0001	**0.0107**
229420_at		0.0001	**0.0117** RPL23A

211934_x_at		0.0001	**0.0122** G2AN
214651_s_at	+	0.0001	**0.0123** HOXA9
208581_x_at		0.0001	**0.0127** MT1X
202718_at		0.0001	**0.0128** IGFBP2
200825_s_at		0.0001	**0.0135** ORP150
212185_x_at		0.0001	**0.0135** MT2A
219868_s_at		0.0001	**0.0135** ANKHZN
203939_at		0.0001	**0.0136** NT5E
200649_at		0.0001	**0.0144** NUCB1
206850_at		0.0001	**0.0144** RRP22
AFFX-r2-Hs28SrRNA-3_at - HG-U133B		0.0001	**0.0144**
218051_s_at		0.0001	**0.0146** FLJ12442
208629_s_at	+	0.0001	**0.0147** HADHA
209523_at	+	0.0001	**0.0147**
AFFX-r2-Hs28SrRNA-3_at - HG-U133A		0.0001	**0.0148**
57588_at		0.0001	**0.0156** SLC24A3
221902_at		0.0001	**0.0163**
225547_at	+	0.0001	**0.0163**
200047_s_at - HG-U133B		0.0001	**0.0172** YY1
200023_s_at - HG-U133B	+	0.0001	**0.0175** EIF3S5
201008_s_at		0.0001	**0.0175** TXNIP
205624_at	*	0.0001	**0.0178** CPA3
AFFX-HSAC07/X00351_5_at - HG-U133A		0.0001	**0.0178** ACTB
200935_at		0.0001	**0.0179** CALR
228083_at	*	0.0001	**0.0179**
222229_x_at	+	0.0001	**0.0183**
224724_at	+	0.0001	**0.0186** KIAA1247
211748_x_at		0.0001	**0.0194** PTGDS
209190_s_at	*	0.0001	**0.0206** DIAPH1
214316_x_at		0.0001	**0.021** CALR
205110_s_at		0.0001	**0.0212** FGF13
233555_s_at	+	0.0001	**0.0215**
202655_at		0.0001	**0.0216** ARMET
AFFX-HUMRGE/M10098_3_at - HG-U133B	+	0.0001	**0.0217**
200008_s_at - HG-U133A		0.0001	**0.022** GDI2
209961_s_at		0.0001	**0.022** HGF
222916_s_at		0.0001	**0.0228**
211456_x_at		0.0001	**0.0229**
219138_at		0.0001	**0.023** RPL14
242845_at		0.0001	**0.023**
202028_s_at		0.0001	**0.0232** RPL38

222862_s_at	+	0.0001	0.0232 AK5
AFFX-HSAC07/X00351_5_at - HG-U133B		0.0001	0.0232 ACTB
238022_at	+	0.0001	0.0233
222977_at		0.0001	0.0234 SURF4
211474_s_at		0.0001	0.0236
204306_s_at		0.0001	0.0237 CD151
212013_at		0.0001	0.0237 D2S448
201922_at	*	0.0001	0.0238 YR-29
203857_s_at		0.0001	0.0238 PDIR
AFFX-M27830_5_at - HG-U133B		0.0001	0.0238
242738_s_at		0.0001	0.024
AFFX-r2-Hs18SrRNA-3_s_at - HG-U133B		0.0001	0.0241
215450_at		0.0001	0.0245 SNRPE
222955_s_at		0.0001	0.0245 HT011
AFFX-M27830_5_at - HG-U133A		0.0001	0.0259
202148_s_at		0.0001	0.026 PYCR1
216609_at		0.0001	0.026
214500_at		0.0001	0.0264 H2AFY
241975_at		0.0001	0.0268
226014_at		0.0001	0.0273 EIF3S5
224407_s_at		0.0001	0.0274 MST4
AFFX-HSAC07/X00351_M_at - HG-U133B		0.0001	0.0275 ACTB
210973_s_at		0.0001	0.0276 FGFR1
213963_s_at		0.0001	0.0279 SAP30
209616_s_at	+	0.0001	0.0288 CES1
201004_at		0.0001	0.0289 SSR4
214228_x_at		0.0001	0.0289
214501_s_at		0.0001	0.0289 H2AFY
208229_at		0.0001	0.029 FGFR2
208819_at		0.0001	0.029 MEL
201564_s_at		0.0001	0.0296 SNL
201437_s_at		0.0001	0.0297 EIF4E
213048_s_at		0.0001	0.0297 SET
221943_x_at		0.0001	0.0297 RPL38
202747_s_at	+	0.0001	0.0299 ITM2A
208611_s_at		0.0001	0.0299 SPTAN1
212012_at		0.0001	0.0304 D2S448
205380_at		0.0001	0.0311 PDZK1
209975_at	+	0.0001	0.0316 CYP2E
208858_s_at		0.0001	0.0317 KIAA0747
206461_x_at		0.0001	0.0322 MT1H
210794_s_at		0.0001	0.0325

212187_x_at		0.0001	**0.0326** PTGDS
AFFX-HSAC07/X00351_M_at - HG-U133A		0.0001	**0.0338** ACTB
200008_s_at - HG-U133B		0.0001	**0.0346** GDI2
222477_s_at		0.0001	**0.0346** TM7SF3
223054_at		0.0001	**0.0347** DNAJB11
231118_at		0.0001	**0.0351**
238367_s_at		0.0001	**0.0357**
201352_at		0.0001	**0.0358** YME1L1
AFFX-M27830_M_at - HG-U133A		0.0001	**0.0358**
210933_s_at		0.0001	**0.0363** MGC4655
200598_s_at		0.0001	**0.0368** TRA1
213942_at		0.0001	**0.037** EGFL3
222692_s_at		0.0001	**0.037** FLJ23399
AFFX-r2-Hs18SrRNA-M_x_at - HG-U133A		0.0001	**0.037**
200646_s_at		0.0001	**0.0372** NUCB1
201005_at		0.0001	**0.0372** CD9
222979_s_at		0.0001	**0.0373**
226210_s_at		0.0001	**0.0388**
AFFX-r2-Hs18SrRNA-M_x_at - HG-U133B		0.0001	**0.0391**
214700_x_at	+	0.0001	**0.0393**
207076_s_at		0.0001	**0.0402** ASS
216450_x_at		0.0001	**0.0402**
202746_at	*	0.0001	**0.0404**
200770_s_at		0.0001	**0.0409** LAMC1
217816_s_at	+	0.0001	**0.0409** pcnp
226531_at		0.0001	**0.0409** FLJ14466
200093_s_at - HG-U133B	+	0.0001	**0.0413** HINT1
AFFX-HUMRGE/M10098_3_at - HG-U133A		0.0001	**0.0413**
219793_at	+	0.0001	**0.0418** SNX16
212032_s_at		0.0001	**0.0423** PTOV1
228193_s_at		0.0001	**0.0423** RGC32
202413_s_at	+	0.0001	**0.0424** USP1
216449_x_at		0.0001	**0.0427**
205131_x_at		0.0001	**0.0432** SCGF
217225_x_at		0.0001	**0.0438** PM5
202406_s_at	+	0.0001	**0.0439** TIAL1
203729_at		0.0001	**0.0439** EMP3
200630_x_at		0.0001	**0.0447** SET
227299_at		0.0001	**0.0448** CCNI
AFFX-r2-Hs18SrRNA-3_s_at - HG-U133A		0.0001	**0.0448**
209905_at	+	0.0001	**0.0449** HOXA9
208033_s_at		0.0001	**0.0452** ATBF1

214395_x_at		0.0001	**0.0452** FLJ20897
217383_at		0.0001	**0.0452**
201377_at	+	0.0001	**0.0454** KIAA0144
206871_at		0.0001	**0.0454** ELA2
203859_s_at		0.0001	**0.0461** PALM
200968_s_at		0.0001	**0.0462** PPIB
219634_at		0.0001	**0.0463** C4ST
220798_x_at	+	0.0001	**0.0463** FLJ11535
201825_s_at		0.0001	**0.0466** LOC51097
224553_s_at		0.0001	**0.0468** TNFRSF18
227353_at		0.0001	**0.0468**
225406_at	*	0.0001	**0.0473** TSG
227145_at		0.0001	**0.0478** LOXL4
201164_s_at	+	0.0001	**0.0484** PUM1
210140_at		0.0001	**0.0484** CST7
202600_s_at		0.0001	**0.0487** NRIP1
210616_s_at		0.0001	**0.0487** KIAA0905
212107_s_at		0.0001	**0.0487** DDX9
200071_at - HG-U133A	+	0.0001	**0.0491** SPF30
204082_at		0.0001	**0.0491** PBX3'
200707_at		0.0001	**0.0492** PRKCSH
200967_at		0.0001	**0.0493** PPIB
206634_at		0.0001	**0.0493** SIX3
AFFX-HUMRGE/M10098_M_at - HG-U133B		0.0001	**0.05**

Table 37a: In total 32 cases of CLL were analyzed. 31 of 32 cases (96.9%) were assigned to the correct CLL subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	+12	11q-	13q-	17p-	normal	total	sensitivity %	specificity %
+12	5					5	100.00	100.00
11q-		4				4	100.00	100.00
13q-			9		1	10	90.00	100.00
17p-				4		4	100.00	100.00
Normal					9	9	100.00	90.00
Total	5	4	9	4	10	32		

Table 37b: In total 128 individual assignments of CLL were analyzed. 127 of 128 assignments (99.2%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	tri 12	11q	13q	17p	normal	total	sensitivity %	specificity %
tri 12	20					20	100.00	100.00
11q		16				16	100.00	100.00
13q			39		1	40	97.50	100.00
17p				16		16	100.00	97.30
Normal					36	36	100.00	100.00
Total	20	16	39	16	37	128		

Table 38: Analysis of 5 CLL subtypes according to the method described by Golub et al.

trisomy 12	5
11q-	4
13q-	10
17p-	4
normal	9

trisomy 12 vs. all other	samples: 5 / 27			
accuracy	1			
confidence	0.935014380126868			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205855_at	-1.76663664947048	0.01		ZNF197
203787_at	1.48888776879594	0*	186.05	SSBP2
240785_at	-1.47915794453041	0*	1	
241930_x_at	1.43687618531343	0		
227527_at	1.43424381736709	0		
233106_at	1.39680763010583	0		
219234_x_at	-1.36406381959263	0*	1	FLJ23142
204992_s_at	-1.35580671258705	0		PFN2
229722_at	-1.35323423840642	0		HSPC072
225772_s_at	1.34357943208416	0		MGC14288
240801_at	1.33658031665266	0		C21orf37
236535_at	-1.28816401084294	0		FLJ22116
213850_s_at	1.28242512478545	0		SFRS2IP
239651_at	1.27623762574996	0		
218692_at	-1.26869683284091	0		FLJ20366
210117_at	1.26847772500135	0		SPAG1
229833_at	-1.2612893100757	0		
243859_at	-1.24636980625822	0.01		
242695_at	1.24259108808825	0		

trisomy 12 vs.11q-	samples: 5 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
233106_at	11.446952458547	0*	17.2	
240801_at	9.47372393833846	0		C21orf37
209876_at	5.71702357037612	0		GIT2
240785_at	-5.41366689652617	0.01		
238651_at	4.44936662944647	0		
224559_at	4.28565210000215	0		
204992_s_at	-4.18799798922824	0.01		PFN2
218089_at	-3.71376785745491	0		C20orf4
233520_s_at	3.68368733311458	0.01		
244248_at	-3.51882915292872	0.01		
202973_x_at	3.46577082978451	0		KIAA0914
238304_at	3.40683085127986	0.02		
209018_s_at	3.33636546986144	0.01		PINK1
235414_at	3.31145415432861	0		
228737_at	-3.19150189531835	0		C20orf100
205841_at	3.0783309837118	0.01		JAK2
210251_s_at	3.06884121765458	0		KIAA0871
227237_x_at	-3.04881893527751	0		KIAA1273
204101_at	2.96540851000724	0		MTM1
214152_at	2.94086839898829	0		PIGB

trisomy 12 vs.13q-	samples: 5 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
241930_x_at	3.41574881140311	0*	30.05	
201125_s_at	2.1330030439147	0.01		ITGB5
214030_at	1.99357501958234	0		FLJ14393
220764_at	1.83054202690279	0		PPP4R2
229711_s_at	1.77592202191897	0		MGC5370
204422_s_at	1.73100503057285	0		FGF2
206519_x_at	1.72950110576936	0		SIGLEC6
229722_at	-1.72165455873558	0		HSPC072
224254_x_at	1.69291666318009	0.01		
244550_at	1.69227307532627	0		
240785_at	-1.67627283307722	0		
219234_x_at	-1.67623751680922	0		FLJ23142
239651_at	1.67596732335477	0		
225803_at	1.66876599612634	0		FBXO32
202371_at	-1.66225791751365	0		FLJ21174
238686_at	1.65936349841951	0		FBXO3
213249_at	-1.65347132783467	0.01		FBXL7
232841_at	-1.61894883955233	0		
37424_at	-1.60782342430755	0		HCR
238651_at	1.5823504522053	0		

trisomy 12 vs.17p-	samples: 5 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
240801_at	9.47372393833846	0.01*	12.2	C21orf37
205855_at	-6.0211187391758	0		ZNF197
35666_at	-5.5825628661131	0		SEMA3F
210807_s_at	4.67905037269957	0		SLC16A7
238756_at	4.46774787106986	0		
213081_at	4.28614856394104	0.01		ZNF297
209992_at	3.83963180828656	0.02		PFKFB2
213922_at	3.58392947846265	0.01		KIAA0847
221642_at	3.54894468199149	0		TREX1
234862_at	3.18446048786689	0.01		
204101_at	2.96540851000724	0		MTM1
240842_at	-2.91868570817753	0		
225270_at	2.79620139853395	0		
240785_at	-2.79597266226518	0.01		
202156_s_at	2.55016914645743	0.02		CUGBP2
242738_s_at	2.48714106974951	0		
222229_x_at	2.4826745391349	0		
221761_at	2.43735081046452	0.01		ADSS
239651_at	2.38139601357287	0.01		
44065_at	1.72880244676984	0.03		FLJ14827

trisomy 12 vs. normal	samples: 5 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
204227_s_at	-2.97871472113278	0*	52.6	TK2
239956_at	-2.19763940812654	0		
229833_at	-2.15561256145124	0		
235259_at	-2.13615684750119	0		
219234_x_at	-2.00077179509905	0		FLJ23142
205225_at	-1.99449483927763	0		ESR1
207871_s_at	-1.92495926735556	0.01		ST7
214849_at	-1.85640805976258	0		
229368_s_at	1.79940595243311	0		ZNF216
241969_at	1.7405112334814	0		ITM2B
206519_x_at	1.72950110576936	0		SIGLEC6
238752_at	-1.70821051414766	0.02		
231269_at	1.70133376942788	0.01		DJ467N11.1
210117_at	1.68428381889367	0		SPAG1
244248_at	-1.64325597313785	0		
227527_at	1.63698066130033	0		
205855_at	-1.62998714380688	0		ZNF197
230775_s_at	1.62302128109514	0		KIAA0610
235428_at	-1.61224208443187	0.01		

11q- vs. all other	samples: 4 / 28			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
218089_at	2.10620905507106	0*	646.5	C20orf4
219846_at	-1.81092435144239	0		FLJ23040
227988_s_at	-1.72174284840356	0		CHAC
214152_at	-1.67765936203123	0		PIGB
218379_at	-1.46433593517939	0		RBM7
226743_at	-1.46222822597622	0		
211297_s_at	1.44946792759264	0		CDK7
201034_at	-1.42442867101326	0		ADD3
241754_at	-1.42345184824601	0.01		
236914_at	-1.4155743735673	0.01		
202883_s_at	-1.40974035083074	0		PPP2R1B
222619_at	1.40836172115026	0		ZNF281
210251_s_at	-1.40353417348001	0		KIAA0871
243764_at	-1.39232414452409	0.01		
232080_at	-1.38768407694403	0.01		KIAA1301
225469_at	-1.33954570434399	0.01		KRAS2
228916_at	-1.33432050535623	0		
231837_at	-1.32753771112964	0		USP28
41553_at	1.12064197016153	0		C8orf1

11q- vs.13q-	samples: 4 / 10			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
219846_at	-3.42496729223506	0*	29.05	FLJ23040
243579_at	2.5422955569836	0		MSI2
218089_at	2.2192149690658	0		C20orf4
236557_at	2.13608221931199	0		
236914_at	-2.11513443853125	0		
211097_s_at	-2.10829683608662	0.01		PBX2
222619_at	1.99497428726409	0		ZNF281
210563_x_at	1.98835546697322	0		CFLAR
203910_at	-1.93770224600631	0		PARG1
214152_at	-1.85345818448696	0.02		PIGB
211665_s_at	1.85212714314444	0		
224727_at	1.79450625074427	0		
212973_at	1.77498087389291	0		RPIA
216363_at	-1.75505428599984	0		
232080_at	-1.71428429043072	0.02		KIAA1301
209939_x_at	1.70364770022483	0		CFLAR
216640_s_at	1.66791014400825	0		
211015_s_at	1.66234655451608	0		HSPA4
241754_at	-1.65521937202397	0.02		
200072_s_at - HG-U133B	1.62143771744332	0		HNRPM

11q- vs.17p-	samples: 4 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203910_at	-12.0891239887758	0.02*	25.2	PARG1
219788_at	-8.01365237890759	0.01		PILR
210807_s_at	5.81727222348978	0		SLC16A7
202973_x_at	-5.54682446497201	0.01		KIAA0914
224727_at	5.47118118794136	0.04		
243538_at	-5.45690493183292	0.01		
220653_at	5.40495669550229	0.01		ZIM2
236557_at	4.79134791840039	0.03		
202535_at	4.6597238034407	0.02		FADD
219846_at	-4.50391195213954	0.03		FLJ23040
223036_at	-4.37417074055808	0.04		FRSB
41553_at	4.17139530611346	0.02		C8orf1
232080_at	-3.7905538055378	0.04		KIAA1301
227212_s_at	3.74958483811803	0		
231538_at	-3.66357978886211	0.03		FLJ23499
223981_at	-3.20166631174034	0.01		NIN
210095_s_at	-3.18292733506553	0.03		IGFBP3
44669_at	1.48597424301687	0.03		

11q- vs. normal	samples: 4 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
227988_s_at	-3.59181544150717	0*	42.9	CHAC
202883_s_at	-3.42911376512134	0		PPP2R1B
239824_s_at	-2.86491576775498	0		MGC10744
208741_at	-2.57358498823744	0		SAP18
235446_at	-2.44561600023568	0		
243024_at	-2.32550716609078	0		
214152_at	-2.28116624754023	0		PIGB
205945_at	-2.2501933683546	0		IL6R
230405_at	-2.2154536025941	0		RAD50
240449_at	-2.16736443161623	0		ZNF341
226735_at	2.13097198546745	0		
235719_at	-2.04486139000124	0		
240269_at	-2.00407877559944	0.02		
231837_at	-1.99281259915495	0.01		USP28
211584_s_at	-1.92263813056307	0		NPAT
212397_at	-1.91363941690428	0		RDX
228083_at	-1.91262419018279	0		
217185_s_at	-1.90105615613598	0		
201034_at	-1.87885968131857	0		ADD3
244636_at	1.41086397558577	0.01		

13q- vs. all other	samples: 10 / 22			
accuracy	0.90625			
confidence	0.758934573190992			
failed:	1,4,10			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
240239_at	1.12265317688576	0		FLJ14779
225803_at	-1.11955038091099	0		FBXO32
214030_at	-1.07932639824253	0		FLJ14393
208612_at	-1.04692103821733	0		GRP58
205059_s_at	-1.02298997137232	0		IDUA
224324_at	-1.0017529706033	0.01		B29
220050_at	-0.942587733303296	0		C9orf9
212133_at	-0.939561276009625	0		MGC5466
209561_at	-0.895424188378393	0.01*	1	THBS3
212346_s_at	-0.86343267965412	0.01*	1	
210563_x_at	-0.857353032891431	0		CFLAR
219846_at	0.851391806455573	0		FLJ23040
200917_s_at	-0.847094054810162	0		SRPR
214693_x_at	-0.842327739447741	0*	513.4	DJ328E19.C1.1
224254_x_at	-0.840493461837671	0*	1	
216363_at	0.840371719572254	0		
206178_at	-0.839970145359486	0.01*	1	PLA2G5
201829_at	-0.83771452268015	0		NET1
242065_x_at	0.752061453727533	0		KIAA0982

13q- vs.17p-	samples: 10 / 4			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
205074_at	3.93082740953048	0*	47.2	SLC22A5
205059_s_at	-2.86213992210757	0		IDUA
206530_at	-2.83791228863181	0		RAB30
239302_s_at	2.16473291745382	0		
211097_s_at	2.10829683608662	0		PBX2
213922_at	2.01548216857792	0		KIAA0847
206748_s_at	-1.88775766295876	0		SPAG9
230960_at	1.78981943765595	0		
219099_at	-1.78601869648563	0		C12orf5
209399_at	1.77172423634645	0		HLCS
234682_at	-1.75764919544644	0.02		
201247_at	-1.75383479254057	0		SREBF2
227047_x_at	1.70965672311403	0		KIAA1538
227336_at	-1.67331959955983	0		DTX1
44563_at	1.6395923566301	0		FLJ10385
202137_s_at	1.63835350305949	0		BS69
204703_at	1.63405057461184	0		TG737
232841_at	1.61894883955233	0		

13q- vs. normal	samples: 10 / 9			
accuracy	0.947368421052632			
confidence	0.767885192437171			
failed:	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212133_at	-1.49179585241618	0		MGC5466
231945_at	1.34403975576724	0		KIAA1275
236707_at	-1.3127085187848	0		DAPP1
240113_at	1.29988454092314	0.01		
233137_at	-1.24704962815733	0*	72.3	
239279_at	1.17173879184892	0*	10.95	
217920_at	-1.16948313904991	0*	100.65	
220050_at	-1.1554548232117	0.01		C9orf9
214693_x_at	-1.12710287831488	0*	785.75	DJ328E19.C1.1
240239_at	1.12265317688576	0		FLJ14779
206633_at	1.11411516845923	0		CHRNA1
233845_at	1.10899780853203	0		
214030_at	-1.10624113689033	0		FLJ14393
214452_at	-1.10585601374159	0.01		BCAT1
244636_at	1.09426538931965	0		
229711_s_at	-1.08284772025586	0*	175.2	MGC5370
208612_at	-1.04802029197291	0		GRP58
201829_at	-1.04541705234559	0		NET1
225025_at	-1.04209808409802	0		IGSF8
56919_at	0.843685137333952	0		KIAA1449

17p- vs. all other	samples: 4 / 28			
accuracy	1			
confidence	0.964568811002079			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
213922_at	-2.38687598396346	0		KIAA0847
239302_s_at	-1.90616910234578	0		
210807_s_at	-1.80157318540302	0*	1	SLC16A7
227047_x_at	-1.74312208164522	0*	1	KIAA1538
243493_at	-1.58349220512196	0.01*	1	
212601_at	-1.53446329571692	0		KIAA0399
231069_at	-1.52786491236881	0		
228183_s_at	-1.52482033281554	0		MGC4189
218938_at	-1.52269705250236	0		MGC11279
209754_s_at	-1.51357080613702	0		
229487_at	1.48496465895187	0.01		
202101_s_at	-1.48060713997599	0		RALB
204075_s_at	-1.44015391162326	0		KIAA0562
225064_at	-1.43255380391079	0		
211800_s_at	-1.42133619880381	0		USP4
44563_at	-1.41946867497272	0		FLJ10385
209003_at	-1.41936503927243	0.01		SLC25A11
233261_at	1.41906569641121	0		

17p- vs. normal	samples: 4 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
239263_at	-5.06986350689012	0*	28.95	
224389_s_at	4.8522042820775 6	0.01		LOC84570
218938_at	-4.37035592768397	0		MGC11279
209558_s_at	3.96926728013304	0.01		HIP12
209003_at	-3.83037277930439	0		SLC25A11
213922_at	-3.70320846722859	0		KIAA0847
227277_at	-3.14601684537179	0		
201247_at	3.13384207920433	0.01		SREBF2
239824_s_at	-2.86491576775498	0		MGC10744
243493_at	-2.55548617887833	0		
202101_s_at	-2.51633093119791	0		RALB
238208_at	2.48580500500254	0		
232641_at	-2.43239639363709	0		
38340_at	2.39155889740356	0		HIP12
225565_at	-2.36688673011482	0		
235692_at	-2.35357613574803	0		
212587_s_at	-2.31297420341289	0		PTPRC
209178_at	2.30977713582653	0		DDX38
226101_at	-2.30435376005559	0		

normal vs. all other	samples: 9 / 23			
accuracy	1			
confidence	0.752908435315332			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
217920_at	1.12626688471637	0*	120.8	
233845_at	-1.11422356526216	0		
239279_at	-1.07195619687299	0*	1	
231945_at	-1.04730583025734	0*	47.05	KIAA1275
240113_at	-1.03819026438649	0*	1	
219641_at	1.01342862157126	0*	68.05	FLJ10103
219457_s_at	1.01203293419066	0*	653.6	RIN3
211349_at	-0.983993758419454	0		SLC15A1
228408_s_at	0.980977651352115	0*	301.7	FLJ10498
214949_at	0.970683369936125	0		
235052_at	0.970295482117812	0*	18.2	
212417_at	0.947300555400096	0		SCAMP1
244636_at	-0.940508403486097	0.01		
226060_at	0.905224209711651	0		RFT1
239263_at	0.904436494271519	0.01		
200890_s_at	0.896568314554417	0		SSR1
208042_at	0.88315849081967	0		HSU84971
206550_s_at	-0.869633758548337	0		NUP155
201813_s_at	0.854527572567661	0		KIAA0210
221543_s_at	0.842343687568175	0		C8orf2

Table 39: Analysis of 5 CLL subgroups according to the method described by Westfall & Young. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

geneID	Golub	rawp	adjp	
229487_at	+	0.0016	0.4057	
233261_at	+	0.0016	0.6404	
235421_at		0.0003	0.7273	
244876_at		0.0016	0.831	
212133_at	+	0.0001	0.8508	MGC5466
232204_at		0.0008	0.889	EBF
244147_at		0.0014	0.9084	
240740_at		0.0016	0.926	
227527_at	+	0.0001	0.943	
206519_x_at	+	0.0007	0.9529	SIGLEC6
213922_at	+	0.0001	0.9568	KIAA0847
207801_s_at		0.0011	0.9745	RNF10
212812_at		0.0003	0.9763	
242329_at		0.0016	0.9777	
221004_s_at		0.0012	0.9807	ITM3
209321_s_at		0.0005	0.9837	ADCY3
44563_at	+	0.0003	0.9839	FLJ10385
212813_at		0.0013	0.984	FLJ14529
217156_at		0.0012	0.9862	
219099_at	+	0.0004	0.9864	C12orf5
238365_s_at		0.0004	0.988	
219846_at	*	0.0003	0.9957	FLJ23040
227936_at		0.0001	0.9975	
228497_at		0.0002	0.9992	DKFZp761G0313
244523_at		0.0007	0.9992	MMD
222108_at		0.0008	0.9994	
212601_at	+	0.0003	0.9996	KIAA0399
222313_at		0.0015	0.9996	
204208_at		0.0016	0.9997	RNGTT
210916_s_at		0.0009	0.9997	
224872_at		0.0006	0.9997	KIAA1463
241930_x_at	*	0.0006	0.9997	
202530_at		0.0007	0.9998	MAPK14
203026_at		0.0004	0.9998	KIAA0354
203394_s_at		0.001	0.9998	HRY

215227_x_at	0.0002	0.9998 ACP1
229138_at	0.0012	0.9998

Table 40a: In total 280 cases of leukemia and normal bone marrow (BM) were analyzed. 263 of 280 cases (93.9%) were assigned to the correct leukemia subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL	AML	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL	36	9	1	1		47	76.60	94.74
AML	2	172			1	175	98.29	93.48
CLL		1	34			35	97.14	97.14
CML		1		13		14	92.86	92.86
normal BM		1			8	9	88.89	88.89
total	38	184	35	14	9	280		

Table 40b: In total 1120 individual assignments of leukemia were analyzed. 1103 of 1120 assignments (98.5%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

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	ALL	AML	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL	177	9	1	1		188	94.15	98.88
AML	2	698			1	700	99.71	98.31
CLL		1	139			140	99.29	99.29
CML		1		55		56	98.21	98.21
normal BM		1			35	36	97.22	97.22
total	179	710	140	56	36	1120		

Table 41: Analysis of 4 leukemia subtypes and normal bone marrow according to the method described by Golub et al.

ALL	47
AML	175
CLL	35
CML	14
normal BM	9

ALL vs. all other	samples: 47 / 233
accuracy	0.960714285714286
confidence	0.912089069819735
failed:	11,12,13,14,16,20,24,41,42,45,46

gene	signal-to-noise	p	decision limit	gene symbol
214761_at	0.970557084257439	0		OAZ
219013_at	-0.898496343314981	0*	66.1	FLJ21634
243362_s_at	0.885999523838621	0*	72.85	LEF1
229487_at	0.879786130972461	0		
224918_x_at	-0.87724222950274	0		MGST1
231736_x_at	-0.869791217148163	0		MGST1
203373_at	0.858710621146821	0		STATI2
201540_at	0.85206943650763	0		FHL1
218589_at	0.849690653983403	0		P2Y5
210487_at	0.84637653892686	0		DNTT
219753_at	0.825247459991453	0		STAG3
223703_at	-0.822007469078868	0		CDA017
203372_s_at	0.821441808884396	0		STATI2
243363_at	0.820493794299965	0		LEF1
208248_x_at	-0.812940151824066	0		APLP2
208702_x_at	-0.8015522739222	0		APLP2
200661_at	-0.791253715797081	0		PPGB
34726_at	0.790007042454156	0		CACNB3
203795_s_at	0.78850089331931	0		BCL7A
230292_at	0.788256600173715	0		

ALL vs. AML	samples: 47 / 175			
accuracy	0.95045045045045			
confidence	0.894203385037297			
failed:	11,12,14,15,16,24,27,36,42,67 ,115			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
221558_s_at	1.12614883575596	0		LEF1
224918_x_at	-1.11745973177444	0		MGST1
41220_at	1.1150066427645	0		MSF
231736_x_at	-1.10060017375911	0		MGST1
205382_s_at	-1.01589067961124	0		DF
200661_at	-1.01253920985203	0		PPGB
208702_x_at	-1.00158300302362	0		APLP2
223703_at	-0.995387894243593	0		CDA017
211404_s_at	-0.985001465936684	0		APLP2
208248_x_at	-0.981211344877388	0		APLP2
210948_s_at	0.973218284228957	0		LEF1
243363_at	0.96583392519617	0		LEF1
214875_x_at	-0.960268914986593	0		APLP2
214761_at	0.959842337636482	0		OAZ
219013_at	-0.956595406819358	0		FLJ21634
243362_s_at	0.953556737247221	0		LEF1
204215_at	0.94873841769727	0*	886.4	MGC4175
217989_at	-0.944775256168326	0		LOC51170
203041_s_at	-0.944024039515523	0		LAMP2
AFFX-r2-Bs-dap-3_at - HG-U133A	0.252552477574741	0		

ALL vs. CLL	samples: 47 / 35			
accuracy	0.98780487804878			
confidence	1			
failed:	42			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
225927_at	-2.54386605255744	0*	1826.45	MAP3K1
224838_at	-2.29762422456477	0		
239287_at	-2.24993335468714	0		
202625_at	-2.06005808097774	0		LYN
208091_s_at	-2.03821117161393	0		DKFZP564K0822
204511_at	-2.00374139556454	0		KIAA0793
AFFX-HUMGAPDH/M33197_3_at - HG-U133B	1.9580832868002	0		GAPD
201417_at	1.9394827392449	0		
212914_at	-1.89064460393095	0		PKP4
207616_s_at	-1.88874561163207	0		TANK
223391_at	-1.87749885738082	0		LOC81537
201416_at	1.87582200205394	0		SOX4
44790_s_at	-1.85742303821942	0		FLJ21562
201462_at	-1.84559373056342	0		KIAA0193
205997_at	-1.82244878004852	0		ADAM28
219471_at	-1.82048094941098	0		FLJ21562
228390_at	-1.81369080029951	0		
206337_at	-1.81234629147377	0		CCR7
218191_s_at	-1.80317310126938	0		FLJ11240
AFFX-HUMGAPDH/M33197_M_at - HG-U133A	1.47237903994758	0		GAPD

ALL vs. CML	samples: 47 / 14			
accuracy	0.983606557377049			
confidence	1			
failed:	14			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
206440_at	-2.27699665329749	0		VELI1
210254_at	-2.24512948903079	0		
205557_at	-2.24379338781824	0*	8347.8	BPI
200654_at	-2.2057677822486	0		P4HB
206676_at	-2.19594220925272	0		CEACAM8
206111_at	-2.12209587819278	0		RNASE2
212268_at	-2.06787563904532	0		SERPINB1
214317_x_at	2.05505121682362	0		RPS9
211275_s_at	-2.0481841650404	0		GYG
212531_at	-1.99958187859813	0		LCN2
206207_at	-1.98193517857499	0		CLC
203757_s_at	-1.92761412477345	0		CEACAM6
204174_at	-1.91747003112972	0		ALOX5AP
207802_at	-1.90928433527318	0		SGP28
211657_at	-1.8921241480708	0		
213572_s_at	-1.87212093424446	0		SERPINB1
203949_at	-1.85990729100683	0		MPO
204351_at	-1.8590267215838	0		S100P
229790_at	1.85536512952314	0		TERF2
231854_at	1.67066719911877	0		

ALL vs. normal BM	samples: 47 / 9			
accuracy	1			
confidence	0.957516862739848			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
203645_s_at	-2.39693596113584	0		CD163
224976_at	-2.31479350464798	0		NFIA
224975_at	-2.18458278616315	0		NFIA
218424_s_at	-2.15949227895441	0		FLJ10829
223044_at	-2.14051279056572	0		SLC11A3
230988_at	-2.14049582400222	0		
225792_at	-2.11616520995308	0		
223280_x_at	-2.05336993376349	0*	2365.65	MS4A6A
224970_at	-2.02013541876615	0		NFIA
215049_x_at	-1.97618634292152	0		CD163
224356_x_at	-1.93812195252731	0*	2203.55	MS4A6A
218916_at	1.86645836675574	0*	26.2	FLJ23436
201506_at	-1.80048485113822	0		TGFBI
202443_x_at	-1.76350311549162	0		NOTCH2
226751_at	-1.75212231661127	0		DKFZP566K1924
218516_s_at	1.74956324093924	0		FLJ20421
201416_at	1.74432934603701	0		SOX4
226448_at	-1.73849176051715	0		
221731_x_at	-1.73207109032378	0		CSPG2
40189_at	1.37012925113272	0		SET

AML vs. all other	samples: 175 / 105
accuracy	0.882142857142857
confidence	0.867062232379983
failed:	17,20,35,51,64,68,86,143,145,189,191,199,217,253,258,259,260, 261,262,263,264,265,266,267,268,269,270,271,272,273,274,275, 280

gene	signal-to-noise	p	decision limit	gene symbol
205382_s_at	0.993761979191943	0		DF
221558_s_at	-0.953118583183064	0		LEF1
233177_s_at	0.898951559660059	0		KIAA1184
221969_at	-0.897763040671617	0*	607.75	PAX5
206398_s_at	-0.887949095602823	0*	365.2	CD19
41220_at	-0.874923766956177	0		MSF
200661_at	0.864835685361425	0		PPGB
203005_at	0.859889652633032	0		LTBR
211404_s_at	0.848185516601275	0		APLP2
208702_x_at	0.844435105361934	0		APLP2
210948_s_at	-0.841151060868526	0		LEF1
221739_at	0.821598909550794	0		IL27
206255_at	-0.821040810957811	0		BLK
205049_s_at	-0.820101703791881	0		CD79A
231736_x_at	0.818968232559464	0		MGST1
214875_x_at	0.818667567167621	0		APLP2
241353_s_at	0.816044719173918	0		
215785_s_at	-0.815070063021364	0		CYFIP2
242774_at	-0.813216814821168	0		SYNE-2
201200_at	0.812769337801728	0		CREG

AML vs. CLL	samples: 175 / 35			
accuracy	0.995238095238095			
confidence	1			
failed:	206			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
224838_at	-3.02914553670118	0		
243780_at	-2.47595031535238	0		
223514_at	-2.32616269321224	0*	401.75	CARD11
212827_at	-2.28998110195367	0		IGHM
239287_at	-2.23009354706297	0		
44790_s_at	-2.21489306728323	0		FLJ21562
228390_at	-2.19221126790713	0		
229072_at	-2.17738285030653	0		
224837_at	-2.17198876436932	0		FOXP1
223391_at	-2.16212129696244	0		LOC81537
219471_at	-2.15559694298803	0		FLJ21562
208456_s_at	-2.12547066951316	0		RRAS2
201998_at	-2.10911401275474	0		SIAT1
223287_s_at	-2.10564435434002	0		FOXP1
212590_at	-2.10270770151805	0		
229844_at	-2.06808415651229	0		
236280_at	-2.03990689910927	0		
230768_at	-2.02994432200127	0		
208091_s_at	-2.02423665232113	0		DKFZP564K0822
208864_s_at	2.01877334646697	0		TXN

AML vs. CML	samples: 175 / 14			
accuracy	0.994708994708995			
confidence	0.981183073260496			
failed:	180			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212531_at	-2.81906069321688	0		LCN2
205557_at	-2.2207882876404	0		BPI
207802_at	-2.21833080555492	0*	3039.3	SGP28
209772_s_at	-2.16935748435446	0*	3429.4	CD24
206676_at	-2.13938671438891	0*	7865.1	CEACAM8
210244_at	-2.09652835954526	0		CAMP
216379_x_at	-2.08891207162947	0		
209771_x_at	-2.07371303677609	0		CD24
203936_s_at	-2.04218257187719	0*	7297.15	MMP9
202018_s_at	-1.88089473759452	0		LTF
201029_s_at	1.75719687256454	0*	1592.95	MIC2
223894_s_at	-1.74095406790845	0*	455.2	FTS
207269_at	-1.71722340830381	0*	15756.25	DEFA4
203757_s_at	-1.70294141320522	0		CEACAM6
205863_at	-1.70288697664328	0		S100A12
211657_at	-1.69693858255424	0		
205513_at	-1.64900632810016	0		TCN1
223839_s_at	-1.60135318115808	0		
210254_at	-1.56841234039023	0		
39835_at	1.23907392901905	0		SBF1

AML vs. normal BM	samples: 175 / 9			
accuracy	0.989130434782609			
confidence	1			
failed:	48,179			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212531_at	-2.40063827757397	0		LCN2
210244_at	-2.19732582937896	0		CAMP
202018_s_at	-2.14183206922033	0*	12387	LTF
231241_at	-2.03350599733901	0		
218516_s_at	1.74555082511394	0		FLJ20421
225792_at	-1.63422305998419	0		
228377_at	-1.59923589910665	0		KIAA1384
244652_at	-1.53426287521002	0		
225700_at	-1.53281555961668	0		
201396_s_at	1.46522297092893	0		SGT
207802_at	-1.44831955629631	0		SGP28
208141_s_at	1.43174521272245	0		MGC4293
207269_at	-1.42268720126305	0		DEFA4
200631_s_at	1.40042176845386	0		SET
208651_x_at	-1.39706589332311	0		CD24
227151_at	1.39359540599557	0		
210004_at	-1.38874742675296	0		OLR1
203367_at	1.38466765321816	0		DUSP14
218916_at	1.37378311700267	0		FLJ23436
40189_at	1.35679082157773	0		SET

CLL vs. all other	samples: 35 / 245			
accuracy	0.996428571428571			
confidence	1			
failed:	31			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
224838_at	2.79416338027605	0		
239287_at	2.23575554655226	0*	630.55	
223514_at	2.14355675231863	0		CARD11
44790_s_at	2.09543551175381	0		FLJ21562
228390_at	2.08427210739342	0		
223391_at	2.06238950802763	0		LOC81537
208091_s_at	2.03394814388952	0		DKFZP564K0822
219471_at	2.03307120566838	0		FLJ21562
229072_at	2.02056757302765	0		
243780_at	2.01909938888062	0		
223287_s_at	2.00808281461583	0		FOXP1
212590_at	1.988255009037	0		
229844_at	1.97715993452055	0		
208456_s_at	1.97615733325	0		RRAS2
201998_at	1.97574573382318	0		SIAT1
225927_at	1.95021458529306	0		MAP3K1
202589_at	-1.92898152025988	0		TYMS
230768_at	1.92227084324811	0		
224837_at	1.91127793077848	0		FOXP1
214615_at	1.91102072539205	0		P2Y10

CLL vs. CML	samples: 35 / 14			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210254_at	-4.916136683483	0*	3718.45	
205557_at	-4.69748391957959	0		BPI
206111_at	-4.58827527010058	0		RNASE2
206871_at	-4.44599783341785	0		ELA2
202503_s_at	-4.43537957592345	0		KIAA0101
209619_at	4.43385248113705	0		CD74
203949_at	-4.37548189755698	0		MPO
202589_at	-4.23719643920935	0		TYMS
212268_at	-4.17631489395545	0		SERPINB1
212531_at	-4.14992393038831	0		LCN2
206676_at	-4.00803780946535	0		CEACAM8
210334_x_at	-3.95114669210453	0		BIRC5
204670_x_at	3.87175276162045	0		HLA-DRB5
224838_at	3.70493413772712	0		
208306_x_at	3.70225355884714	0		HLA-DRB4
212750_at	3.65712314278563	0		PPP1R16B
200654_at	-3.65009107919176	0		P4HB
213572_s_at	-3.6081864481715	0		SERPINB1
207269_at	-3.56289987570257	0		DEFA4
41577_at	3.23509608373299	0		PPP1R16B

CLL vs. normal BM	samples: 35 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
210613_s_at	-4.82300971873091	0*	459.4	SYNGR1
204776_at	-4.80025506569938	0		THBS4
218662_s_at	-4.51907004754891	0		HCAP-G
205051_s_at	-4.20900192886026	0		KIT
202503_s_at	-4.20172034150208	0		KIAA0101
202580_x_at	-4.18939678293477	0		FOXM1
202018_s_at	-4.17647701264208	0		LTF
206871_at	-4.05443661323157	0		ELA2
230988_at	-4.04866661866689	0		
224975_at	-3.82592750915745	0		NFIA
227230_s_at	-3.69195069014623	0		KIAA1211
209714_s_at	-3.58566958034221	0		CDKN3
212531_at	-3.57925128815766	0		LCN2
214575_s_at	-3.54194227378832	0		AZU1
223785_at	-3.42904648124574	0		FLJ10719
224976_at	-3.40063969780409	0		NFIA
218424_s_at	-3.38874340856322	0		FLJ10829
202705_at	-3.38096906634746	0		CCNB2
202589_at	-3.36383889155021	0		TYMS

CML vs. all other	samples: 14 / 266			
accuracy	0.982142857142857			
confidence	0.984872053615011			
failed:	1,5,7,11,28			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
212531_at	2.22285326348413	0		LCN2
205557_at	2.21595356438375	0*	11581.65	BPI
206676_at	2.03792028235761	0		CEACAM8
209772_s_at	1.92045186041392	0*	3429.4	CD24
207802_at	1.85737448791579	0		SGP28
216379_x_at	1.78690596201348	0		
209771_x_at	1.78099473628645	0		CD24
203936_s_at	1.76415242821485	0		MMP9
211657_at	1.70950599523981	0		
203757_s_at	1.69567517095366	0		CEACAM6
210254_at	1.67886160490067	0		
202018_s_at	1.66318733776484	0		LTF
211275_s_at	1.64178539863162	0		GYG
205513_at	1.62356154923572	0		TCN1
205863_at	1.61881375489405	0		S100A12
223839_s_at	1.58264885795695	0		
206440_at	1.58048354996482	0		VELI1
210244_at	1.57522288410986	0		CAMP
207269_at	1.5628690030838	0		DEFA4
204174_at	1.55441937407586	0		ALOX5AP

OML vs. normal BM	samples: 14 / 9			
accuracy	1			
confidence	1			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
227198_at	-3.96995770729437	0*	39.95	
204562_at	-3.83910818190111	0		IRF4
227749_at	-3.11980636745679	0		
228377_at	-2.65145492785893	0		KIAA1384
226713_at	-2.28229285614419	0		
209619_at	-2.27384420268273	0		CD74
227375_at	-2.22184735546056	0		DKFZP566D1346
204057_at	-2.13119125485665	0		ICSBP1
201506_at	-2.05058862618543	0		TGFBI
221558_s_at	-2.0055054625083	0		LEF1
227867_at	-2.00414646646454	0		
225331_at	-1.95134035825926	0		
223280_x_at	-1.95125537387335	0		MS4A6A
243780_at	-1.94601159348593	0		
228055_at	-1.94418493221925	0		
204670_x_at	-1.94197079510435	0		HLA-DRB5
208683_at	-1.93662356244796	0		CAPN2
210356_x_at	-1.92014292171279	0		MS4A2
209670_at	-1.89146017871026	0		TRA
AFFX-HUMGAPDH/M33197_3_at - HG-U133B	1.0887744230798	0		GAPD

normal BM vs. all other	samples: 9 / 271			
accuracy	0.975			
confidence	0.993135080527801			
failed:	1,3,4,5,6,8,9			
gene	**signal-to-noise**	**p**	**decision limit**	**gene symbol**
231241_at	1.74993445464942	0*	145.7	
202018_s_at	1.72201479004034	0		LTF
212531_at	1.63441866839502	0		LCN2
210244_at	1.48912390888008	0		CAMP
244652_at	1.41243941049484	0		
224976_at	1.41100451645958	0		NFIA
218916_at	-1.39948677493198	0		FLJ23436
218516_s_at	-1.39516117721544	0		FLJ20421
208141_s_at	-1.38238694283986	0		MGC4293
201396_s_at	-1.3585420884411	0		SGT
230988_at	1.30213323583922	0		
200631_s_at	-1.2906273376207	0		SET
224975_at	1.28440445542309	0		NFIA
227497_at	1.2690169947779	0*	317.95	
203535_at	1.26454687252909	0		S100A9
203367_at	-1.25252661696593	0		DUSP14
40189_at	-1.24465725545763	0		SET
223785_at	1.23866083411764	0		FLJ10719
225700_at	1.22842543098158	0		
207269_at	1.22161055733689	0		DEFA4

Table 42: Analysis of 4 leukemia subgroups and normal bone marrow (BM) according to the method described by Westfall & Young. The 499 significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

geneID	Golub	rawp	adjp	
200998_s_at		0.0001	**0.0001**	CKAP4
201012_at		0.0001	**0.0001**	ANXA1
201079_at		0.0001	**0.0001**	SYNGR2
201189_s_at		0.0001	**0.0001**	ITPR3
201200_at	+	0.0001	**0.0001**	CREG
201362_at		0.0001	**0.0001**	NS1-BP
201812_s_at		0.0001	**0.0001**	LOC54543
201853_s_at		0.0001	**0.0001**	CDC25B
201858_s_at		0.0001	**0.0001**	PRG1
201889_at		0.0001	**0.0001**	GS3786
201962_s_at		0.0001	**0.0001**	SBB103
201998_at	+	0.0001	**0.0001**	SIAT1
202018_s_at	*	0.0001	**0.0001**	LTF
202080_s_at		0.0001	**0.0001**	KIAA1042
202254_at		0.0001	**0.0001**	KIAA0440
202421_at		0.0001	**0.0001**	IGSF3
202441_at		0.0001	**0.0001**	KEO4
202524_s_at		0.0001	**0.0001**	KIAA0275
202606_s_at		0.0001	**0.0001**	TLK1
202709_at		0.0001	**0.0001**	FMOD
202723_s_at		0.0001	**0.0001**	FOXO1A
202761_s_at		0.0001	**0.0001**	SYNE-2
202822_at		0.0001	**0.0001**	LPP
202880_s_at		0.0001	**0.0001**	PSCD1
203020_at		0.0001	**0.0001**	KIAA0471
203037_s_at		0.0001	**0.0001**	KIAA0429
203057_s_at		0.0001	**0.0001**	PRDM2
203143_s_at		0.0001	**0.0001**	KIAA0040
203217_s_at		0.0001	**0.0001**	SIAT9
203233_at		0.0001	**0.0001**	IL4R
203241_at		0.0001	**0.0001**	UVRAG
203288_at		0.0001	**0.0001**	KIAA0355
203385_at		0.0001	**0.0001**	DGKA
203607_at		0.0001	**0.0001**	SAC2

203685_at		0.0001	**0.0001** BCL2
203753_at		0.0001	**0.0001** TCF4
203757_s_at	+	0.0001	**0.0001** CEACAM6
203881_s_at		0.0001	**0.0001** DMD
203936_s_at	*	0.0001	**0.0001** MMP9
204000_at		0.0001	**0.0001** GNB5
204118_at		0.0001	**0.0001** CD48
204192_at		0.0001	**0.0001** CD37
204199_at		0.0001	**0.0001** RALGPS1A
204205_at		0.0001	**0.0001** MDS019
204215_at	*	0.0001	**0.0001** MGC4175
204269_at		0.0001	**0.0001** PIM2
204328_at		0.0001	**0.0001** LAK-4P
204352_at		0.0001	**0.0001** TRAF5
204401_at		0.0001	**0.0001** KCNN4
204511_at	+	0.0001	**0.0001** KIAA0793
204512_at		0.0001	**0.0001** HIVEP1
204604_at		0.0001	**0.0001** PFTK1
204674_at		0.0001	**0.0001** LRMP
204731_at		0.0001	**0.0001** TGFBR3
204793_at		0.0001	**0.0001** KIAA0443
204882_at		0.0001	**0.0001** KIAA0053
204922_at		0.0001	**0.0001** FLJ22531
204951_at		0.0001	**0.0001** ARHH
205019_s_at		0.0001	**0.0001** VIPR1
205040_at		0.0001	**0.0001** ORM1
205041_s_at		0.0001	**0.0001** ORM1
205049_s_at	+	0.0001	**0.0001** CD79A
205105_at		0.0001	**0.0001** MAN2A1
205192_at		0.0001	**0.0001** MAP3K14
205223_at		0.0001	**0.0001** KIAA0645
205267_at		0.0001	**0.0001** POU2AF1
205306_x_at		0.0001	**0.0001** KMO
205308_at		0.0001	**0.0001** LOC51101
205383_s_at		0.0001	**0.0001** ZNF288
205414_s_at		0.0001	**0.0001** KIAA0672
205513_at	+	0.0001	**0.0001** TCN1
205547_s_at		0.0001	**0.0001** TAGLN
205557_at	*	0.0001	**0.0001** BPI
205599_at		0.0001	**0.0001** TRAF1
205613_at		0.0001	**0.0001** LOC51760
205627_at		0.0001	**0.0001** CDA

205671_s_at		0.0001	**0.0001** HLA-DOB
205691_at		0.0001	**0.0001** SYNGR3
205790_at		0.0001	**0.0001** SCAP1
205801_s_at		0.0001	**0.0001** GRP3
205805_s_at		0.0001	**0.0001** ROR1
205863_at	+	0.0001	**0.0001** S100A12
205901_at		0.0001	**0.0001** PNOC
205933_at		0.0001	**0.0001** SETBP1
205997_at	+	0.0001	**0.0001** ADAM28
206111_at	+	0.0001	**0.0001** RNASE2
206126_at		0.0001	**0.0001** BLR1
206150_at		0.0001	**0.0001** TNFRSF7
206177_s_at		0.0001	**0.0001** ARG1
206245_s_at		0.0001	**0.0001** NS1-BP
206255_at	+	0.0001	**0.0001** BLK
206337_at	+	0.0001	**0.0001** CCR7
206398_s_at	*	0.0001	**0.0001** CD19
206513_at		0.0001	**0.0001** AIM2
206515_at		0.0001	**0.0001** CYP4F3
206676_at	*	0.0001	**0.0001** CEACAM8
206759_at		0.0001	**0.0001** FCER2
206760_s_at		0.0001	**0.0001** FCER2
207000_s_at		0.0001	**0.0001** PPP3CC
207168_s_at		0.0001	**0.0001** H2AFY
207269_at	*	0.0001	**0.0001** DEFA4
207384_at		0.0001	**0.0001** PGLYRP
207641_at		0.0001	**0.0001** TACI
207700_s_at		0.0001	**0.0001** NCOA3
207734_at		0.0001	**0.0001** FLJ20340
207777_s_at		0.0001	**0.0001** SP140
207802_at	*	0.0001	**0.0001** SGP28
207819_s_at		0.0001	**0.0001** ABCB4
207957_s_at		0.0001	**0.0001** PRKCB1
208091_s_at	+	0.0001	**0.0001** DKFZP564K0822
208168_s_at		0.0001	**0.0001** CHIT1
208190_s_at		0.0001	**0.0001** LISCH7
208195_at		0.0001	**0.0001** TTN
208268_at		0.0001	**0.0001** ADAM28
208456_s_at	+	0.0001	**0.0001** RRAS2
208470_s_at		0.0001	**0.0001** HPR
208623_s_at		0.0001	**0.0001** VIL2
208657_s_at		0.0001	**0.0001** MSF

208864_s_at	+	0.0001	**0.0001** TXN
208913_at		0.0001	**0.0001** GGA2
208914_at		0.0001	**0.0001** GGA2
209060_x_at		0.0001	**0.0001** NCOA3
209061_at		0.0001	**0.0001** NCOA3
209062_x_at		0.0001	**0.0001** NCOA3
209075_s_at		0.0001	**0.0001** NIFU
209236_at		0.0001	**0.0001**
209306_s_at		0.0001	**0.0001** SWAP70
209307_at		0.0001	**0.0001** SWAP70
209374_s_at		0.0001	**0.0001** IGHM
209412_at		0.0001	**0.0001** TMEM1
209682_at		0.0001	**0.0001** CBLB
209685_s_at		0.0001	**0.0001** PRKCB1
209761_s_at		0.0001	**0.0001** SP110
209765_at		0.0001	**0.0001** ADAM19
209772_s_at	*	0.0001	**0.0001** CD24
209780_at		0.0001	**0.0001** DKFZP564F013
209827_s_at		0.0001	**0.0001** IL16
209994_s_at		0.0001	**0.0001** ABCB1
210004_at	+	0.0001	**0.0001** OLR1
210244_at	+	0.0001	**0.0001** CAMP
210262_at		0.0001	**0.0001** TPX1
210268_at		0.0001	**0.0001** NFX1
210279_at		0.0001	**0.0001** GPR18
210356_x_at	+	0.0001	**0.0001** MS4A2
210658_s_at		0.0001	**0.0001** GGA2
210763_x_at		0.0001	**0.0001** LY117
210789_x_at		0.0001	**0.0001** CEACAM3
210948_s_at	+	0.0001	**0.0001** LEF1
211105_s_at		0.0001	**0.0001** NFATC1
211138_s_at		0.0001	**0.0001** KMO
211352_s_at		0.0001	**0.0001** NCOA3
211502_s_at		0.0001	**0.0001** PFTK1
211657_at	+	0.0001	**0.0001**
211771_s_at		0.0001	**0.0001** POU2F2
211883_x_at		0.0001	**0.0001** CEACAM1
211889_x_at		0.0001	**0.0001** CEACAM1
211984_at		0.0001	**0.0001**
212074_at		0.0001	**0.0001** KIAA0810
212229_s_at		0.0001	**0.0001**
212231_at		0.0001	**0.0001** FBXO21

212268_at	+	0.0001	**0.0001** SERPINB1
212311_at		0.0001	**0.0001** KIAA0746
212313_at		0.0001	**0.0001**
212314_at		0.0001	**0.0001** KIAA0746
212345_s_at		0.0001	**0.0001** DKFZP586F2423
212382_at		0.0001	**0.0001**
212385_at		0.0001	**0.0001**
212386_at		0.0001	**0.0001**
212387_at		0.0001	**0.0001**
212400_at		0.0001	**0.0001**
212531_at	+	0.0001	**0.0001** LCN2
212569_at		0.0001	**0.0001** KIAA0650
212577_at		0.0001	**0.0001** KIAA0650
212579_at		0.0001	**0.0001** KIAA0650
212589_at		0.0001	**0.0001** RRAS2
212590_at	+	0.0001	**0.0001**
212614_at		0.0001	**0.0001**
212660_at		0.0001	**0.0001** KIAA0239
212733_at		0.0001	**0.0001** KIAA0226
212735_at		0.0001	**0.0001** KIAA0226
212827_at	+	0.0001	**0.0001** IGHM
212838_at		0.0001	**0.0001** KIAA1010
212886_at		0.0001	**0.0001** DKFZP434C171
212914_at	+	0.0001	**0.0001** PKP4
212956_at		0.0001	**0.0001** KIAA0882
212960_at		0.0001	**0.0001** KIAA0882
212970_at		0.0001	**0.0001**
212985_at		0.0001	**0.0001**
213049_at		0.0001	**0.0001** DKFZp566D133
213142_x_at		0.0001	**0.0001** LOC54103
213295_at		0.0001	**0.0001**
213309_at		0.0001	**0.0001** PLCL2
213353_at		0.0001	**0.0001** ABCA5
213370_s_at		0.0001	**0.0001** DKFZP434L243
213453_x_at		0.0001	**0.0001** GAPD
213511_s_at		0.0001	**0.0001**
213572_s_at	+	0.0001	**0.0001** SERPINB1
213600_at		0.0001	**0.0001** KIAA0545
213622_at		0.0001	**0.0001** COL9A2
213674_x_at		0.0001	**0.0001** IGHG3
213689_x_at		0.0001	**0.0001** RPL5
213772_s_at		0.0001	**0.0001** GGA2

213891_s_at		0.0001	0.0001
213927_at		0.0001	0.0001
214238_at		0.0001	0.0001
214615_at	+	0.0001	0.0001 P2Y10
214686_at		0.0001	0.0001 ZNF266
214786_at		0.0001	0.0001 MAP3K1
214924_s_at		0.0001	0.0001
215100_at		0.0001	0.0001
215346_at		0.0001	0.0001 TNFRSF5
215785_s_at	+	0.0001	0.0001 CYFIP2
216044_x_at		0.0001	0.0001
216095_x_at		0.0001	0.0001 MTMR1
216218_s_at		0.0001	0.0001 PLCL2
216356_x_at		0.0001	0.0001 BAIAP3
217398_x_at		0.0001	0.0001
217418_x_at		0.0001	0.0001 MS4A2
217478_s_at		0.0001	0.0001
217504_at		0.0001	0.0001 ABCA6
217838_s_at		0.0001	0.0001 RNB6
217950_at		0.0001	0.0001 NOSIP
218090_s_at		0.0001	0.0001
218100_s_at		0.0001	0.0001 ESRRBL1
218329_at		0.0001	0.0001 PRDM4
218354_at		0.0001	0.0001 LOC51693
218531_at		0.0001	0.0001 FLJ21749
218614_at		0.0001	0.0001 FLJ10652
218974_at		0.0001	0.0001 FLJ10159
219029_at		0.0001	0.0001 FLJ21657
219073_s_at		0.0001	0.0001 OSBPL10
219221_at		0.0001	0.0001 FLJ22332
219471_at	+	0.0001	0.0001 FLJ21562
219574_at		0.0001	0.0001 FLJ20668
219690_at		0.0001	0.0001 FLJ22573
219734_at		0.0001	0.0001 FLJ20174
219820_at		0.0001	0.0001 NTT5
220001_at		0.0001	0.0001 PADI5
220007_at		0.0001	0.0001 FLJ13984
220059_at		0.0001	0.0001 BRDG1
220118_at		0.0001	0.0001 TZFP
220338_at		0.0001	0.0001 FLJ10244
220987_s_at		0.0001	0.0001 DKFZP434J037
220999_s_at		0.0001	0.0001 PRO1331

221011_s_at		0.0001	**0.0001** DKFZP566J091
221030_s_at		0.0001	**0.0001** DKFZP564B1162
221234_s_at		0.0001	**0.0001** BACH2
221239_s_at		0.0001	**0.0001** SPAP1
221268_s_at		0.0001	**0.0001** LOC81537
221331_x_at		0.0001	**0.0001** CTLA4
221558_s_at	+	0.0001	**0.0001** LEF1
221586_s_at		0.0001	**0.0001** E2F5
221601_s_at		0.0001	**0.0001** TOSO
221602_s_at		0.0001	**0.0001** TOSO
221778_at		0.0001	**0.0001** KIAA1718
221865_at		0.0001	**0.0001**
221969_at	*	0.0001	**0.0001** PAX5
222073_at		0.0001	**0.0001** COL4A3
222146_s_at		0.0001	**0.0001**
222150_s_at		0.0001	**0.0001**
222520_s_at		0.0001	**0.0001** ESRRBL1
222996_s_at		0.0001	**0.0001** HSPC195
223287_s_at	+	0.0001	**0.0001** FOXP1
223391_at	+	0.0001	**0.0001** LOC81537
223422_s_at		0.0001	**0.0001** DKFZP564B1162
223514_at	*	0.0001	**0.0001** CARD11
223522_at		0.0001	**0.0001** GL012
223595_at		0.0001	**0.0001** AD031
223894_s_at	*	0.0001	**0.0001** FTS
224404_s_at		0.0001	**0.0001** IRTA2
224405_at		0.0001	**0.0001** IRTA2
224406_s_at		0.0001	**0.0001** IRTA2
224482_s_at		0.0001	**0.0001** MGC11316
224516_s_at		0.0001	**0.0001** HSPC195
224609_at		0.0001	**0.0001** CTL2
224735_at		0.0001	**0.0001**
224811_at		0.0001	**0.0001**
224833_at		0.0001	**0.0001** ETS1
224837_at	+	0.0001	**0.0001** FOXP1
224838_at	+	0.0001	**0.0001**
224994_at		0.0001	**0.0001** CAMK2D
225136_at		0.0001	**0.0001**
225144_at		0.0001	**0.0001**
225230_at		0.0001	**0.0001** CEPT1
225246_at		0.0001	**0.0001** STIM2
225250_at		0.0001	**0.0001** STIM2

225327_at		0.0001	0.0001 FLJ10980
225512_at		0.0001	0.0001
225624_at		0.0001	0.0001
225629_s_at		0.0001	0.0001 KIAA1538
225635_s_at		0.0001	0.0001
225640_at		0.0001	0.0001
225917_at		0.0001	0.0001 DKFZp762B226
225927_at	*	0.0001	0.0001 MAP3K1
226005_at		0.0001	0.0001
226008_at		0.0001	0.0001 HCA4
226013_at		0.0001	0.0001
226063_at		0.0001	0.0001
226122_at		0.0001	0.0001
226147_s_at		0.0001	0.0001
226156_at		0.0001	0.0001 AKT2
226247_at		0.0001	0.0001
226250_at		0.0001	0.0001
226252_at		0.0001	0.0001
226258_at		0.0001	0.0001
226301_at		0.0001	0.0001 dJ55C23.6
226326_at		0.0001	0.0001
226384_at		0.0001	0.0001 HTPAP
226408_at		0.0001	0.0001 TEAD2
226454_at		0.0001	0.0001 LOC92979
226508_at		0.0001	0.0001
226538_at		0.0001	0.0001 MAN2A1
226550_at		0.0001	0.0001
226560_at		0.0001	0.0001
226625_at		0.0001	0.0001 TGFBR3
226635_at		0.0001	0.0001
226641_at		0.0001	0.0001
226713_at	+	0.0001	0.0001
226878_at		0.0001	0.0001
226905_at		0.0001	0.0001
226989_at		0.0001	0.0001
227030_at		0.0001	0.0001
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227121_at		0.0001	0.0001
227146_at		0.0001	0.0001
227152_at		0.0001	0.0001
227167_s_at		0.0001	0.0001
227173_s_at		0.0001	0.0001 BACH2

227189_at		0.0001	**0.0001** KIAA1599
227198_at	*	0.0001	**0.0001**
227224_at		0.0001	**0.0001**
227261_at		0.0001	**0.0001** KLF12
227393_at		0.0001	**0.0001**
227396_at		0.0001	**0.0001**
227408_s_at		0.0001	**0.0001** MSTP043
227414_at		0.0001	**0.0001** DKFZp547E052
227478_at		0.0001	**0.0001**
227533_at		0.0001	**0.0001**
227568_at		0.0001	**0.0001**
227606_s_at		0.0001	**0.0001** KIAA1373
227607_at		0.0001	**0.0001** KIAA1373
227670_at		0.0001	**0.0001**
227749_at	+	0.0001	**0.0001**
227767_at		0.0001	**0.0001** CSNK1G3
227817_at		0.0001	**0.0001**
227900_at		0.0001	**0.0001**
228003_at		0.0001	**0.0001**
228007_at		0.0001	**0.0001**
228029_at		0.0001	**0.0001** KIAA1982
228298_at		0.0001	**0.0001** LOC91523
228343_at		0.0001	**0.0001** POU2F2
228345_at		0.0001	**0.0001**
228377_at	+	0.0001	**0.0001** KIAA1384
228390_at	+	0.0001	**0.0001**
228471_at		0.0001	**0.0001**
228476_at		0.0001	**0.0001** KIAA1407
228518_at		0.0001	**0.0001** IGHG3
228551_at		0.0001	**0.0001**
228555_at		0.0001	**0.0001**
228592_at		0.0001	**0.0001**
228599_at		0.0001	**0.0001**
228693_at		0.0001	**0.0001**
228984_at		0.0001	**0.0001** KIAA1394
229001_at		0.0001	**0.0001**
229070_at		0.0001	**0.0001** MGC12335
229072_at	+	0.0001	**0.0001**
229194_at		0.0001	**0.0001**
229310_at		0.0001	**0.0001** KIAA1921
229383_at		0.0001	**0.0001**
229513_at		0.0001	**0.0001**

229659_s_at		0.0001	0.0001
229681_at		0.0001	0.0001
229750_at		0.0001	0.0001
229779_at		0.0001	0.0001
229844_at	+	0.0001	0.0001
229872_s_at		0.0001	0.0001 KIAA0493
229923_at		0.0001	0.0001
229934_at		0.0001	0.0001
230110_at		0.0001	0.0001
230245_s_at		0.0001	0.0001
230363_s_at		0.0001	0.0001 SAC2
230489_at		0.0001	0.0001 CD5
230499_at		0.0001	0.0001
230551_at		0.0001	0.0001
230648_at		0.0001	0.0001
230689_at		0.0001	0.0001
230753_at		0.0001	0.0001
230768_at	+	0.0001	0.0001
230793_at		0.0001	0.0001 FLJ20048
230802_at		0.0001	0.0001 DKFZP564B1162
230803_s_at		0.0001	0.0001 DKFZP564B1162
230834_at		0.0001	0.0001
230877_at		0.0001	0.0001 IGHG3
230917_at		0.0001	0.0001
230939_at		0.0001	0.0001
230983_at		0.0001	0.0001
230986_at		0.0001	0.0001
230997_at		0.0001	0.0001
231093_at		0.0001	0.0001 FCRH3
231332_at		0.0001	0.0001
231406_at		0.0001	0.0001
231418_at		0.0001	0.0001 MS4A2
231647_s_at		0.0001	0.0001 IRTA2
231656_x_at		0.0001	0.0001 OSBPL10
231775_at		0.0001	0.0001 TNFRSF10A
231793_s_at		0.0001	0.0001 CAMK2D
231794_at		0.0001	0.0001 CTLA4
231873_at		0.0001	0.0001
232027_at		0.0001	0.0001
232060_at		0.0001	0.0001
232112_at		0.0001	0.0001
232125_at		0.0001	0.0001

232210_at	0.0001	0.0001	
232614_at	0.0001	0.0001	
232739_at	0.0001	0.0001	
232950_s_at	0.0001	0.0001	NIR3
233483_at	0.0001	0.0001	
233955_x_at	0.0001	0.0001	HSPC195
234140_s_at	0.0001	0.0001	STIM2
234362_s_at	0.0001	0.0001	CTLA4
234725_s_at	0.0001	0.0001	SEMA4B
235023_at	0.0001	0.0001	
235051_at	0.0001	0.0001	
235061_at	0.0001	0.0001	
235331_x_at	0.0001	0.0001	
235353_at	0.0001	0.0001	KIAA0746
235372_at	0.0001	0.0001	FREB
235385_at	0.0001	0.0001	FLJ20668
235400_at	0.0001	0.0001	FREB
235401_s_at	0.0001	0.0001	FREB
235422_at	0.0001	0.0001	FALZ
235444_at	0.0001	0.0001	
235459_at	0.0001	0.0001	
235674_at	0.0001	0.0001	
235982_at	0.0001	0.0001	FCRH1
236190_at	0.0001	0.0001	
236226_at	0.0001	0.0001	
236248_x_at	0.0001	0.0001	
236265_at	0.0001	0.0001	
236280_at	0.0001	0.0001	
236293_at	0.0001	0.0001	
236301_at	0.0001	0.0001	
236341_at	0.0001	0.0001	CTLA4
236458_at	0.0001	0.0001	
236796_at	0.0001	0.0001	
236854_at	0.0001	0.0001	
236979_at	0.0001	0.0001	
237411_at	0.0001	0.0001	LOC153516
238055_at	0.0001	0.0001	
238057_at	0.0001	0.0001	
238376_at	0.0001	0.0001	
238516_at	0.0001	0.0001	BMPR2
238593_at	0.0001	0.0001	
238604_at	0.0001	0.0001	

238790_at		0.0001	0.0001
239054_at		0.0001	0.0001
239122_at		0.0001	0.0001 IL24
239152_at		0.0001	0.0001
239229_at		0.0001	0.0001
239231_at		0.0001	0.0001
239278_at		0.0001	0.0001
239287_at	*	0.0001	0.0001
239292_at		0.0001	0.0001
239442_at		0.0001	0.0001
239679_at		0.0001	0.0001
240061_at		0.0001	0.0001
240572_s_at		0.0001	0.0001
241483_at		0.0001	0.0001
242104_at		0.0001	0.0001
242388_x_at		0.0001	0.0001
242404_at		0.0001	0.0001
242458_at		0.0001	0.0001
242463_x_at		0.0001	0.0001
242541_at		0.0001	0.0001 ABCA9
242633_x_at		0.0001	0.0001
242774_at	+	0.0001	0.0001 SYNE-2
242866_x_at		0.0001	0.0001
242932_at		0.0001	0.0001
243030_at		0.0001	0.0001
243154_at		0.0001	0.0001
243780_at	+	0.0001	0.0001
243798_at		0.0001	0.0001
243932_at		0.0001	0.0001
243968_x_at		0.0001	0.0001
244261_at		0.0001	0.0001
32541_at		0.0001	0.0001 PPP3CC
35974_at		0.0001	0.0001 LRMP
37152_at		0.0001	0.0001 PPARD
37831_at		0.0001	0.0001 KIAA0545
38149_at		0.0001	0.0001 KIAA0053
41220_at	+	0.0001	0.0001 MSF
41660_at		0.0001	0.0001 CELSR1
44790_s_at	+	0.0001	0.0001 FLJ21562
49485_at		0.0001	0.0001 PRDM4
54970_at		0.0001	0.0001 DKFZP761I2123
74694_s_at		0.0001	0.0001 FLJ23282

AFFX-HUMGAPDH/M33197_3_at - HG-U133A	0.0001	**0.0001** GAPD
AFFX-HUMGAPDH/M33197_3_at + - HG-U133B	0.0001	**0.0001** GAPD
AFFX-HUMGAPDH/M33197_M_at + - HG-U133A	0.0001	**0.0001** GAPD

Table 43a: Functional annotation of all genes identified with relevance to leukemia subtyping

ID	Gene Symbol	Unigene_Cluster	SWISS-PROT	Locus Link	Map Location
1007_s_at_HG-U133A	DDR1	Hs.75562	Q08345	780	6p21.3
1729_at_HG-U133A	TRADD	Hs.89862	Q15628	8717	16q22
200008_s_at_HG-U133A	GDI2	Hs.56845	P50395	2665	10p15
200008_s_at_HG-U133B	GDI2	Hs.56845	P50395	2665	10p15
200023_s_at_HG-U133A	EIF3S5	Hs.7811	O00303	8665	2p16.1
200040_at_HG-U133A	KHDRBS1	Hs.119537	Q99760	10657	1p32
200047_s_at_HG-U133A	YY1	Hs.97496	P25490	7528	14q
200047_s_at_HG-U133B	YY1	Hs.97496	P25490	7528	14q
200056_s_at_HG-U133A	C1D	Hs.15164	Q13901	10438	2p13-p12
200068_s_at_HG-U133B	CANX	Hs.155560	P27824	821	5q35
200071_at_HG-U133A	SPF30	Hs.79968	O75940	10285	10q23
200072_s_at_HG-U133A	HNRPM	Hs.79024	P52272	4670	19p13.3-p13.2
200093_s_at_HG-U133A	HINT1	Hs.256697	P49773	3094	5q31.2
200094_s_at_HG-U133A	EEF2	Hs.75309	P13639	1938	19pter-q12
200598_s_at_HG-U133A	TRA1	Hs.82689	P14625	7184	12q24.2-q24.3
200608_s_at_HG-U133A	RAD21	Hs.81848	O60216	5885	8q24
200620_at_HG-U133A	C1orf8	Hs.11441	Q9BXS4	9528	1p36-p31
200625_s_at_HG-U133A	CAP	Hs.104125	Q01518	10487	1p34.3
200630_x_at_HG-U133A	SET	Hs.145279	Q15541	6418	9q34
200631_s_at_HG-U133A	SET	Hs.145279	Q01105	6418	9q34
200646_s_at_HG-U133A	NUCB1	Hs.172609	Q96BA4	4924	19q13.2-q13.4
200649_at_HG-U133A	NUCB1	Hs.172609	Q96BA4	4924	19q13.2-q13.4
200650_s_at_HG-U133A	LDHA	Hs.2795	P00338	3939	11p15.4
200654_at_HG-U133A	P4HB	Hs.75655	P07237	5034	17q25
200655_s_at_HG-U133A	CALM1	Hs.177656	AAH08597	801	14q24-q31
200656_s_at_HG-U133A	P4HB	Hs.75655	AAH10859	5034	17q25
200659_s_at_HG-U133A	PHB	Hs.75323	P35232	5245	17q21
200661_at_HG-U133A	PPGB	Hs.118126	P10619	5476	20q13.1
200665_s_at_HG-U133A	SPARC	Hs.111779	AAH08011	6678	5q31.3-q32
200673_at_HG-U133A	LAPTM4A	Hs.111894	Q15012	9741	2p24.3
200675_at_HG-U133A	CD81	Hs.54457	P18582	975	11p15.5
200679_x_at_HG-U133A	HMG1	Hs.337757	P09429	3146	13q12
200707_at_HG-U133A	PRKCSH	Hs.1432	Q96D06	5589	19p13.1-p13.2
200742_s_at_HG-U133A	CLN2	Hs.20478	O14773	1200	11p15
200743_s_at_HG-U133A	CLN2	Hs.20478	O14773	1200	11p15
200765_x_at_HG-U133A	CTNNA1	Hs.178452	AAH00385	1495	5q31
200770_s_at_HG-U133A	LAMC1	Hs.214982	P11047	3915	1q31
200825_s_at_HG-U133A	ORP150	Hs.277704	Q9Y4L1	10525	11q23.1-q23.3

200829_x_at_HG-U133A	ZNF207	Hs.62112	O43670	7756	17q11.2
200832_s_at_HG-U133A	SCD	Hs.119597	O00767	6319	10q23-q24
200867_at_HG-U133A					
200872_at_HG-U133A	S100A10	Hs.119301	P08206	6281	1q21
200890_s_at_HG-U133A	SSR1	Hs.250773	P43307	6745	6p23
200906_s_at_HG-U133A					
200907_s_at_HG-U133A	KIAA0992	Hs.194431	Q8WX93	23022	4q32.3
200917_s_at_HG-U133A	SRPR	Hs.75730	P08240	6734	11q23-q24
200931_s_at_HG-U133A	VCL	Hs.75350	P18206	7414	10q22.1-q23
200935_at_HG-U133A	CALR	Hs.16488	P27797	811	19p13.3-p13.2
200951_s_at_HG-U133A	CCND2	Hs.75586	P30279	894	12p13
200952_s_at_HG-U133A	CCND2	Hs.75586	P30279	894	12p13
200953_s_at_HG-U133A	CCND2	Hs.75586	P30279	894	12p13
200967_at_HG-U133A	PPIB	Hs.699	Q9BVK5	5479	15q21-q22
200968_s_at_HG-U133A	PPIB	Hs.699	P23284	5479	15q21-q22
200984_s_at_HG-U133A	CD59	Hs.278573	P13987	966	11p13
200985_s_at_HG-U133A	CD59	Hs.278573	AAH01506	966	11p13
200986_at_HG-U133A	SERPING1	Hs.151242	P05155	710	11q12-q13.1
200996_at_HG-U133A	ACTR3	Hs.5321	AAD51904	10096	2q13
200998_s_at_HG-U133A	CKAP4	Hs.74368	Q07065	10970	12q23.3
201004_at_HG-U133A	SSR4	Hs.102135	Q96BQ0	6748	Xq28
201005_at_HG-U133A	CD9	Hs.1244	P21926	928	12p13.3
201008_s_at_HG-U133A	TXNIP	Hs.179526	Q16226	10628	1q12
201012_at_HG-U133A	ANXA1	Hs.78225	P04083	301	9q12-q21.2
201015_s_at_HG-U133A	JUP	Hs.2340	Q15151	3728	17q21
201029_s_at_HG-U133A	MIC2	Hs.177543	AAH02584	4267	Xp22.32
201034_at_HG-U133A	ADD3	Hs.324470	Q9UEY8	120	10q24.2-q24.3
201061_s_at_HG-U133A	EPB72	Hs.160483	P27105	2040	9q34.1
201069_at_HG-U133A	MMP2	Hs.111301	P08253	4313	16q13-q21
201079_at_HG-U133A	SYNGR2	Hs.5097	O43760	9144	17qter
201105_at_HG-U133A	LGALS1	Hs.227751	P09382	3956	22q13.1
201125_s_at_HG-U133A	ITGB5	Hs.149846	AAH06541	3693	3q21.3
201137_s_at_HG-U133A	HLA-DPB1	Hs.814	Q30174	3115	6p21.3
201152_s_at_HG-U133A	MBNL	Hs.28578	Q96P92	4154	3q25
201153_s_at_HG-U133A	MBNL	Hs.28578	Q96RE3	4154	3q25
201162_at_HG-U133A	IGFBP7	Hs.119206	Q16270	3490	4q12
201163_s_at_HG-U133A	IGFBP7	Hs.119206	Q07822	3490	4q12
201164_s_at_HG-U133A	PUM1	Hs.153834	Q14671	9698	1p35.2
201189_s_at_HG-U133A	ITPR3	Hs.77515	Q14573	3710	6p21
201200_at_HG-U133A	CREG	Hs.5710	O75629	8804	1q24
201247_at_HG-U133A	SREBF2	Hs.108689	Q12772	6721	22q13
201263_at_HG-U133A	TARS	Hs.84131	P26639	6897	5p13-cen

201278_at_HG-U133A	DAB2	Hs.81988	P98082	1601	5p13
201281_at_HG-U133A	ADRM1	Hs.90107	Q16186	11047	20q13.33
201324_at_HG-U133A	EMP1	Hs.79368	P54849	2012	12p12.3
201334_s_at_HG-U133A	ARHGEF12	Hs.6582	O15086	23365	11q23.3
201338_x_at_HG-U133A	GTF3A	Hs.75113	Q9H2K0	2971	13q12.3-q13.1
201352_at_HG-U133A	YME1L1	Hs.206521	Q9UMR9	10730	10p14
201358_s_at_HG-U133A	COPB	Hs.3059	AAL39009	1315	11p15.2
201359_at_HG-U133A	COPB	Hs.3059	P53618	1315	11p15.2
201360_at_HG-U133A	CST3	Hs.135084	P01034	1471	20p11.21
201362_at_HG-U133A	NS1-BP	Hs.197298	Q9Y480	10625	1q25.1-q31.1
201377_at_HG-U133A	KIAA0144	Hs.8127	Q9BTU3	9898	1q21.2
201396_s_at_HG-U133A	SGT	Hs.203910	O43765	6449	19p13
201416_at_HG-U133A	SOX4	Hs.83484	Q99687	6659	6p22.3
201417_at_HG-U133A					
201425_at_HG-U133A	ALDH2	Hs.195432	P05091	217	12q24.2
201433_s_at_HG-U133A	PTDSS1	Hs.77329	Q9BUQ5	9791	8q22
201437_s_at_HG-U133A	EIF4E	Hs.79306	P06730	1977	4q21-q25
201462_at_HG-U133A	KIAA0193	Hs.75137	BAA12106	9805	7p14.3-p14.1
201463_s_at_HG-U133A	TALDO1	Hs.77290	P37837	6888	11p15.5-p15.4
201482_at_HG-U133A	QSCN6	Hs.77266	O00391	5768	1q24
201485_s_at_HG-U133A	RCN2	Hs.79088	AAH04892	5955	15q23
201486_at_HG-U133A	RCN2	Hs.79088	AAH04892	5955	15q23
201496_x_at_HG-U133A	MYH11	Hs.78344	O14729	4629	16p13.13-p13.12
201497_x_at_HG-U133A	MYH11	Hs.78344	O14729	4629	16p13.13-p13.12
201506_at_HG-U133A	TGFBI	Hs.118787	Q96IU7	7045	5q31
201530_x_at_HG-U133A	EIF4A1	Hs.129673	Q9BRB1	1973	17p13
201537_s_at_HG-U133A	DUSP3	Hs.181046	Q96HQ4	1845	17q21
201540_at_HG-U133A	FHL1	Hs.239069	Q13642	2273	Xq26
201548_s_at_HG-U133A	PLU-1	Hs.143323	O95811	10765	1q32.1
201564_s_at_HG-U133A	SNL	Hs.118400	Q96IH1	6624	7p22
201585_s_at_HG-U133A	SFPQ	Hs.180610	P23246	6421	1p34.2
201592_at_HG-U133A	EIF3S3	Hs.58189	O15372	8667	8q24.11
201595_s_at_HG-U133A	HT010	Hs.6375	Q9NZ37	55854	2q32.2
201596_x_at_HG-U133A	KRT18	Hs.65114	Q96GD2	3875	12q13
201602_s_at_HG-U133A	PPP1R12A	Hs.16533	Q96L23	4659	12q15-q21
201640_x_at_HG-U133A	CLPTM1	Hs.106671	Q9BSS5	1209	19q13.2-q13.3
201644_at_HG-U133A	TSTA3	Hs.264428	Q13630	7264	8q24.3
201652_at_HG-U133A	COPS5	Hs.198767	Q9BQ17	10987	8q12.3
201753_s_at_HG-U133A	ADD3	Hs.324470	Q9UEY8	120	10q24.2-q24.3
201761_at_HG-U133A	MTHFD2	Hs.154672	P13995	10797	2p12
201810_s_at_HG-U133A	SH3BP5	Hs.109150	O60239	9467	3p24.3
201811_x_at_HG-U133A	SH3BP5	Hs.109150	Q9BRM4	9467	3p24.3

201812_s_at_HG-U133A	LOC54543	Hs.112318	Q9P0U1	54543	7p21.3
201813_s_at_HG-U133A	KIAA0210	Hs.115740	Q92609	9779	3p24.3
201825_s_at_HG-U133A	LOC51097	Hs.238126	AAH26185	51097	1q44
201828_x_at_HG-U133A	CXX1	Hs.250708	O15255	8933	Xq26
201829_at_HG-U133A	NET1	Hs.25155	Q9UEN6	10276	10p15
201830_s_at_HG-U133A	NET1	Hs.25155	Q96D82	10276	10p15
201851_at_HG-U133A	SH3GL1	Hs.97616	Q9BWP4	6455	19p13.3
201853_s_at_HG-U133A	CDC25B	Hs.153752	P30305	994	20p13
201858_s_at_HG-U133A	PRG1	Hs.1908	P10124	5552	10q22.1
201874_at_HG-U133A	FLJ21047	Hs.14891	Q8WUP4	79620	1q23.2
201889_at_HG-U133A	GS3786	Hs.29882	Q92520	10447	7q22.1-q31.1
201922_at_HG-U133A	YR-29	Hs.8170	O95478	10412	5q13.3-q14.1
201923_at_HG-U133A	PRDX4	Hs.83383	AAH03609	10549	Xp22.13
201962_s_at_HG-U133A	SBB103	Hs.153639	O75598	10193	12q12
201968_s_at_HG-U133A	PGM1	Hs.1869	AAH19920	5236	1p31
201974_s_at_HG-U133A	LOC51622	Hs.289112	O95766	51622	7p22.1
201985_at_HG-U133A	KIAA0196	Hs.8294	AAH26951	9897	8p22
201988_s_at_HG-U133A	CREBL2	Hs.13313	O60519	1389	12p13
201998_at_HG-U133A	SIAT1	Hs.2554	P15907	6480	3q27-q28
202016_at_HG-U133A	MEST	Hs.79284	O15007	4232	7q32
202018_s_at_HG-U133A	LTF	Hs.105938	Q96KZ4	4057	3q21-q23
202028_s_at_HG-U133A	RPL38	Hs.2017	AAH00603	6169	17q23-q25
202052_s_at_HG-U133A	RAI14	Hs.15165	Q9Y3T5	26064	5p13.3-p13.2
202074_s_at_HG-U133A	OPTN	Hs.278898	AAL76327	10133	10p12.33
202080_s_at_HG-U133A	KIAA1042	Hs.6705	Q9UPV9	22906	3p25.3-p24.1
202085_at_HG-U133A	TJP2	Hs.75608	Q9UDY2	9414	9q13-q21
202095_s_at_HG-U133A	BIRC5	Hs.1578	Q969L1	332	17q25
202101_s_at_HG-U133A	RALB	Hs.348024	P11234	5899	2cen-q13
202113_s_at_HG-U133A	SNX2	Hs.11183	O60749	6643	5q23
202123_s_at_HG-U133A	ABL1	Hs.146355	P00519	25	9q34.1
202137_s_at_HG-U133A	BS69	Hs.301449	Q15326	10771	10p14
202148_s_at_HG-U133A	PYCR1	Hs.79217	P32322	5831	17q25.3
202150_s_at_HG-U133A	HEF1	Hs.80261	Q14511	10543	6p25-p24
202156_s_at_HG-U133A	CUGBP2	Hs.211610	Q92950	10659	10p13
202206_at_HG-U133A	ARL7	Hs.111554	AAM12606	10123	2q37.2
202249_s_at_HG-U133A	H326	Hs.110707	Q12839	50717	1q22-q23
202254_at_HG-U133A	KIAA0440	Hs.172180	BAA23712	26037	14q24.1
202262_x_at_HG-U133A	DDAH2	Hs.247362	O95865	23564	6p21.3
202265_at_HG-U133A	BMI1	Hs.431	P35226	648	10p13
202283_at_HG-U133A	SERPINF1	Hs.173594	P36955	5176	17p13.1
202288_at_HG-U133A	FRAP1	Hs.338207	P42345	2475	1p36.2
202328_s_at_HG-U133A	PKD1	Hs.75813	Q15140	5310	16p13.3

202332_at_HG-U133A	CSNK1E	Hs.79658	AAH06490	1454	22q13.1
202340_x_at_HG-U133A	NR4A1	Hs.1119	P22736	3164	12q13
202370_s_at_HG-U133A	CBFB	Hs.179881	Q13951	865	16q22.1
202371_at_HG-U133A	FLJ21174	Hs.194329	Q8WY12	79921	Xq22.1
202377_at_HG-U133A	HSOBRGRP	Hs.23581	O15243	54741	1
202382_s_at_HG-U133A	GNPI	Hs.278500	P46926	10007	5q21
202391_at_HG-U133A	BASP1	Hs.79516	Q9BWA5	10409	5p15.1-p14
202406_s_at_HG-U133A	TIAL1	Hs.182741	Q01085	7073	10q
202413_s_at_HG-U133A	USP1	Hs.35086	O94782	7398	1p32.1-p31.3
202421_at_HG-U133A	IGSF3	Hs.81234	O75054	3321	1p13
202441_at_HG-U133A	KEO4	Hs.285818	O75477	10613	10q21-q22
202443_x_at_HG-U133A	NOTCH2	Hs.8121	Q04721	4853	1p13-p11
202477_s_at_HG-U133A	GCP2	Hs.13386	Q9BSJ2	10844	10q26.3
202479_s_at_HG-U133A	GS3955	Hs.155418	Q92519	28951	2p25.1
202481_at_HG-U133A	SDR1	Hs.17144	Q9BUC8	9249	1p36.1
202503_s_at_HG-U133A	KIAA0101	Hs.81892	Q15004	9768	15q22.1
202519_at_HG-U133A	MONDOA	Hs.52081	Q8WYA5	22877	12q21.31
202524_s_at_HG-U133A	KIAA0275	Hs.74583	Q92563	9806	10pter-q25.3
202530_at_HG-U133A	MAPK14	Hs.79107	AAF36770	1432	6p21.3-p21.2
202535_at_HG-U133A	FADD	Hs.86131	Q13158	8772	11q13.3
202545_at_HG-U133A	PRKCD	Hs.155342	Q05655	5580	3p21.31
202551_s_at_HG-U133A	CRIM1	Hs.19280	Q9NZV1	51232	2p21
202552_s_at_HG-U133A	CRIM1	Hs.19280	Q9NZV1	51232	2p21
202572_s_at_HG-U133A	KIAA0964	Hs.177425	Q9Y2H0	22839	20q11.22
202580_x_at_HG-U133A	FOXM1	Hs.239	Q9BRL2	2305	12p13
202589_at_HG-U133A	TYMS	Hs.82962	P04818	7298	18p11.32
202600_s_at_HG-U133A	NRIP1	Hs.155017	P48552	8204	21q11.2
202606_s_at_HG-U133A	TLK1	Hs.18895	Q9UKI8	9874	2q31.1
202619_s_at_HG-U133A	PLOD2	Hs.41270	O00469	5352	3q23-q24
202625_at_HG-U133A	LYN	Hs.80887	P07948	4067	8q13
202626_s_at_HG-U133A	LYN	Hs.80887	P07948	4067	8q13
202655_at_HG-U133A	ARMET	Hs.75412	Q96IS4	7873	3p21.1
202705_at_HG-U133A	CCNB2	Hs.194698	O95067	9133	15q21.2
202709_at_HG-U133A	FMOD	Hs.230	Q12833	2331	1q32
202718_at_HG-U133A	IGFBP2	Hs.162	P18065	3485	2q33-q34
202723_s_at_HG-U133A	FOXO1A	Hs.170133	Q12778	2308	13q14.1
202729_s_at_HG-U133A	LTBP1	Hs.241257	Q14766	4052	2p22-p21
202746_at_HG-U133A					
202747_s_at_HG-U133A	ITM2A	Hs.17109		9452	Xq13.3-Xq21.2
202761_s_at_HG-U133A	SYNE-2	Hs.57749	Q8WXH0	23224	14q23.1-q23.2
202819_s_at_HG-U133A	TCEB3	Hs.155202	Q14241	6924	1p36.1
202822_at_HG-U133A	LPP	Hs.180398	Q93052	4026	3q27-q28

202823_at_HG-U133A	TCEB1	Hs.184693	Q15369	6921	8q13.2
202853_s_at_HG-U133A	RYK	Hs.79350	P34925	6259	3q22
202862_at_HG-U133A	FAH	Hs.73875	P16930	2184	15q23-q25
202863_at_HG-U133A	SP100	Hs.77617	Q96T95	6672	2q36.1
202880_s_at_HG-U133A	PSCD1	Hs.1050	Q15438	9267	17q25
202883_s_at_HG-U133A	PPP2R1B	Hs.108705	AAH27596	5519	11q23
202926_at_HG-U133A	NAG	Hs.15430	O95790	51594	2p24
202944_at_HG-U133A	NAGA	Hs.75372	P17050	4668	22q13-qter
202945_at_HG-U133A	FPGS	Hs.754	Q05932	2356	9cen-q34
202956_at_HG-U133A	BIG1	Hs.94631	Q9Y6D6	10565	8q13
202973_x_at_HG-U133A	KIAA0914	Hs.177664	O94988	10144	4q21.3
203005_at_HG-U133A	LTBR	Hs.1116	P36941	4055	12p13
203007_x_at_HG-U133A					
203020_at_HG-U133A	KIAA0471	Hs.242271	Q9UEL5	9910	1q24-q25
203021_at_HG-U133A	SLPI	Hs.251754	AAH20708	6590	20q12
203026_at_HG-U133A	KIAA0354	Hs.3682	O15062	9925	9p11.1
203037_s_at_HG-U133A	KIAA0429	Hs.77694	AAH23998	9788	8p22
203041_s_at_HG-U133A	LAMP2	Hs.8262	P13473	3920	Xq24
203053_at_HG-U133A	BCAS2	Hs.22960	AAH22880	10286	1p21-p13.3
203057_s_at_HG-U133A	PRDM2	Hs.26719	Q13029	7799	1p36
203074_at_HG-U133A	ANXA8	Hs.87268	Q96H89	244	10q11.2
203092_at_HG-U133A	TIMM44	Hs.123178	O43615	10469	19p13.3-p13.2
203104_at_HG-U133A	CSF1R	Hs.174142	P07333	1436	5q33-q35
203110_at_HG-U133A	PTK2B	Hs.20313	Q14289	2185	8p21.1
203133_at_HG-U133A	SEC61B	Hs.77028	P38391	10952	9q22.32-q31.3
203143_s_at_HG-U133A	KIAA0040	Hs.158282	CAB42560	9674	1q24-25
203177_x_at_HG-U133A	TFAM	Hs.75133	Q00059	7019	10q21
203188_at_HG-U133A	B3GNT6	Hs.8526	O43505	11041	11q12.1
203217_s_at_HG-U133A	SIAT9	Hs.225939	O94902	8869	2p11.2
203233_at_HG-U133A	IL4R	Hs.75545	P24394	3566	16p11.2-12.1
203241_at_HG-U133A	UVRAG	Hs.13137	Q9P2Y5	7405	11q13.5
203288_at_HG-U133A	KIAA0355	Hs.186840	O15063	9710	19q13.12
203345_s_at_HG-U133A	M96	Hs.31016	Q96G26	22823	1p22.1
203355_s_at_HG-U133A	KIAA0942	Hs.6763	Q9Y2F1	23362	8pter-p23.3
203367_at_HG-U133A	DUSP14	Hs.91448	O95147	11072	17q12
203370_s_at_HG-U133A	ENIGMA	Hs.102948	Q9BXB8	9260	5q35.3
203372_s_at_HG-U133A	STATI2	Hs.110776	O14508	8835	12q
203373_at_HG-U133A	STATI2	Hs.110776	O14508	8835	12q
203380_x_at_HG-U133A	SFRS5	Hs.166975	Q13243	6430	14q24
203385_at_HG-U133A	DGKA	Hs.172690	O75484	1606	12q13.3
203386_at_HG-U133A	KIAA0603	Hs.173802	O60343	9882	13q21.33
203387_s_at_HG-U133A	KIAA0603	Hs.173802	O60343	9882	13q21.33

203394_s_at_HG-U133A	HRY	Hs.250666	Q9BS99	3280	3q28-q29
203535_at_HG-U133A	S100A9	Hs.112405	P06702	6280	1q21
203544_s_at_HG-U133A	STAM	Hs.153487	Q92783	8027	10p14-p13
203556_at_HG-U133A	KIAA0854	Hs.30209	Q9Y6X8	22882	8q24.13
203593_at_HG-U133A	CD2AP	Hs.343211	Q9UG97	23607	6p12
203602_s_at_HG-U133A	ZNF151	Hs.33532	Q13105	7709	1p36.2-p36.1
203607_at_HG-U133A	SAC2	Hs.52463	Q9NT51	22876	10q26.13
203645_s_at_HG-U133A	CD163	Hs.74076	Q07901	9332	12p13.3
203679_at_HG-U133A	IL1RL1LG	Hs.54411	Q13445	11018	19p13.2
203685_at_HG-U133A	BCL2	Hs.79241	AAH27258	596	18q21.3
203725_at_HG-U133A	GADD45A	Hs.80409	P24522	1647	1p31.2-p31.1
203729_at_HG-U133A	EMP3	Hs.9999	P54852	2014	19q13.3
203731_s_at_HG-U133A	ZFP95	Hs.110839	Q9Y2L8	23660	7q22
203753_at_HG-U133A	TCF4	Hs.326198	P15884	6925	18q21.1
203757_s_at_HG-U133A	CEACAM6	Hs.73848	Q13774	4680	19q13.2
203787_at_HG-U133A	SSBP2	Hs.169833	Q9BWW6	23635	5q14.1
203795_s_at_HG-U133A	BCL7A	Hs.211563	Q13843	605	12q24.13
203796_s_at_HG-U133A	BCL7A	Hs.211563	Q13843	605	12q24.13
203808_at_HG-U133A	AKT2	Hs.326445	P31751	208	19q13.1-q13.2
203818_s_at_HG-U133A	SF3A3	Hs.77897	Q12874	10946	1p35.2
203857_s_at_HG-U133A	PDIR	Hs.372612	Q14554	10954	3q21.2
203859_s_at_HG-U133A	PALM	Hs.78482	O75781	5064	19p13.3
203881_s_at_HG-U133A	DMD	Hs.169470	P11532	1756	Xp21.2
203897_at_HG-U133A	LOC57149	Hs.28607	AAH17039	57149	16p11.2
203904_x_at_HG-U133A	KAI1	Hs.323949	P27701	3732	11p11.2
203910_at_HG-U133A	PARG1	Hs.70983	AAH22483	9411	1p22.1
203932_at_HG-U133A	HLA-DMB	Hs.1162	P28068	3109	6p21.3
203936_s_at_HG-U133A	MMP9	Hs.151738	P14780	4318	20q11.2-q13.1
203939_at_HG-U133A	NT5E	Hs.153952	P21589	4907	6q14-q21
203948_s_at_HG-U133A	MPO	Hs.1817	P05164	4353	17q23.1
203949_at_HG-U133A	MPO	Hs.1817	P05164	4353	17q23.1
203973_s_at_HG-U133A	CEBPD	Hs.76722	P49716	1052	8p11.2-p11.1
204000_at_HG-U133A	GNB5	Hs.155090	AAM15921	10681	15q15.3
204030_s_at_HG-U133A	SCHIP1	Hs.61490	Q9P0W5	29970	3q25.32
204044_at_HG-U133A	QPRT	Hs.8935	Q9BSG6	23475	16q13
204057_at_HG-U133A	ICSBP1	Hs.14453	Q02556	3394	16q24.1
204069_at_HG-U133A	MEIS1	Hs.170177	O00470	4211	2p14-p13
204075_s_at_HG-U133A	KIAA0562	Hs.200595	O60308	9731	1p36.32
204082_at_HG-U133A	PBX3	Hs.294101	Q96AL5	5090	9q33-q34
204101_at_HG-U133A	MTM1	Hs.75302	Q13496	4534	Xq28
204112_s_at_HG-U133A	HNMT	Hs.81182	P50135	3176	2q21.1
204116_at_HG-U133A	IL2RG	Hs.84	P31785	3561	Xq13.1

204118_at_HG-U133A	CD48	Hs.901	P09326	962	1q21.3-q22
204150_at_HG-U133A	STAB1	Hs.301989	Q9NY15	23166	3p21.31
204163_at_HG-U133A	EMILIN	Hs.63348	Q9Y6C2	11117	2p23.3-p23.2
204174_at_HG-U133A	ALOX5AP	Hs.100194	AAH18538	241	13q12
204192_at_HG-U133A	CD37	Hs.153053	Q96LM7	951	19p13-q13.4
204199_at_HG-U133A	RALGPS1A	Hs.374518	O15059	9649	9q34.13
204205_at_HG-U133A	MDS019	Hs.250619	Q9HC16	60489	22q
204208_at_HG-U133A	RNGTT	Hs.27345	Q8WUM8	8732	6q16
204214_s_at_HG-U133A	RAB32	Hs.32217	AAM21106	10981	6q24.3
204215_at_HG-U133A	MGC4175	Hs.322404	Q9BU79	79161	7q21.1-q21.2
204225_at_HG-U133A	HDAC4	Hs.91400	P56524	9759	2q37.2
204227_s_at_HG-U133A	TK2	Hs.274701	O00142	7084	16q22
204249_s_at_HG-U133A	LMO2	Hs.184585	P25791	4005	11p13
204269_at_HG-U133A	PIM2	Hs.80205	Q9P1W9	11040	Xp11.23
204285_s_at_HG-U133A	PMAIP1	Hs.96	Q13794	5366	18q21.31
204306_s_at_HG-U133A	CD151	Hs.75564	P48509	977	11p15.5
204319_s_at_HG-U133A	RGS10	Hs.82280	Q96GN0	6001	10q25
204328_at_HG-U133A	LAK-4P	Hs.16165	Q9HAG5	11322	17q25
204348_s_at_HG-U133A	AK3	Hs.274691	P27144	205	9p24-p13
204351_at_HG-U133A	S100P	Hs.2962	P25815	6286	4p16
204352_at_HG-U133A	TRAF5	Hs.29736	O00463	7188	1q32
204401_at_HG-U133A	KCNN4	Hs.10082	AAH15337	3783	19q13.2
204422_s_at_HG-U133A	FGF2	Hs.284244	P09038	2247	4q26-q27
204425_at_HG-U133A	ARHGAP4	Hs.3109	P98171	393	Xq28
204446_s_at_HG-U133A	ALOX5	Hs.89499	P09917	240	10q11.2
204484_at_HG-U133A	PIK3C2B	Hs.132463	O00750	5287	1q32
204495_s_at_HG-U133A	DKFZP434H132	Hs.17936	Q9H3J1	25958	15q22.33
204501_at_HG-U133A	NOV	Hs.235935	AAL92490	4856	8q24.1
204511_at_HG-U133A	KIAA0793	Hs.301283	Q9UFE7	9855	2q37.3
204512_at_HG-U133A	HIVEP1	Hs.306	Q14122	3096	6p24-p22.3
204562_at_HG-U133A	IRF4	Hs.82132	Q15306	3662	6p25-p23
204563_at_HG-U133A	SELL	Hs.82848	P14151	6402	1q23-q25
204604_at_HG-U133A	PFTK1	Hs.57856	Q9H3D7	5218	7q21-q22
204638_at_HG-U133A	ACP5	Hs.1211	AAH25414	54	19p13.3-p13.2
204647_at_HG-U133A	HOMER-3	Hs.166146	O95350	9454	19p13.11
204661_at_HG-U133A	CDW52	Hs.276770	P31358	1043	1p36
204663_at_HG-U133A	ME3	Hs.2838	Q16798	10873	11cen-q22.3
204670_x_at_HG-U133A	HLA-DRB5	Hs.352392	Q29972	3127	6p21.3
204672_s_at_HG-U133A	ANKRD6	Hs.30991	Q9BVM3	22881	6q14.2-q16.1
204674_at_HG-U133A	LRMP	Hs.40202	Q12912	4033	12p12.3
204703_at_HG-U133A	TG737	Hs.2291	Q13099	8100	13q12.1
204731_at_HG-U133A	TGFBR3	Hs.342874	Q9UGI2	7049	1p33-p32

204776_at_HG-U133A	THBS4	Hs.75774	P35443	7060	5q13
204793_at_HG-U133A	KIAA0443	Hs.113082	Q96LA1	9737	Xq22.1
204798_at_HG-U133A	MYB	Hs.1334	Q14024	4602	6q22-q23
204811_s_at_HG-U133A	CACNA2D2	Hs.127436	Q9UEW0	9254	3p21.3
204858_s_at_HG-U133A	ECGF1	Hs.73946	P19971	1890	22q13.33
204882_at_HG-U133A	KIAA0053	Hs.1528	P42331	9938	2p13.1
204891_s_at_HG-U133A	LCK	Hs.1765	P06239	3932	1p34.3
204922_at_HG-U133A	FLJ22531	Hs.55613	AAH28240	79703	11q12.1
204951_at_HG-U133A	ARHH	Hs.109918	Q15669	399	4p13
204992_s_at_HG-U133A	PFN2	Hs.91747	P35080	5217	3q25.1-q25.2
205019_s_at_HG-U133A	VIPR1	Hs.348500	P32241	7433	3p22
205040_at_HG-U133A	ORM1	Hs.572	P02763	5004	9q31-q32
205041_s_at_HG-U133A	ORM1	Hs.572	AAH26238	5004	9q31-q32
205049_s_at_HG-U133A	CD79A	Hs.79630	P11912	973	19q13.2
205051_s_at_HG-U133A	KIT	Hs.81665	P10721	3815	4q11-q12
205055_at_HG-U133A	ITGAE	Hs.851	P38570	3682	17p13
205059_s_at_HG-U133A	IDUA	Hs.89560	P35475	3425	4p16.3
205074_at_HG-U133A	SLC22A5	Hs.15813	O76082	6584	5q31
205076_s_at_HG-U133A	CRA	Hs.166066	Q99753	10903	1q12-q21
205101_at_HG-U133A	MHC2TA	Hs.3076	Q29675	4261	16p13
205105_at_HG-U133A	MAN2A1	Hs.63368	Q16706	4124	5q21-q22
205110_s_at_HG-U133A	FGF13	Hs.6540	Q92913	2258	Xq26.3
205131_x_at_HG-U133A	SCGF	Hs.105927	Q9Y240	6320	19q13.3
205145_s_at_HG-U133A	MYL5	Hs.170482	Q02045	4636	4p16.3
205192_at_HG-U133A	MAP3K14	Hs.47007	Q99558	9020	17q21
205223_at_HG-U133A	KIAA0645	Hs.155987	O75140	9681	22q12.3
205225_at_HG-U133A	ESR1	Hs.1657	Q9H2M0	2099	6q25.1
205267_at_HG-U133A	POU2AF1	Hs.2407	Q16633	5450	11q23.1
205306_x_at_HG-U133A	KMO	Hs.107318	O15229	8564	1q42-q44
205308_at_HG-U133A	LOC51101	Hs.118821	Q9Y372	51101	8q21.11
205312_at_HG-U133A	SPI1	Hs.157441	P17947	6688	11p11.2
205316_at_HG-U133A	SLC15A2	Hs.182575	Q16348	6565	3q21.1
205349_at_HG-U133A	GNA15	Hs.73797	P30679	2769	19p13.3
205355_at_HG-U133A	ACADSB	Hs.81934	P45954	36	10q25-q26
205366_s_at_HG-U133A	HOXB6	Hs.98428	P17509	3216	17q21-q22
205380_at_HG-U133A	PDZK1	Hs.15456	O60450	5174	1q21
205382_s_at_HG-U133A	DF	Hs.155597	P00746	1675	19p13.3
205383_s_at_HG-U133A	ZNF288	Hs.159456	Q9HC78	26137	3q13.2
205414_s_at_HG-U133A	KIAA0672	Hs.6336	O75160	9912	17p11.2
205420_at_HG-U133A	PEX7	Hs.79993	O00628	5191	6q21-q22.2
205436_s_at_HG-U133A	H2AFX	Hs.147097	P16104	3014	11q23.2-q23.3
205453_at_HG-U133A	HOXB2	Hs.2733	P14652	3212	17q21-q22

205471_s_at_HG-U133A	DACH	Hs.63931	Q9UMH4	1602	13q22
205472_s_at_HG-U133A	DACH	Hs.63931	Q9UI36	1602	13q22
205504_at_HG-U133A	BTK	Hs.159494	Q9NPI3	695	Xq21.33-q22
205513_at_HG-U133A	TCN1	Hs.2012	P20061	6947	11q11-q12
205528_s_at_HG-U133A	CBFA2T1	Hs.31551	Q06455	862	8q22
205529_s_at_HG-U133A	CBFA2T1	Hs.31551	Q06455	862	8q22
205541_s_at_HG-U133A	GSPT2	Hs.59523	Q9H909	23708	
205547_s_at_HG-U133A	TAGLN	Hs.75777	AAH04927	6876	11q23.2
205557_at_HG-U133A	BPI	Hs.89535	P17213	671	20q11.23-q12
205599_at_HG-U133A	TRAF1	Hs.2134	Q13077	7185	9q33-q34
205600_x_at_HG-U133A	HOXB5	Hs.22554	P09067	3215	17q21-q22
205601_s_at_HG-U133A	HOXB5	Hs.22554	Q96H37	3215	17q21-q22
205607_s_at_HG-U133A	LOC57147	Hs.24243	Q96C56	57147	1q22
205613_at_HG-U133A	LOC51760	Hs.26971	Q9NZ18	51760	16p13.13
205614_x_at_HG-U133A	MST1	Hs.349110	P26927	4485	3p21
205624_at_HG-U133A	CPA3	Hs.646	P15088	1359	3q21-q25
205627_at_HG-U133A	CDA	Hs.72924	P32320	978	1p36.2-p35
205640_at_HG-U133A	ALDH3B1	Hs.83155	Q9BUJ8	221	11q13
205653_at_HG-U133A	CTSG	Hs.100764	P08311	1511	14q11.2
205663_at_HG-U133A	PCBP3	Hs.121241	Q96EP6	54039	21q22.3
205668_at_HG-U133A	LY75	Hs.153563	O75913	4065	2q24
205671_s_at_HG-U133A	HLA-DOB	Hs.1802	AAH06097	3112	6p21.3
205674_x_at_HG-U133A	FXYD2	Hs.19520	Q15332	486	11q23
205690_s_at_HG-U133A	G10	Hs.330310	P41223	8896	7q11.21
205691_at_HG-U133A	SYNGR3	Hs.6467	Q96L30	9143	16pter
205718_at_HG-U133A	ITGB7	Hs.1741	P26010	3695	12q13.13
205790_at_HG-U133A	SCAP1	Hs.19126	O15268	8631	17q21.32
205801_s_at_HG-U133A	GRP3	Hs.24024	O94931	25780	2p25.1-p24.1
205805_s_at_HG-U133A	ROR1	Hs.274243	Q01973	4919	1p32-p31
205821_at_HG-U133A	D12S2489E	Hs.74085	Q8WZ67	22914	12p13.2-p12.3
205837_s_at_HG-U133A	GYPA	Hs.108694	Q03870	2993	4q28.2-q31.1
205841_at_HG-U133A	JAK2	Hs.115541	O60674	3717	9p24
205849_s_at_HG-U133A	UQCRB	Hs.131255	P14927	7381	8q22
205855_at_HG-U133A	ZNF197	Hs.170341	O14709	10168	3p21
205863_at_HG-U133A	S100A12	Hs.19413	P80511	6283	1q21
205899_at_HG-U133A	CCNA1	Hs.79378	P78396	8900	13q12.3-q13
205901_at_HG-U133A	PNOC	Hs.89040	Q13519	5368	8p21
205911_at_HG-U133A	PTHR1	Hs.1019	Q03431	5745	3p22-p21.1
205933_at_HG-U133A	SETBP1	Hs.151717	BAA24826	26040	18q21.1
205945_at_HG-U133A	IL6R	Hs.193400	P08887	3570	1q21
205997_at_HG-U133A	ADAM28	Hs.174030	Q9UKQ2	10863	8p12
206009_at_HG-U133A	ITGA9	Hs.222	Q13797	3680	3p21.3

206090_s_at_HG-U133A	DISC1	Hs.26985	Q9NRI5	27185	1q42.1
206111_at_HG-U133A	RNASE2	Hs.728	P10153	6036	14q24-q31
206126_at_HG-U133A	BLR1	Hs.113916	P32302	643	11q23.3
206135_at_HG-U133A	KIAA0535	Hs.151449	O60284	9705	8q11.21
206150_at_HG-U133A	TNFRSF7	Hs.180841	P26842	939	12p13
206177_s_at_HG-U133A	ARG1	Hs.332405	AAL71547	383	6q23
206178_at_HG-U133A	PLA2G5	Hs.290	P39877	5322	1p36-p34
206207_at_HG-U133A	CLC	Hs.889	Q05315	1178	19q13.1
206241_at_HG-U133A	KPNA5	Hs.182971	O15131	3841	6q22.31
206245_s_at_HG-U133A	NS1-BP	Hs.197298	Q9Y6Y0	10625	1q25.1-q31.1
206255_at_HG-U133A	BLK	Hs.2243	P51451	640	8p23-p22
206295_at_HG-U133A	IL18	Hs.83077	Q14116	3606	11q22.2-q22.3
206302_s_at_HG-U133A	NUDT4	Hs.92381	Q9NZK0	11163	
206337_at_HG-U133A	CCR7	Hs.1652	P32248	1236	17q12-q21.2
206380_s_at_HG-U133A	PFC	Hs.53155	P27918	5199	Xp11.3-p11.23
206398_s_at_HG-U133A	CD19	Hs.96023	Q9BRD6	930	16p11.2
206438_x_at_HG-U133A	FLJ12975	Hs.167165	Q96GX1	79867	12q24.31
206440_at_HG-U133A	VELI1	Hs.178215	O14910	8825	12q21
206461_x_at_HG-U133A	MT1H	Hs.2667	AAH08408	4496	16q13
206488_s_at_HG-U133A	CD36	Hs.75613	P16671	948	7q11.2
206513_at_HG-U133A	AIM2	Hs.105115	O14862	9447	1q22
206515_at_HG-U133A	CYP4F3	Hs.106242	Q08477	4051	19p13.2
206519_x_at_HG-U133A	SIGLEC6	Hs.117992	O15388	946	19q13.3
206530_at_HG-U133A	RAB30	Hs.159505	AAM21104	27314	11q12-q14
206550_s_at_HG-U133A	NUP155	Hs.23255	O75694	9631	5p13
206576_s_at_HG-U133A	CEACAM1	Hs.50964	Q15600	634	19q13.2
206622_at_HG-U133A	TRH	Hs.182231		7200	3q13.3-q21
206633_at_HG-U133A	CHRNA1	Hs.2266	P02708	1134	2q24-q32
206634_at_HG-U133A	SIX3	Hs.227277	O95343	6496	2p16-p21
206676_at_HG-U133A	CEACAM8	Hs.41	AAH26263	1088	19q13.2
206748_s_at_HG-U133A	SPAG9	Hs.129872	O60271	9043	17q24.1
206759_at_HG-U133A	FCER2	Hs.1416	P06734	2208	19p13.3
206760_s_at_HG-U133A	FCER2	Hs.1416	P06734	2208	19p13.3
206761_at_HG-U133A	TACTILE	Hs.142023	Q8WUE2	10225	3q13.2
206772_at_HG-U133A	PTHR2	Hs.159499	P49190	5746	2q33
206781_at_HG-U133A	DNAJC4	Hs.172847	Q9NNZ3	3338	11q13
206804_at_HG-U133A	CD3G	Hs.2259	P09693	917	11q23
206847_s_at_HG-U133A	HOXA7	Hs.355540	P31268	3204	7p15-p14
206850_at_HG-U133A	RRP22	Hs.73088	Q92737	10633	22q12.2
206871_at_HG-U133A	ELA2	Hs.99863	AAA35792	1991	19p13.3
206940_s_at_HG-U133A	POU4F1	Hs.211588	Q01851	5457	13q21.1-q22
206956_at_HG-U133A	BGLAP	Hs.2558	P02818	632	1q25-q31

206995_x_at_HG-U133A	SREC	Hs.57735	Q14162	8578	17p13.3
207000_s_at_HG-U133A	PPP3CC	Hs.75206	Q9BSS6	5533	8p21.2
207030_s_at_HG-U133A	CSRP2	Hs.10526	Q16527	1466	12q21.1
207057_at_HG-U133A	SLC16A7	Hs.132183	O60669	9194	12q13
207076_s_at_HG-U133A	ASS	Hs.160786	P00966	445	9q34.1
207168_s_at_HG-U133A	H2AFY	Hs.75258	Q9H8P3	9555	5q31.3-q32
207194_s_at_HG-U133A	ICAM4	Hs.108287	Q14773	3386	19p13.2-cen
207224_s_at_HG-U133A	SIGLEC7	Hs.274470	Q9UJ86	27036	19q13.3
207269_at_HG-U133A	DEFA4	Hs.2582	P12838	1669	8p23
207384_at_HG-U133A	PGLYRP	Hs.137583	O75594	8993	19q13.2-q13.3
207403_at_HG-U133A	IRS4	Hs.159609	O14654	8471	Xq22.3
207520_at_HG-U133A					
207543_s_at_HG-U133A	P4HA1	Hs.76768	P13674	5033	10q21.3-q23.1
207616_s_at_HG-U133A	TANK	Hs.146847	Q92844	10010	2q24-q31
207641_at_HG-U133A	TACI	Hs.158341	O14836	23495	17p11.2
207654_x_at_HG-U133A	DR1	Hs.16697	Q01658	1810	1p22.1
207655_s_at_HG-U133A	BLNK	Hs.167746	O75499	29760	10q23.2-q23.33
207697_x_at_HG-U133A	LILRB2	Hs.22405	O75017	10288	19q13.4
207700_s_at_HG-U133A	NCOA3	Hs.225977	Q9UPG7	8202	20q12
207734_at_HG-U133A	FLJ20340	Hs.272794	Q9NXB4	54900	1q31.1
207760_s_at_HG-U133A	NCOR2	Hs.287994	Q9Y618	9612	12q24
207777_s_at_HG-U133A	SP140	Hs.309943	Q13342	11262	2q36.1
207801_s_at_HG-U133A	RNF10	Hs.5094	Q9ULW4	9921	12q24.23
207802_at_HG-U133A	SGP28	Hs.54431	P54108	10321	6p12.2
207809_s_at_HG-U133A	ATP6IP1	Hs.6551	AAH00724	537	Xq28
207819_s_at_HG-U133A	ABCB4	Hs.73812	P21439	5244	7q21.1
207871_s_at_HG-U133A	ST7	Hs.5814	Q9NRC1	7982	7q31.1-q31.3
207957_s_at_HG-U133A	PRKCB1	Hs.77202	P05771	5579	16p11.2
207971_s_at_HG-U133A	KIAA0582	Hs.79507	O60326	23177	2p14
207983_s_at_HG-U133A	STAG2	Hs.8217	Q9H1N8	10735	Xq25
207996_s_at_HG-U133A	C18orf1	Hs.153498	O15165	753	18p11.2
208033_s_at_HG-U133A	ATBF1	Hs.101842	Q15911	463	16q22.3-q23.1
208042_at_HG-U133A	HSU84971	Hs.104530	Q9BU84	29905	5q14.1
208091_s_at_HG-U133A	DKFZP564K0822	Hs.4750	Q9H0W4	81552	7p14.1
208141_s_at_HG-U133A	MGC4293	Hs.91103	Q9BU89	83475	19p13.3
208146_s_at_HG-U133A	CPVL	Hs.95594	Q96AR7	54504	7p15-p14
208168_s_at_HG-U133A	CHIT1	Hs.91093	Q9H3V8	1118	1q31-q32
208190_s_at_HG-U133A	LISCH7	Hs.361379	Q9UQL3	51599	19q13.13
208195_at_HG-U133A	TTN	Hs.172004	Q15598	7273	2q24.3
208217_at_HG-U133A	GABRR2	Hs.99927	P28476	2570	6q13-q16.3
208229_at_HG-U133A	FGFR2	Hs.278581	Q9UIH4	2263	10q26
208248_x_at_HG-U133A	APLP2	Hs.279518	Q06481	334	11q24

208268_at_HG-U133A	ADAM28	Hs.174030	Q9UKQ2	10863	8p12
208302_at_HG-U133A	HB-1	Hs.158320	O97980	57824	5q33.1
208306_x_at_HG-U133A	HLA-DRB4	Hs.318720	AAM00252	3126	6p21.3
208456_s_at_HG-U133A	RRAS2	Hs.206097	P17082	22800	11p15.2
208470_s_at_HG-U133A	HPR	Hs.328822	Q92659	3250	16q22.1
208581_x_at_HG-U133A	MT1X	Hs.278462		4501	16q13
208611_s_at_HG-U133A	SPTAN1	Hs.77196	Q13813	6709	9q33-q34
208612_at_HG-U133A	GRP58	Hs.289101	P30101	2923	15q15
208614_s_at_HG-U133A	FLNB	Hs.81008	Q9NT26	2317	3p14.3
208623_s_at_HG-U133A	VIL2	Hs.155191	Q9UJU1	7430	6q25-q26
208629_s_at_HG-U133A	HADHA	Hs.75860	P40939	3030	2p23
208645_s_at_HG-U133A					
208646_at_HG-U133A					
208650_s_at_HG-U133A	CD24	Hs.286124	AAH07674	934	6q21
208651_x_at_HG-U133A	CD24	Hs.286124	AAH07674	934	6q21
208657_s_at_HG-U133A	MSF	Hs.181002	Q96QF3	10801	17q25
208664_s_at_HG-U133A	TTC3	Hs.118174	P53804	7267	21q22.2
208674_x_at_HG-U133A	DDOST	Hs.34789	Q9BUI2	1650	1p36.1
208683_at_HG-U133A	CAPN2	Hs.76288	Q9HBB1	824	1q41-q42
208689_s_at_HG-U133A	RPN2	Hs.75722	AAH20222	6185	20q12-q13.1
208697_s_at_HG-U133A	EIF3S6	Hs.106673	AAH08419	3646	8q22-q23
208702_x_at_HG-U133A	APLP2	Hs.279518	AAD47291	334	11q24
208703_s_at_HG-U133A	APLP2	Hs.279518	Q9BT36	334	11q24
208710_s_at_HG-U133A	AP3D1	Hs.75056	O14617	8943	19p13.3
208741_at_HG-U133A	SAP18	Hs.23964	O00422	10284	13q11
208754_s_at_HG-U133A	NAP1L1	Hs.302649	P55209	4673	12q14.1
208819_at_HG-U133A	MEL	Hs.5947	AAM21091	4218	19p13.1
208852_s_at_HG-U133A	CANX	Hs.155560	P27824	821	5q35
208858_s_at_HG-U133A	KIAA0747	Hs.8309	O94848	23344	12q12
208864_s_at_HG-U133A	TXN	Hs.76136	P10599	7295	9q31
208890_s_at_HG-U133A	PLXNB2	Hs.3989	Q9BSU7	23654	22q13.33
208894_at_HG-U133A	HLA-DRA	Hs.76807	P01903	3122	6p21.3
208908_s_at_HG-U133A	CAST	Hs.359682	O95360	831	5q14-q22
208913_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
208914_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
208918_s_at_HG-U133A	FLJ13052	Hs.220324	AAM01195	65220	1p36.33-p36.21
209003_at_HG-U133A	SLC25A11	Hs.184877	Q02978	8402	17p13.3
209018_s_at_HG-U133A	PINK1	Hs.6163	Q9BXM7	65018	1p36
209019_s_at_HG-U133A	PINK1	Hs.6163	AAH28215	65018	1p36
209023_s_at_HG-U133A	STAG2	Hs.8217	Q9H1N8	10735	Xq25
209055_s_at_HG-U133A	CDC5L	Hs.155174	BAA24862	988	6p21
209060_x_at_HG-U133A	NCOA3	Hs.225977	O15406	8202	20q12

209061_at_HG-U133A	NCOA3	Hs.225977	O15406	8202	20q12
209062_x_at_HG-U133A	NCOA3	Hs.225977	O15406	8202	20q12
209075_s_at_HG-U133A	NIFU	Hs.9908	Q99617	23479	12q24.1
209085_x_at_HG-U133A	RFC1	Hs.166563	P35251	5981	4p14-p13
209101_at_HG-U133A	CTGF	Hs.75511	AAA75378	1490	6q23.1
209135_at_HG-U133A	ASPH	Hs.283664	AAH25236	444	8q12.1
209160_at_HG-U133A	AKR1C3	Hs.78183	Q9UKL9	8644	10p15-p14
209167_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209168_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209169_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209170_s_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209178_at_HG-U133A	DDX38	Hs.78054	Q92620	9785	16q21-q22.3
209186_at_HG-U133A	ATP2A2	Hs.1526	P16615	488	12q23-q24.1
209188_x_at_HG-U133A	DR1	Hs.16697	Q01658	1810	1p22.1
209190_s_at_HG-U133A	DIAPH1	Hs.26584	O60610	1729	5q31
209197_at_HG-U133A	KIAA0080	Hs.74554	Q14998	23208	1
209236_at_HG-U133A					
209253_at_HG-U133A	SCAM-1	Hs.33787	O60504	10174	8p21.2
209259_s_at_HG-U133A	CSPG6	Hs.24485	O60464	9126	10q25
209267_s_at_HG-U133A	LOC64116	Hs.284205	Q96SM9	64116	4q22-q24
209306_s_at_HG-U133A	SWAP70	Hs.153026	O75135	23075	11p15
209307_at_HG-U133A	SWAP70	Hs.153026	O75135	23075	11p15
209312_x_at_HG-U133A	HLA-DRB1	Hs.308026	Q9TQE1	3123	6p21.3
209321_s_at_HG-U133A	ADCY3	Hs.8402	O60266	109	2p24-p22
209344_at_HG-U133A	TPM4	Hs.250641	P07226	7171	19p13.1
209354_at_HG-U133A	TNFRSF14	Hs.279899	Q92956	8764	1p36.3-p36.2
209365_s_at_HG-U133A	ECM1	Hs.81071	O43266	1893	1q21
209369_at_HG-U133A	ANXA3	Hs.1378	P12429	306	4q13-q22
209374_s_at_HG-U133A	IGHM	Hs.153261	Q8WUX4	3507	14q32.33
209380_s_at_HG-U133A	ABCC5	Hs.108660	O15440	10057	3q27
209399_at_HG-U133A	HLCS	Hs.79375	P50747	3141	21q22.13
209412_at_HG-U133A	TMEM1	Hs.94479	P48553	7109	21q22.3
209428_s_at_HG-U133A	ZFPL1	Hs.155165	O14616	7542	11q13
209490_s_at_HG-U133A	PPT2	Hs.81737	Q9UMR5	9374	6p21.3
209499_x_at_HG-U133A	TNFSF13	Hs.54673	Q96HV6	8741	17p13.1
209500_x_at_HG-U133A	TNFSF13	Hs.54673	O75888	8741	17p13.1
209522_s_at_HG-U133A	CRAT	Hs.12068	Q9BW16	1384	9q34.1
209523_at_HG-U133A					
209558_s_at_HG-U133A	HIP12	Hs.96731	O75146	9026	12q24
209561_at_HG-U133A	THBS3	Hs.169875	P49746	7059	1q21
209604_s_at_HG-U133A	GATA3	Hs.169946	Q96J04	2625	10p15
209616_s_at_HG-U133A	CES1	Hs.76688	Q96EE8	1066	16q13-q22.1

209619_at_HG-U133A	CD74	Hs.84298	P04233	972	5q32
209628_at_HG-U133A	P15-2	Hs.25010	Q9NPJ8	55916	Xq22.3
209670_at_HG-U133A	TRA	Hs.74647	Q8WUD0	6955	14q11.2
209679_s_at_HG-U133A	LOC57228	Hs.206501	O95332	57228	12q11
209682_at_HG-U133A	CBLB	Hs.3144	Q13191	868	3q13.12
209685_s_at_HG-U133A	PRKCB1	Hs.77202	P05771	5579	16p11.2
209686_at_HG-U133A	S100B	Hs.83384	P04271	6285	21q22.3
209714_s_at_HG-U133A	CDKN3	Hs.84113	Q9BPW7	1033	14q22
209732_at_HG-U133A	CLECSF2	Hs.85201	Q9BS74	9976	12p13-p12
209735_at_HG-U133A	ABCG2	Hs.194720	Q96LD6	9429	4q22
209754_s_at_HG-U133A					
209761_s_at_HG-U133A	SP110	Hs.38125	Q14976	3431	2q37.1
209765_at_HG-U133A	ADAM19	Hs.278679	Q9H013	8728	5q32-q33
209771_x_at_HG-U133A	CD24	Hs.286124	P25063	934	6q21
209772_s_at_HG-U133A	CD24	Hs.286124	P25063	934	6q21
209780_at_HG-U133A	DKFZP564F013	Hs.128653	Q9H099	57157	7q11.23-q21
209806_at_HG-U133A	H2B/S	Hs.247817	O60814	85236	6p21.33
209815_at_HG-U133A	PTCH	Hs.159526	Q13635	5727	9q22.3
209822_s_at_HG-U133A	VLDLR	Hs.73729	P98155	7436	9p24
209825_s_at_HG-U133A	UMPK	Hs.75939	Q92528	7371	1q23
209827_s_at_HG-U133A	IL16	Hs.82127	Q14005	3603	15q26.3
209831_x_at_HG-U133A	DNASE2	Hs.118243	O00115	1777	19p13.2
209876_at_HG-U133A	GIT2	Hs.57734	Q96CI2	9815	12q24.1
209891_at_HG-U133A	AD024	Hs.21137	Q9HBM1	57405	2q31.1
209905_at_HG-U133A	HOXA9	Hs.127428	AAH06537	3205	7p15-p14
209939_x_at_HG-U133A	CFLAR	Hs.195175	O15519	8837	2q33-q34
209961_s_at_HG-U133A	HGF	Hs.809	Q13494	3082	7q21.1
209975_at_HG-U133A	CYP2E	Hs.75183	P05181	1571	10q24.3-qter
209992_at_HG-U133A	PFKFB2	Hs.211585	Q9H3P1	5208	1q31
209994_s_at_HG-U133A	ABCB1	Hs.21330	P08183	5243	7q21.1
210004_at_HG-U133A	OLR1	Hs.77729	AAH22295	4973	12p13.2-p12.3
210024_s_at_HG-U133A	UBE2E3	Hs.4890	Q969T4	10477	2q32.1
210036_s_at_HG-U133A	KCNH2	Hs.188021	AAL37559	3757	7q35-q36
210038_at_HG-U133A					
210045_at_HG-U133A	IDH2	Hs.5337	P48735	3418	15q26.1
210052_s_at_HG-U133A	C20orf1	Hs.9329	AAD33965	22974	20q11.2
210053_at_HG-U133A	TAF5	Hs.96103	Q15542	6877	10q24-q25.2
210095_s_at_HG-U133A	IGFBP3	Hs.77326	P17936	3486	7p13-p12
210116_at_HG-U133A	SH2D1A	Hs.151544	AAH20732	4068	Xq25-q26
210117_at_HG-U133A	SPAG1	Hs.153057	Q07617	6674	8q22
210128_s_at_HG-U133A	LTB4R	Hs.28408	Q15722	1241	14q11.2-q12
210140_at_HG-U133A	CST7	Hs.143212	O76096	8530	20p11.21

210145_at_HG-U133A	PLA2G4A	Hs.211587	P47712	5321	1q25
210151_s_at_HG-U133A	DYRK3	Hs.38018	O43781	8444	1q32
210192_at_HG-U133A	ATP8A1	Hs.144931	Q9Y2Q0	10396	4p14-p12
210244_at_HG-U133A	CAMP	Hs.51120	P49913	820	3p21.3
210251_s_at_HG-U133A	KIAA0871	Hs.7972	O94948	22902	4q13.2
210254_at_HG-U133A					
210262_at_HG-U133A	TPX1	Hs.2042	AAH22011	7180	6p21-qter
210268_at_HG-U133A	NFX1	Hs.3187	Q12986	4799	9p12
210279_at_HG-U133A	GPR18	Hs.88269	Q96HI6	2841	13q32
210298_x_at_HG-U133A	FHL1	Hs.239069	O95212	2273	Xq26
210299_s_at_HG-U133A	FHL1	Hs.239069	O95212	2273	Xq26
210314_x_at_HG-U133A	TNFSF13	Hs.54673	O75888	8741	17p13.1
210334_x_at_HG-U133A	BIRC5	Hs.1578	O15392	332	17q25
210356_x_at_HG-U133A	MS4A2	Hs.89751	P11836	931	11q12-q13.1
210358_x_at_HG-U133A	MGC2306	Hs.760	P23769	84724	3q22.1
210448_s_at_HG-U133A	P2RX5	Hs.77807	Q93086	5026	17p13
210487_at_HG-U133A	DNTT	Hs.272537	Q96E50	1791	10q23-q24
210519_s_at_HG-U133A					
210563_x_at_HG-U133A	CFLAR	Hs.195175	O15519	8837	2q33-q34
210609_s_at_HG-U133A	PIG3	Hs.50649	Q9BWB8	9540	2p23.3
210613_s_at_HG-U133A	SYNGR1	Hs.6139	O43759	9145	22q13.1
210616_s_at_HG-U133A	KIAA0905	Hs.70266	O94979	22872	4q21.22
210658_s_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
210664_s_at_HG-U133A	TFPI	Hs.170279	P10646	7035	2q31-q32.1
210715_s_at_HG-U133A	SPINT2	Hs.31439	O43291	10653	19q13.1
210749_x_at_HG-U133A	DDR1	Hs.75562	Q08345	780	6p21.3
210755_at_HG-U133A	HGF	Hs.809	Q02935	3082	7q21.1
210763_x_at_HG-U133A	LY117	Hs.88411	O00452	7940	6p21.3
210788_s_at_HG-U133A	LOC51635	Hs.109201	Q9UKU2	51635	14q22.3
210789_x_at_HG-U133A	CEACAM3	Hs.11	P40198	1084	19q13.2
210794_s_at_HG-U133A					
210807_s_at_HG-U133A	SLC16A7	Hs.132183	O60669	9194	12q13
210817_s_at_HG-U133A	NDP52	Hs.154230	Q9BTF7	10241	17q23.2
210896_s_at_HG-U133A	ASPH	Hs.283664	AAH25236	444	8q12.1
210916_s_at_HG-U133A		Hs.306278	O95370		
210933_s_at_HG-U133A	MGC4655	Hs.55923	Q9BSU1	84752	16q23.1
210934_at_HG-U133A	BLK	Hs.2243	P51451	640	8p23-p22
210948_s_at_HG-U133A	LEF1	Hs.44865	Q9UJU2	51176	4q23-q25
210973_s_at_HG-U133A	FGFR1	Hs.748	Q02063	2260	8p11.2-p11.1
210982_s_at_HG-U133A	HLA-DRA	Hs.76807	P01903	3122	6p21.3
210997_at_HG-U133A	HGF	Hs.809	Q02935	3082	7q21.1
210998_s_at_HG-U133A	HGF	Hs.809	P14210	3082	7q21.1

211015_s_at_HG-U133A	HSPA4	Hs.90093	Q9BUK9	3308	5q31.1-q31.2
211031_s_at_HG-U133A	CYLN2	Hs.104717	Q9BRH8	7461	7q11.23
211097_s_at_HG-U133A	PBX2	Hs.93728	Q9BTW4	5089	6p21.3
211101_x_at_HG-U133A	LILRA2	Hs.94498	O75020	11027	19q13.4
211105_s_at_HG-U133A	NFATC1	Hs.96149	O95644	4772	18q23
211126_s_at_HG-U133A	CSRP2	Hs.10526	Q16527	1466	12q21.1
211138_s_at_HG-U133A	KMO	Hs.107318	O15229	8564	1q42-q44
211275_s_at_HG-U133A	GYG	Hs.174071	P46976	2992	3q24-q25.1
211297_s_at_HG-U133A	CDK7	Hs.184298	P50613	1022	2p15-cen
211341_at_HG-U133A	POU4F1	Hs.211588	Q01851	5457	13q21.1-q22
211349_at_HG-U133A	SLC15A1	Hs.2217	O14496	6564	13q33-q34
211352_s_at_HG-U133A	NCOA3	Hs.225977	Q9UPG7	8202	20q12
211404_s_at_HG-U133A	APLP2	Hs.279518	AAD47291	334	11q24
211456_x_at_HG-U133A		Hs.367850	Q9BXG3		
211474_s_at_HG-U133A		Hs.355890	Q9BSM3		
211495_x_at_HG-U133A	TNFSF13	Hs.54673	O75888	8741	17p13.1
211502_s_at_HG-U133A	PFTK1	Hs.57856	O94921	5218	7q21-q22
211540_s_at_HG-U133A	RB1	Hs.75770	P06400	5925	13q14.2
211574_s_at_HG-U133A	MCP	Hs.83532	Q15429	4179	1q32
211584_s_at_HG-U133A	NPAT	Hs.89385	Q13632	4863	11q22-q23
211657_at_HG-U133A					
211665_s_at_HG-U133A					
211668_s_at_HG-U133A	PLAU	Hs.77274	Q96SE8	5328	10q24
211709_s_at_HG-U133A	SCGF	Hs.105927	Q9Y470	6320	19q13.3
211743_s_at_HG-U133A	PRG2	Hs.99962	P13727	5553	11q12
211748_x_at_HG-U133A	PTGDS	Hs.8272	P41222	5730	9q34.2-q34.3
211771_s_at_HG-U133A	POU2F2	Hs.1101	Q9BRS4	5452	19q13.31
211787_s_at_HG-U133A	EIF4A1	Hs.129673	Q9BRB1	1973	17p13
211796_s_at_HG-U133A	TRB	Hs.303157	P04435	6957	7q34
211800_s_at_HG-U133A	USP4	Hs.77500	Q13107	7375	3p21.3
211819_s_at_HG-U133A	SH3D5	Hs.108924	Q9BX64	10580	10q23.3-q24.1
211824_x_at_HG-U133A	DEFCAP	Hs.104305	Q9H5Z7	22861	17p13
211852_s_at_HG-U133A	ATRN	Hs.194019	O75882	8455	20p13
211883_x_at_HG-U133A	CEACAM1	Hs.50964	Q13854	634	19q13.2
211889_x_at_HG-U133A	CEACAM1	Hs.50964	Q13854	634	19q13.2
211918_x_at_HG-U133A	PLAC3	Hs.293896	Q96PH7	60676	1q23-q25
211934_x_at_HG-U133A	G2AN	Hs.76847	Q9P0X0	23193	11q13.1
211950_at_HG-U133A	RBAF600	Hs.297641	AAL83880	23352	1p36.13
211953_s_at_HG-U133A	KPNB3	Hs.113503	AAH01497	3843	13q32.2
211984_at_HG-U133A		Hs.374441			
211990_at_HG-U133A	HLA-DPA1	Hs.914	Q95HB9	3113	6p21.3
211991_s_at_HG-U133A	HLA-DPA1	Hs.914	Q95HB9	3113	6p21.3

212012_at_HG-U133A	D2S448	Hs.118893	Q92626	7837	2pter-p25.1
212013_at_HG-U133A	D2S448	Hs.118893	Q92626	7837	2pter-p25.1
212020_s_at_HG-U133A	MKI67	Hs.80976	P46013	4288	10q25-qter
212022_s_at_HG-U133A	MKI67	Hs.80976	P46013	4288	10q25-qter
212032_s_at_HG-U133A	PTOV1	Hs.19555	Q9HBN4	53635	19q13.33
212058_at_HG-U133A	KIAA0332	Hs.7976	O15042	23350	3q24
212074_at_HG-U133A	KIAA0810	Hs.7531	Q96CZ7	23353	7p22.3
212107_s_at_HG-U133A	DDX9	Hs.74578	Q12803	1660	1q25
212133_at_HG-U133A	MGC5466	Hs.83724	Q96F03	81614	15q11.1
212146_at_HG-U133A	KIAA0842	Hs.74569	O94928	23207	1p36.13
212150_at_HG-U133A	KIAA0143	Hs.84087	Q14156	23167	8q24.12
212171_x_at_HG-U133A	VEGF	Hs.73793	Q96KJ0	7422	6p12
212185_x_at_HG-U133A	MT2A	Hs.118786	P02795	4502	16q13
212187_x_at_HG-U133A	PTGDS	Hs.8272	P41222	5730	9q34.2-q34.3
212188_at_HG-U133A	LOC115207	Hs.109438	Q96CX2	115207	13q22.1
212207_at_HG-U133A	KIAA1025	Hs.4084	Q9UFD8	23389	12q24.21
212222_at_HG-U133A	KIAA0077	Hs.112396	Q14997	23198	2p16.2
212229_s_at_HG-U133A					
212231_at_HG-U133A	FBXO21	Hs.184227	O94952	23014	12q24.21
212232_at_HG-U133A	KIAA1014	Hs.6834	Q9H985	23360	11q12.1
212236_x_at_HG-U133A					
212250_at_HG-U133A		Hs.243901	AAL92861		
212251_at_HG-U133A		Hs.243901	AAL92861		
212259_s_at_HG-U133A	HPIP	Hs.8068	Q9HA02	57326	1q21.2
212268_at_HG-U133A	SERPINB1	Hs.183583	P30740	1992	6p25
212271_at_HG-U133A	MAPK1	Hs.324473	P28482	5594	22q11.21
212281_s_at_HG-U133A	MAC30	Hs.199695	Q07823	27346	17q11.1
212285_s_at_HG-U133A	AGRN	Hs.273330	Q96IC1	180	1p36.3-p32
212287_at_HG-U133A	JJAZ1	Hs.197803	Q15022	23512	17q11.2
212293_at_HG-U133A	KIAA0630	Hs.12259	AAH28408	23323	1p11.2
212309_at_HG-U133A	CLASP2	Hs.108614	Q9H7A3	23122	3p22.2-p22.1
212311_at_HG-U133A	KIAA0746	Hs.49500	Q96G59	23231	4p15.31
212313_at_HG-U133A		Hs.5019	Q8WUX9		
212314_at_HG-U133A	KIAA0746	Hs.49500	O94847	23231	4p15.31
212345_s_at_HG-U133A	DKFZP586F2423	Hs.13659	Q9H6N8	64764	7q34
212346_s_at_HG-U133A					
212349_at_HG-U133A	POFUT1	Hs.178292	BAA11497	23509	
212357_at_HG-U133A	KIAA0280	Hs.75400	Q92567	23201	11q13.3
212365_at_HG-U133A	MYO1B	Hs.121576	O43795	4430	2q12-q34
212382_at_HG-U133A		Hs.289068			
212385_at_HG-U133A		Hs.289068			
212386_at_HG-U133A		Hs.289068			

212387_at_HG-U133A		Hs.289068				
212397_at_HG-U133A	RDX	Hs.263671	P35241	5962	11q23	
212400_at_HG-U133A		Hs.349755				
212417_at_HG-U133A	SCAMP1	Hs.31218	Q96BX1	9522	5q13.3-q14.1	
212449_s_at_HG-U133A	LYPLA1	Hs.12540	O75608	10434	8q11.23	
212463_at_HG-U133A		Hs.99766				
212469_at_HG-U133A	IDN3	Hs.225767	Q9Y6Y4	25836	5p13.1	
212479_s_at_HG-U133A	FLJ13910	Hs.75277	Q9H6W5	64795	2p11.1	
212480_at_HG-U133A	KIAA0376	Hs.4791	O15081	23384	22q11.21	
212481_s_at_HG-U133A	TPM4	Hs.250641	P07226	7171	19p13.1	
212484_at_HG-U133A	MTVR	Hs.18686		23625		
212509_s_at_HG-U133A		Hs.356623				
212531_at_HG-U133A	LCN2	Hs.204238	P80188	3934	9q34	
212535_at_HG-U133A		Hs.288993				
212538_at_HG-U133A	KIAA1058	Hs.8021	Q9BZ29	23348	13q32.3	
212549_at_HG-U133A		Hs.24064				
212569_at_HG-U133A	KIAA0650	Hs.8118	Q9UG39	23347	18p11.31	
212577_at_HG-U133A	KIAA0650	Hs.8118	O75141	23347	18p11.31	
212579_at_HG-U133A	KIAA0650	Hs.8118	O75141	23347	18p11.31	
212586_at_HG-U133A	ARTS-1	Hs.247043	AAK37778	51752	5q15	
212587_s_at_HG-U133A	PTPRC	Hs.170121	P08575	5788	1q31-q32	
212589_at_HG-U133A	RRAS2	Hs.206097	AAM12638	22800	11p15.2	
212590_at_HG-U133A						
212592_at_HG-U133A		Hs.76325	Q8WW49			
212601_at_HG-U133A	KIAA0399	Hs.100955	BAB85062	23140	17p13.3	
212614_at_HG-U133A		Hs.12702				
212629_s_at_HG-U133A	PRKCL2	Hs.69171	Q16513	5586	1p22.1	
212658_at_HG-U133A	LHFPL2	Hs.79299	Q92605	10184	5q13.3	
212660_at_HG-U133A	KIAA0239	Hs.9729	Q96GQ6	23338	5q31.1	
212667_at_HG-U133A	SPARC	Hs.111779	AAH04974	6678	5q31.3-q32	
212686_at_HG-U133A	KIAA1157	Hs.21894	Q9ULR3	57460	12q13.13	
212719_at_HG-U133A	SCOP	Hs.38176	BAA25532	23239	18q21.32	
212733_at_HG-U133A	KIAA0226	Hs.141296	Q92622	9711	3q29	
212735_at_HG-U133A	KIAA0226	Hs.141296	Q92622	9711	3q29	
212750_at_HG-U133A	PPP1R16B	Hs.45719	O94912	26051	20q11.23	
212778_at_HG-U133A	KIAA0602	Hs.37656	O60342	23241		14
212783_at_HG-U133A	DKFZp761B2423	Hs.91065	Q9NPX4	55524		16
212812_at_HG-U133A		Hs.288232				
212813_at_HG-U133A	FLJ14529	Hs.334703	Q8WWL8	84887	11q25	
212827_at_HG-U133A	IGHM	Hs.153261	Q96GA6	3507	14q32.33	
212828_at_HG-U133A	SYNJ2	Hs.61289	O15056	8871	6q25.3	
212838_at_HG-U133A	KIAA1010	Hs.23860	Q9Y2L3	23268	10q25.1	

212886_at_HG-U133A	DKFZP434C171	Hs.209100	AAH16647	26112	5q33.1
212895_s_at_HG-U133A	ABR	Hs.118021	Q12979	29	17p13.3
212914_at_HG-U133A	PKP4	Hs.152151	Q99569	8502	2q23-q31
212953_x_at_HG-U133A	CALR	Hs.16488	P13796	811	19p13.3-p13.2
212956_at_HG-U133A	KIAA0882	Hs.90419	BAA74905	23158	4q31.1
212960_at_HG-U133A	KIAA0882	Hs.90419	BAA74905	23158	4q31.1
212967_x_at_HG-U133A	NAP1L1	Hs.302649	AAH02387	4673	12q14.1
212970_at_HG-U133A		Hs.15740			
212973_at_HG-U133A	RPIA	Hs.79886	Q96BJ6	22934	2p11.1
212975_at_HG-U133A	KIAA0870	Hs.18166	Q9UFX2	22898	8q24.3
212985_at_HG-U133A		Hs.15740			
212989_at_HG-U133A		Hs.153716			
212998_x_at_HG-U133A	HLA-DQB1	Hs.73931	AAH12106	3119	6p21.3
213048_s_at_HG-U133A	SET	Hs.145279	Q01105	6418	9q34
213049_at_HG-U133A	DKFZp566D133	Hs.167031	Q9Y408	26134	9q31
213073_at_HG-U133A	KIAA0321	Hs.8663	Q96H43	23503	14q23.3
213081_at_HG-U133A	ZNF297	Hs.206770	Q8WV82	9278	6p21.3
213101_s_at_HG-U133A	IL27	Hs.10927	Q9BTK7	56005	19p13.3
213142_x_at_HG-U133A	LOC54103	Hs.12969	Q9UMH3	54103	7p12.3
213147_at_HG-U133A	HOXA10	Hs.110637	AAH13971	3206	7p15-p14
213150_at_HG-U133A	HOXA10	Hs.110637	AAH13971	3206	7p15-p14
213159_at_HG-U133A	KIAA0805	Hs.55947	O94897	23226	14q22.1-q23.3
213238_at_HG-U133A	ATP10D	Hs.173540	Q96SR3	57205	4p12
213249_at_HG-U133A	FBXL7	Hs.76798	O94926	23194	5p15.1
213288_at_HG-U133A		Hs.90797			
213295_at_HG-U133A		Hs.26295			
213309_at_HG-U133A	PLCL2	Hs.54886	Q9H8L0	23228	3p24.3
213313_at_HG-U133A	GAPCENA	Hs.55099	Q9UG67	23637	9q34.11
213353_at_HG-U133A	ABCA5	Hs.180513	Q9NY14	23461	17q24.3
213370_s_at_HG-U133A	DKFZP434L243	Hs.21695	Q9Y4Q9	25944	3
213447_at_HG-U133A	IPW	Hs.5022		3653	15q11-q12
213452_at_HG-U133A	ZNF184	Hs.158174	AAH22992	7738	6p21.3
213453_x_at_HG-U133A	GAPD	Hs.169476	Q16768	2597	12p13
213474_at_HG-U133A		Hs.356517			
213504_at_HG-U133A	MOV34-34KD	Hs.15591	O15387	10980	7q11.1
213511_s_at_HG-U133A		Hs.347187	Q96FD1		
213514_s_at_HG-U133A	DIAPH1	Hs.26584	O60610	1729	5q31
213539_at_HG-U133A	CD3D	Hs.95327		915	11q23
213572_s_at_HG-U133A	SERPINB1	Hs.183583	P30740	1992	6p25
213582_at_HG-U133A	ATP11A	Hs.29189	Q9H7W0	23250	13q34
213600_at_HG-U133A	KIAA0545	Hs.129943	BAA25471	23094	19q13.13
213622_at_HG-U133A	COL9A2	Hs.37165	Q14055	1298	1p33-p32

213624_at_HG-U133A	ASM3A	Hs.42945	Q92484	10924	6
213639_s_at_HG-U133A	KIAA0557	Hs.101414	O60304	26048	16p13.13
213674_x_at_HG-U133A	IGHG3	Hs.300697	AAH24289	3502	14q32.33
213689_x_at_HG-U133A	RPL5	Hs.180946	P46777	6125	1p22.1
213716_s_at_HG-U133A	SECTM1	Hs.95655	O00466	6398	17q25
213725_x_at_HG-U133A		Hs.22907			
213737_x_at_HG-U133A		Hs.205125			
213772_s_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
213779_at_HG-U133A					
213798_s_at_HG-U133A	CAP	Hs.104125	Q01518	10487	1p34.3
213810_s_at_HG-U133A	FLJ10342	Hs.101514	Q9BQB1	55122	6q16.1
213844_at_HG-U133A	HOXA5	Hs.37034	Q96CY6	3202	7p15-p14
213846_at_HG-U133A	COX7C	Hs.3462	P15954	1350	5q14
213850_s_at_HG-U133A	SFRS2IP	Hs.51957	Q99590	9169	12p11.21
213854_at_HG-U133A	SYNGR1	Hs.6139	O43759	9145	22q13.1
213857_s_at_HG-U133A	CD47	Hs.82685	Q96A60	961	3q13.1-q13.2
213891_s_at_HG-U133A		Hs.289068			
213894_at_HG-U133A	KIAA0960	Hs.29900	BAA76804	23249	7p22.1
213895_at_HG-U133A	EMP1	Hs.79368	P54849	2012	12p12.3
213902_at_HG-U133A	ASAH	Hs.75811	Q13510	427	8p22-p21.3
213922_at_HG-U133A	KIAA0847	Hs.125836	O94932	26044	15q14
213927_at_HG-U133A		Hs.170267			
213942_at_HG-U133A	EGFL3	Hs.56186	O75095	1953	1p36.3
213944_x_at_HG-U133A		Hs.323067	Q96DH5		
213963_s_at_HG-U133A	SAP30	Hs.20985	O75446	8819	4q34.1
213979_s_at_HG-U133A	CTBP1	Hs.239737	Q13363	1487	4p16
214000_s_at_HG-U133A	RGS10	Hs.82280	AAM12648	6001	10q25
214017_s_at_HG-U133A	DDX34	Hs.151706	Q14147	9704	19q13.3
214030_at_HG-U133A	FLJ14393	Hs.23294	Q96C17	84864	3q22.1
214051_at_HG-U133A	TMSNB	Hs.56145	Q99406	11013	Xq21.33-q22.3
214109_at_HG-U133A	LRBA	Hs.62354	P50851	987	4q31.22-q31.23
214116_at_HG-U133A	BTD	Hs.78885	P43251	686	3p25
214144_at_HG-U133A	POLR2D	Hs.194638	Q96FU3	5433	2q21
214152_at_HG-U133A	PIGB	Hs.247118	Q8WVN7	9488	15q21-q22
214203_s_at_HG-U133A	PRODH	Hs.343874	Q9UF13	5625	22q11.21
214228_x_at_HG-U133A					
214238_at_HG-U133A		Hs.18081			
214310_s_at_HG-U133A	ZFPL1	Hs.155165	O14616	7542	11q13
214315_x_at_HG-U133A	CALR	Hs.16488	P27797	811	19p13.3-p13.2
214316_x_at_HG-U133A	CALR	Hs.16488	P13796	811	19p13.3-p13.2
214317_x_at_HG-U133A	RPS9	Hs.180920	P46781	6203	19q13.4
214321_at_HG-U133A	NOV	Hs.235935	P48745	4856	8q24.1

214394_x_at_HG-U133A	FLJ20897	Hs.334798	Q96I38	84338	8q24.3
214395_x_at_HG-U133A	FLJ20897	Hs.334798	Q9H7G6	84338	8q24.3
214430_at_HG-U133A	GLA	Hs.69089	BAA34059	2717	Xq22
214439_x_at_HG-U133A	BIN1	Hs.193163	O00499	274	2q14
214450_at_HG-U133A	CTSW	Hs.87450	P56202	1521	11q13.1
214452_at_HG-U133A	BCAT1	Hs.157205	Q96MY9	586	12pter-q12
214475_x_at_HG-U133A	CAPN3	Hs.40300	Q9BQC8	825	15q15.1•q21.1
214500_at_HG-U133A	H2AFY	Hs.75258	Q96D41	9555	5q31.3-q32
214501_s_at_HG-U133A	H2AFY	Hs.75258	O75367	9555	5q31.3-q32
214505_s_at_HG-U133A	FHL1	Hs.239069	O95212	2273	Xq26
214523_at_HG-U133A	CEBPE	Hs.158323	Q15744	1053	14q11.2
214558_at_HG-U133A	GPR12	Hs.123034		2835	13q12
214575_s_at_HG-U133A	AZU1	Hs.72885		566	19p13.3
214615_at_HG-U133A	P2Y10	Hs.296433		27334	Xq21.1
214651_s_at_HG-U133A	HOXA9	Hs.127428	P31269	3205	7p15-p14
214686_at_HG-U133A	ZNF266	Hs.118281	Q14584	10781	19p13.2
214693_x_at_HG-U133A	DJ328E19.C1.1	Hs.218329	Q9UJI9	25832	1q12-1q21.2
214700_x_at_HG-U133A					
214761_at_HG-U133A	OAZ	Hs.137168	BAA34480	23090	16q12
214786_at_HG-U133A	MAP3K1	Hs.170610	Q13233	4214	5q11.2
214789_x_at_HG-U133A	SRP46	Hs.155160	Q96TA3	10929	11q22
214849_at_HG-U133A		Hs.188757	Q9BTH8		
214875_x_at_HG-U133A	APLP2	Hs.279518	Q14662	334	11q24
214894_x_at_HG-U133A	MACF1	Hs.108258	BAA32310	23499	1p32-p31
214911_s_at_HG-U133A					
214924_s_at_HG-U133A					
214949_at_HG-U133A					
214950_at_HG-U133A					
215001_s_at_HG-U133A	GLUL	Hs.170171	AAH11700	2752	1q31
215049_x_at_HG-U133A	CD163	Hs.74076	Q07900	9332	12p13.3
215087_at_HG-U133A					
215100_at_HG-U133A					
215115_x_at_HG-U133A	NTRK3	Hs.26776	Q16288	4916	15q25
215215_s_at_HG-U133A					
215227_x_at_HG-U133A	ACP1	Hs.75393	AAH07422	52	2p25
215346_at_HG-U133A	TNFRSF5	Hs.25648	P25942	958	20q12-q13.2
215379_x_at_HG-U133A	IGLJ3	Hs.181125	Q8WUK3	28831	22q11.1-q11.2
215450_at_HG-U133A	SNRPE	Hs.334612	P08578	6635	1q32
215537_x_at_HG-U133A					
215622_x_at_HG-U133A	HSPC226	Hs.30127	Q9BWX1	51533	3p21.31
215785_s_at_HG-U133A	CYFIP2	Hs.258503	Q14650	26999	5q34
215855_s_at_HG-U133A					

215925_s_at_HG-U133A					
216015_s_at_HG-U133A					
216032_s_at_HG-U133A	SDBCAG84	Hs.169992	Q9H276	51614	20pter-q12
216044_x_at_HG-U133A					
216095_x_at_HG-U133A	MTMR1	Hs.372428	Q13613	8776	Xq28
216218_s_at_HG-U133A	PLCL2	Hs.54886	Q9H8L0	23228	3p24.3
216304_x_at_HG-U133A					
216320_x_at_HG-U133A					
216356_x_at_HG-U133A	BAIAP3	Hs.134846	BAA34454	8938	16p13.3
216363_at_HG-U133A					
216379_x_at_HG-U133A					
216399_s_at_HG-U133A					
216449_x_at_HG-U133A					
216450_x_at_HG-U133A					
216609_at_HG-U133A		Hs.336933	O60744		
216640_s_at_HG-U133A					
216652_s_at_HG-U133A					
216680_s_at_HG-U133A	EPHB4	Hs.155227	Q96L35	2050	7q22
216698_x_at_HG-U133A					
216833_x_at_HG-U133A		Hs.372513	Q12832		
216860_s_at_HG-U133A	GDF11	Hs.339699	O95390	10220	12q12
217047_s_at_HG-U133A					
217080_s_at_HG-U133A	HOMER-2B	Hs.93564	O95349	9455	15q24.3
217156_at_HG-U133A					
217179_x_at_HG-U133A					
217185_s_at_HG-U133A					
217223_s_at_HG-U133A					
217225_x_at_HG-U133A	PM5	Hs.227823	Q9H049	23420	16p13.11
217375_at_HG-U133A					
217383_at_HG-U133A					
217398_x_at_HG-U133A					
217418_x_at_HG-U133A	MS4A2	Hs.89751	AAH02807	931	11q12-q13.1
217419_x_at_HG-U133A					
217478_s_at_HG-U133A					
217504_at_HG-U133A	ABCA6	Hs.15780	Q8WWZ6	23460	17q24.3
217520_x_at_HG-U133A		Hs.356777			
217521_at_HG-U133A		Hs.276590			
217559_at_HG-U133A	RPL10L	Hs.308332	Q96L21	140801	14q13-q21
217716_s_at_HG-U133A	SEC61A1	Hs.306079	Q9BU16	29927	3q21.3
217768_at_HG-U133A	LOC51637	Hs.110803	Q9Y224	51637	14q21.3
217816_s_at_HG-U133A	pcnp	Hs.283728	Q96CU3	57092	3q13.11
217838_s_at_HG-U133A	RNB6	Hs.241471	AAH23997	51466	14q32.32

217916_s_at_HG-U133A	BM-009	Hs.92918	Q9NW21	51571	8q24.22
217920_at_HG-U133A		Hs.362793	AAH15874		
217950_at_HG-U133A	NOSIP	Hs.7236	Q9Y314	51070	19q13.33
217963_s_at_HG-U133A	HCS	Hs.169248	P00001	54205	7p21.2
217966_s_at_HG-U133A	C1orf24	Hs.48778	Q9H9Y8	116496	1q25
217979_at_HG-U133A	NET-6	Hs.284243	O95857	27075	7p21.3
217988_at_HG-U133A	HEI10	Hs.107003	Q9NPC3	57820	14q11.1
217989_at_HG-U133A	LOC51170	Hs.12150	Q9UKU4	51170	4q21.3
217994_x_at_HG-U133A					
218039_at_HG-U133A	ANKT	Hs.279905	AAH24772	51203	15q13.3
218041_x_at_HG-U133A	PRO1068	Hs.343878		55439	
218051_s_at_HG-U133A	FLJ12442	Hs.84753	Q96C80	64943	
218089_at_HG-U133A	C20orf4	Hs.11314	Q9Y312	25980	20pter-q12
218090_s_at_HG-U133A					
218094_s_at_HG-U133A	C20orf35	Hs.179666	Q9BVL1	55861	20q13.11
218100_s_at_HG-U133A	ESRRBL1	Hs.170318	Q9NWB7	55081	3q13.13
218109_s_at_HG-U133A	FLJ14153	Hs.7503	Q9H3U5	64747	3q25.31
218122_s_at_HG-U133A	SENP2	Hs.3355	BAA92569	59343	3q28
218144_s_at_HG-U133A	FLJ22056	Hs.24956	Q9H6N1	64423	14q32.33
218151_x_at_HG-U133A	FLJ11856	Hs.6459	Q9HAB3	79581	8q24.3
218168_s_at_HG-U133A	CABC1	Hs.273186	Q9HBQ1	56997	1q42.11
218172_s_at_HG-U133A	PRO2577	Hs.241576		55493	8q24.13
218191_s_at_HG-U133A	FLJ11240	Hs.339833	Q9BY56	55788	6q14.1
218223_s_at_HG-U133A	LOC51177	Hs.173380	Q9NRV3	51177	1q21.3
218224_at_HG-U133A	PNMA1	Hs.194709	O95144	9240	14q24.1
218237_s_at_HG-U133A	SLC38A1	Hs.18272	Q9H2H9	81539	12p11.21
218259_at_HG-U133A	KIAA1243	Hs.151076	BAA86557	57496	16p13.2
218319_at_HG-U133A	PELI1	Hs.7886	Q9HCX0	57162	2p13.3
218329_at_HG-U133A	PRDM4	Hs.21807	Q9UKN5	11108	12q23-q24.1
218331_s_at_HG-U133A	FLJ20360	Hs.26434	Q9H7A4	54906	10p15.1
218338_at_HG-U133A	EDR1	Hs.305985	Q9BU63	1911	12p13
218341_at_HG-U133A	FLJ11838	Hs.72531	Q9HAB8	79717	1p34.1
218351_at_HG-U133A	FLJ20502	Hs.23956	Q9NX08	54951	
218354_at_HG-U133A	LOC51693	Hs.27445	Q9UL33	51693	16q24.3
218355_at_HG-U133A	KIF4A	Hs.279766	O95239	24137	Xq13.1
218379_at_HG-U133A	RBM7	Hs.5887	Q9NUT4	10179	11q23.1-q23.2
218384_at_HG-U133A	CRHSP-24	Hs.92198	Q9BQ53	23589	16p13.3
218424_s_at_HG-U133A	FLJ10829	Hs.57655	AAM08128	55240	2q21.2
218464_s_at_HG-U133A	FLJ10700	Hs.295909	Q9H6F3	55731	17q11.2
218468_s_at_HG-U133A	CKTSF1B1	Hs.40098	O60565	26585	15q13-q15
218469_at_HG-U133A	CKTSF1B1	Hs.40098	O60565	26585	15q13-q15
218482_at_HG-U133A	DC6	Hs.283740	Q9NPA8	56943	8q23.2

218499_at_HG-U133A	MST4	Hs.23643	Q96SR7	51765	Xq26.1
218516_s_at_HG-U133A	FLJ20421	Hs.13328	Q9NX62	54928	8q11.23
218517_at_HG-U133A	FLJ22479	Hs.238246	Q96SQ1	79960	4q26-q27
218531_at_HG-U133A	FLJ21749	Hs.288761	Q9H6X4	80194	11q12.2
218543_s_at_HG-U133A	FLJ22693	Hs.12646	Q9H610	64761	7q32.2
218549_s_at_HG-U133A	LOC51115	Hs.44222	Q96DB5	51115	8
218577_at_HG-U133A	FLJ20331	Hs.50848	Q9NXC1	55631	1p31.1
218582_at_HG-U133A	FLJ20445	Hs.343748	Q9NX47	54708	10q23.33
218589_at_HG-U133A	P2Y5	Hs.189999	P43657	10161	13q14
218614_at_HG-U133A	FLJ10652	Hs.236844	Q9NVL6	55196	12p12.1
218642_s_at_HG-U133A	MGC2217	Hs.323164	Q9BUK0	79145	8q11.22
218645_at_HG-U133A	ZNF277	Hs.42636	CAD28546	11179	7q31.1
218662_s_at_HG-U133A	HCAP-G	Hs.193602	Q96SV9	64151	4p16-p15
218663_at_HG-U133A	HCAP-G	Hs.193602	Q9BUR3	64151	4p16-p15
218692_at_HG-U133A	FLJ20366	Hs.8358	Q96D80	55638	8q23.2
218718_at_HG-U133A	PDGFC	Hs.43080	Q9NRA1	56034	4q32
218764_at_HG-U133A	MGC5363	Hs.1880	Q9BVQ0	79030	14q22.1-q22.3
218836_at_HG-U133A	FLJ22638	Hs.183232	Q96F16	79897	6p21.31
218913_s_at_HG-U133A	LOC51291	Hs.49427	Q9P107	51291	19p11-p12
218916_at_HG-U133A	FLJ23436	Hs.85658	Q9H5H4	79724	16p11.1
218933_at_HG-U133A	MGC5347	Hs.5555	Q9BVQ7	79029	15q15.1
218938_at_HG-U133A	MGC11279	Hs.10915	Q9H469	79176	10q24.32
218942_at_HG-U133A	FLJ22055	Hs.144502	AAH28596	79837	12q13.11
218974_at_HG-U133A	FLJ10159	Hs.22505	Q9NWB3	55084	6q21
219013_at_HG-U133A	FLJ21634	Hs.97056	Q9H6C2	63917	7q34-q36
219027_s_at_HG-U133A	MYO9A	Hs.23395	Q9NTG2	4649	15q22-q23
219029_at_HG-U133A	FLJ21657	Hs.26498	Q96D39	64417	5p12
219033_at_HG-U133A	FLJ21308	Hs.29977	Q9H754	79668	5q11.1
219036_at_HG-U133A	BITE	Hs.42315	Q96B31	80321	3q22-q23
219073_s_at_HG-U133A	OSBPL10	Hs.321622	Q9NX98	114884	3p22.3
219076_s_at_HG-U133A	PXMP2	Hs.49912	Q96GB0	5827	
219079_at_HG-U133A	b5&b5R	Hs.5741	AAH25380	51167	6pter-q22.33
219084_at_HG-U133A	NSD1	Hs.99010	Q96L73	64324	5q35.3
219090_at_HG-U133A	SLC24A3	Hs.12321	Q9HC58	57419	20p13
219099_at_HG-U133A	C12orf5	Hs.24792	Q9NQ88	57103	12p13.3
219111_s_at_HG-U133A	MGC2835	Hs.70582	AAL85336	79039	12q24.11
219138_at_HG-U133A	RPL14	Hs.738	Q96GR0	9045	3p22-p21.2
219156_at_HG-U133A	FLJ11271	Hs.109654	Q96IA4	55333	14q22.1-q24.3
219202_at_HG-U133A	FLJ22341	Hs.25485	Q9H6E9	79651	17q25.3
219221_at_HG-U133A	FLJ22332	Hs.111092	Q9H6F0	79779	3q24
219229_at_HG-U133A	SLC21A11	Hs.14805	Q9UIG8	28232	15q26
219234_x_at_HG-U133A	FLJ23142	Hs.20999	Q9H5R5	79634	2q31.1

219271_at_HG-U133A	FLJ12691	Hs.15830	Q9BRH1	79623	2p23.2
219280_at_HG-U133A	WDR9	Hs.225674	Q96QH0	54014	21q22.2
219291_at_HG-U133A	MDS009	Hs.64641	Q9NRU6	56986	15q15.2
219312_s_at_HG-U133A	RINZF	Hs.237146	Q96MH9	65986	8q13-q21.1
219329_s_at_HG-U133A	3-Apr	Hs.9527	Q96RT2	51374	2p23.3
219337_at_HG-U133A	FLJ20584	Hs.126704	Q9NWV0	54991	1p36.33
219358_s_at_HG-U133A	CENTA2	Hs.28802	Q96SD5	55803	17q11.2
219360_s_at_HG-U133A	TRPM4	Hs.31608	AAM18083	54795	19q13.33
219362_at_HG-U133A	FLJ22643	Hs.43579	Q9H631	79688	9q21.33
219452_at_HG-U133A	LOC64174	Hs.115537	Q9H4A9	64174	16q22.2
219457_s_at_HG-U133A	RIN3	Hs.180040	Q9H6A5	79890	14q32.13
219463_at_HG-U133A	C20orf103	Hs.22920	Q9UJQ1	24141	20p12
219471_at_HG-U133A	FLJ21562	Hs.288708	Q9H714	80183	13q14.11
219477_s_at_HG-U133A	LOC55901	Hs.325667	Q9NS62	55901	13q14.13
219478_at_HG-U133A	WFDC1	Hs.36688	Q9HAU1	58189	16q24.3
219518_s_at_HG-U133A	FLJ22637	Hs.296178	Q9H634	80237	15q14
219574_at_HG-U133A	FLJ20668	Hs.12920	CAD28529	55016	4q32.2
219598_s_at_HG-U133A					
219615_s_at_HG-U133A	KCNK5	Hs.127007	O95279	8645	6p21
219631_at_HG-U133A	FLJ12929	Hs.278956	Q8WVX8	80002	8q22.3
219634_at_HG-U133A	C4ST	Hs.287402	Q9NPF2	50515	12q
219641_at_HG-U133A	FLJ10103	Hs.42140	Q9NWD5	55070	15q25.3
219654_at_HG-U133A	PTPLA	Hs.114062	Q96FW7	9200	10p14-p13
219667_s_at_HG-U133A	BANK	Hs.193736	Q9NWP2	55024	4q22.2
219690_at_HG-U133A	FLJ22573	Hs.352548	Q9H665	79713	19q13.13
219734_at_HG-U133A	FLJ20174	Hs.114556	Q9NXL6	54847	3q13.31
219753_at_HG-U133A	STAG3	Hs.20132	Q9UJ98	10734	7q22
219763_at_HG-U133A	KIAA1608	Hs.300842	BAB13434	57706	9q34.11
219788_at_HG-U133A	PILR	Hs.122591	Q9UKJ1	29992	7q22
219789_at_HG-U133A	NPR3	Hs.123655	P17342	4883	5p14-p13
219793_at_HG-U133A	SNX16	Hs.128645	P57768	64089	8q21.13
219812_at_HG-U133A	MGC2463	Hs.323634	Q9BVK3	79037	7q11.1
219820_at_HG-U133A	NTT5	Hs.59260	Q9GZN6	28968	19q13.1-q13.4
219837_s_at_HG-U133A	C17	Hs.13872	Q9NRR1	54360	4p16-p15
219846_at_HG-U133A	FLJ23040	Hs.169813	Q9H5U2	80248	1q21.2
219868_s_at_HG-U133A	ANKHZN	Hs.352146	Q9P2R3	51479	17p13
219869_s_at_HG-U133A	LOC64116	Hs.284205	Q9BVC0	64116	4q22-q24
219891_at_HG-U133A	FLJ20208	Hs.131776	Q9NXJ5	54858	19p13.11
220000_at_HG-U133A	SIGLEC5	Hs.117005	O15389	8778	19q13.3
220001_at_HG-U133A	PADI5	Hs.117232	Q9UM07	23569	1p36.13
220007_at_HG-U133A	FLJ13984	Hs.135146	Q9H825	79828	2q31.1
220050_at_HG-U133A	C9orf9	Hs.62595	Q96E40	11092	9q34

220059_at_HG-U133A	BRDG1	Hs.121128	Q9ULZ2	26228	4q13.1
220118_at_HG-U133A	TZFP	Hs.99430	Q8WVP2	27033	19q13.1
220307_at_HG-U133A	CD244	Hs.157872	Q9Y288	51744	1q23.1
220338_at_HG-U133A	FLJ10244	Hs.274419	Q9NW78	55103	1q24.1
220564_at_HG-U133A	FLJ11218	Hs.274413	Q9BS33	55328	10q23.33
220653_at_HG-U133A	ZIM2	Hs.201776	Q9NZV7	23619	19q13.4
220744_s_at_HG-U133A	WDR10	Hs.70202	Q9NV68	55764	3q21
220755_s_at_HG-U133A					
220764_at_HG-U133A	PPP4R2	Hs.356686	Q8WXX6	56340	3q29
220768_s_at_HG-U133A	CSNK1G3	Hs.129206	Q9Y6M4	1456	5q23
220796_x_at_HG-U133A	FLJ14251	Hs.281462	Q96I93	79939	19p13.12
220798_x_at_HG-U133A	FLJ11535	Hs.225170	Q9HAJ4	79948	19p13.3
220924_s_at_HG-U133A	SLC38A2	Hs.298275	Q96QD8	54407	12q
220987_s_at_HG-U133A	DKFZP434J037	Hs.172012	Q9H093	81788	1q31.1-q31.2
220999_s_at_HG-U133A	PRO1331	Hs.301824	AAH26892	81032	5q33.2
221004_s_at_HG-U133A	ITM3	Hs.111577	CAD28460	81618	2q37
221006_s_at_HG-U133A	MY014	Hs.67619	Q96D79	81609	1q21.1
221011_s_at_HG-U133A	DKFZP566J091	Hs.57209	Q9H0Q1	81606	2p23.1
221030_s_at_HG-U133A	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
221188_s_at_HG-U133A	CIDEB	Hs.288835	AAH25332	27141	14q11.2
221206_at_HG-U133A	FLJ21459	Hs.3769	Q9H729	79569	3q21.2
221234_s_at_HG-U133A	BACH2	Hs.88414	Q9BYV9	60468	6q15
221239_s_at_HG-U133A	SPAP1	Hs.194976	AAM12152	79368	1q21
221253_s_at_HG-U133A	MGC3178	Hs.6101	CAD29430	81567	6p25.2
221268_s_at_HG-U133A	LOC81537	Hs.24678	Q9H189	81537	14q23.1
221331_x_at_HG-U133A	CTLA4	Hs.247824	O95653	1493	2q33
221486_at_HG-U133A					
221543_s_at_HG-U133A	C8orf2	Hs.125849	O94905	11160	8p11.2
221555_x_at_HG-U133A	CDC14B	Hs.22116	O60730	8555	9q22.32
221558_s_at_HG-U133A	LEF1	Hs.44865	Q9UJU2	51176	4q23-q25
221581_s_at_HG-U133A	WBSCR5	Hs.56607	Q9BXX8	7462	7q11.23
221586_s_at_HG-U133A	E2F5	Hs.2331	Q15329	1875	8q21.13
221601_s_at_HG-U133A	TOSO	Hs.58831	O60667	9214	1q31.3
221602_s_at_HG-U133A	TOSO	Hs.58831	O60667	9214	1q31.3
221617_at_HG-U133A					
221642_at_HG-U133A	TREX1	Hs.278408	AAD48774	11277	3p21.3-p21.2
221731_x_at_HG-U133A	CSPG2	Hs.81800	P13611	1462	5q14.3
221739_at_HG-U133A	IL27	Hs.10927	Q969H8	56005	19p13.3
221755_at_HG-U133A		Hs.356684	Q9HBR0		
221761_at_HG-U133A	ADSS	Hs.90011	P30520	159	1cen-q12
221770_at_HG-U133A	RPE	Hs.125845	Q96MI0	6120	2q32-q33.3
221778_at_HG-U133A	KIAA1718	Hs.222707	Q9C0E5	80853	7q33-q35

221802_s_at_HG-U133A	KIAA1598	Hs.23740	AAH22348	57698	10q26.2
221834_at_HG-U133A		Hs.351343			
221858_at_HG-U133A	KIAA0608	Hs.100960	Q9UG83	23232	10q24.2
221865_at_HG-U133A		Hs.170226			
221902_at_HG-U133A		Hs.7967			
221943_x_at_HG-U133A	RPL38	Hs.2017	P23411	6169	17q23-q25
221969_at_HG-U133A	PAX5	Hs.22030	Q02548	5079	9p13
221980_at_HG-U133A					
221991_at_HG-U133A	NXPH3	Hs.55069	AAH22541	11248	17q22
222062_at_HG-U133A	WSX1	Hs.132781	AAH28003	9466	19p13.11
222073_at_HG-U133A	COL4A3	Hs.530	Q01955	1285	2q36-q37
222108_at_HG-U133A					
222146_s_at_HG-U133A					
222147_s_at_HG-U133A					
222150_s_at_HG-U133A					
222154_s_at_HG-U133A	DKFZP564A2416	Hs.5297	Q8WV53	26010	2q33.1
222163_s_at_HG-U133A	MGC5347	Hs.5555	Q9HA41	79029	15q15.1
222166_at_HG-U133A					
222203_s_at_HG-U133A					
222229_x_at_HG-U133A					
222237_s_at_HG-U133A					
222275_at_HG-U133A		Hs.27362			
222282_at_HG-U133A		Hs.294014			
222313_at_HG-U133A		Hs.293334			
222335_at_HG-U133A		Hs.44888			
222422_s_at_HG-U133B	MGC10924	Hs.9788	Q9BT67	80762	5q31.3
222448_s_at_HG-U133B	UMP-CMPK	Hs.11463	P30085	51727	
222465_at_HG-U133B	C15orf15	Hs.284162	AAH26267	51187	15q21
222477_s_at_HG-U133B	TM7SF3	Hs.10071	Q9NUS4	51768	12q11-q12
222492_at_HG-U133B	FLJ21324	Hs.4746	Q9BTJ7	60683	21q22.3
222520_s_at_HG-U133B	ESRRBL1	Hs.170318	BAB87803	55081	3q13.13
222619_at_HG-U133B	ZNF281	Hs.59757	Q9Y2X9	23528	1q32.1
222680_s_at_HG-U133B	RAMP	Hs.126774	Q96SN0	51514	
222692_s_at_HG-U133B	FLJ23399	Hs.299883	Q9NSQ8	64778	3q26.31
222698_s_at_HG-U133B	IMPACT	Hs.284245	Q9H2X4	55364	18q11.2-q12.1
222862_s_at_HG-U133B	AK5	Hs.18268	Q9Y6K8	26289	1p31
222915_s_at_HG-U133B	BANK	Hs.193736	Q8WYN5	55024	4q22.2
222916_s_at_HG-U133B					
222955_s_at_HG-U133B	HT011	Hs.355726	Q9NRV0	55855	Xq26.1
222976_s_at_HG-U133B	NTRK1	Hs.85844	AAH15403	4914	1q21-q22
222977_at_HG-U133B	SURF4	Hs.284296	O15260	6836	9q34.2
222979_s_at_HG-U133B					

222982_x_at_HG-U133B	SLC38A2	Hs.298275	BAA92620	54407	12q
222996_s_at_HG-U133B	HSPC195	Hs.15093	Q9NV51	51523	5q31.3
223036_at_HG-U133B	FRSB	Hs.9081	Q9BR63	10056	2q36.3
223044_at_HG-U133B	SLC11A3	Hs.5944	Q9NP59	30061	2q32
223054_at_HG-U133B	DNAJB11	Hs.278605	Q9UBS4	51726	3q28
223226_x_at_HG-U133B	MGC3181	Hs.324618	Q9BWG4	84713	19p13.11
223246_s_at_HG-U133B	STRBP	Hs.8215	Q9BXG4	55342	9q34.11
223253_at_HG-U133B	UCC1	Hs.46721	Q96J80	54749	7p14.1
223276_at_HG-U133B	NID67	Hs.29444	Q9BZL3	85027	
223280_x_at_HG-U133B	MS4A6A	Hs.17914	AAL56223	64231	11q12.1
223287_s_at_HG-U133B	FOXP1	Hs.274344	AAL56661	27086	3p14.1
223314_at_HG-U133B	MGC11352	Hs.101395	Q9BU34	81619	10q23.2
223318_s_at_HG-U133B	MGC10974	Hs.111099	Q9BT30	84266	19p13.3
223321_s_at_HG-U133B	FGFRL1	Hs.193326	Q9H4D7	53834	4p16
223382_s_at_HG-U133B	NIN283	Hs.320834	Q96K16	84937	16q22.3
223385_at_HG-U133B	CYP2S1	Hs.98370	Q96SQ9	29785	19q13.1
223391_at_HG-U133B	LOC81537	Hs.24678	Q9H189	81537	14q23.1
223401_at_HG-U133B	MDS006	Hs.47668	Q9BVD4	56985	17p12
223422_s_at_HG-U133B	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
223449_at_HG-U133B	SEMA6A	Hs.263395	Q96JU9	57556	5q23.1
223462_at_HG-U133B	MGC4618	Hs.89072	Q9BSA9	84286	4p16.3
223467_at_HG-U133B	RASD1	Hs.25829	AAM21071	51655	17p11.2
223469_at_HG-U133B	MGC10812	Hs.4188	Q9BSM8	83542	19p13.11
223471_at_HG-U133B					
223474_at_HG-U133B	C14orf4	Hs.179260	Q96JG2	64207	14q24.3
223482_at_HG-U133B	TMPIT	Hs.314243	Q9BXJ8	83862	7p12.3
223498_at_HG-U133B		Hs.15053	Q9HCQ3		
223514_at_HG-U133B	CARD11	Hs.293867	AAL34460	84433	7p22
223522_at_HG-U133B	GL012	Hs.21379	Q9H2N8	81571	9q34.11
223595_at_HG-U133B	AD031	Hs.44004	Q9H2Q1	83935	11q22.2
223703_at_HG-U133B	CDA017	Hs.39780	Q9H2I8	83938	10q23.1
223712_at_HG-U133B	DCOHM	Hs.150186	AAM18136	84105	5q31.2
223785_at_HG-U133B	FLJ10719	Hs.334828	Q96JN1	55215	15q25-q26
223828_s_at_HG-U133B	LGALS12	Hs.284183	AAH28222	85329	11q13
223839_s_at_HG-U133B					
223894_s_at_HG-U133B	FTS	Hs.288929	Q9H8T0	64400	16q12.2
223939_at_HG-U133B	GPR91	Hs.279575	AAL95690	56670	3q24-3q25.1
223981_at_HG-U133B	NIN	Hs.44054	BAB13391	51199	14q21.3
223982_s_at_HG-U133B	IPLA2	Hs.44198	Q9NP80	50640	7q31
224044_at_HG-U133B	FLJ11040	Hs.14202	Q9H067	55288	17q11.2
224049_at_HG-U133B	KCNK17	Hs.162282	AAH25726	89822	6p21.1
224076_s_at_HG-U133B	WHSC1L1	Hs.27721	Q9BYU8	54904	8p11.2

224221_s_at_HG-U133B	VAV3	Hs.267659	Q9UKW4	10451	1p13.2
224254_x_at_HG-U133B					
224324_at_HG-U133B	B29	Hs.131072	Q9BYG7	83876	18q21
224356_x_at_HG-U133B	MS4A6A	Hs.17914	AAH22854	64231	11q12.1
224389_s_at_HG-U133B	LOC84570	Hs.148642	Q9BXR9	84570	4q24
224404_s_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
224405_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
224406_s_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
224407_s_at_HG-U133B	MST4	Hs.23643	Q9BXC3	51765	Xq26.1
224435_at_HG-U133B	MGC4248	Hs.334437	Q9BRX8	84293	10q23.2
224482_s_at_HG-U133B	MGC11316	Hs.7985	Q9BRI9	85018	17q11.2
224516_s_at_HG-U133B	HSPC195	Hs.15093	Q9NV51	51523	5q31.3
224520_s_at_HG-U133B	MGC13168	Hs.9451	Q9BR80	84821	12q13.2
224553_s_at_HG-U133B	TNFRSF18	Hs.212680	Q9Y5U5	8784	1p36.3
224559_at_HG-U133B					
224570_s_at_HG-U133B		Hs.350268			
224609_at_HG-U133B	CTL2	Hs.105509	Q8WY97	57153	19p13.1
224664_at_HG-U133B		Hs.178485	Q96DE5		
224681_at_HG-U133B	GNA12	Hs.182874	AAM12615	2768	7p22-p21
224710_at_HG-U133B	RAB34	Hs.301853	Q96AR4	83871	17q11.1
224724_at_HG-U133B	KIAA1247	Hs.43857	Q9UJR3	55959	20q12-13.2
224727_at_HG-U133B		Hs.250465			
224735_at_HG-U133B		Hs.22546	Q8WVT9		
224739_at_HG-U133B	MG61	Hs.5326	Q96MW6	64840	Xp11.23
224764_at_HG-U133B	ARHGAP10	Hs.11611	BAA92662	57584	10
224772_at_HG-U133B	MGC14961	Hs.6298	BAA86465	57177	1q32.3
224794_s_at_HG-U133B	LOC51148	Hs.23954	Q9HBP2	51148	9q34.2
224804_s_at_HG-U133B	FLJ00005	Hs.367690	P28906	57184	15
224811_at_HG-U133B		Hs.5724			
224823_at_HG-U133B		Hs.288965			
224833_at_HG-U133B	ETS1	Hs.18063	P14921	2113	11q23.3
224837_at_HG-U133B	FOXP1	Hs.274344	BAB85050	27086	3p14.1
224838_at_HG-U133B					
224839_s_at_HG-U133B	GPT2	Hs.355862	AAK31794	84706	
224847_at_HG-U133B		Hs.180059	AAH27989		
224848_at_HG-U133B		Hs.180059	AAH27989		
224872_at_HG-U133B	KIAA1463	Hs.21104	Q9P265	57609	12q11
224918_x_at_HG-U133B	MGST1	Hs.355733	P10620	4257	12p12.3-p12.1
224928_at_HG-U133B					
224932_at_HG-U133B	PRSS2	Hs.241561	P07478	5645	7q34
224935_at_HG-U133B	EIF2S3	Hs.211539	AAH19906	1968	Xp22.2-p22.1
224967_at_HG-U133B		Hs.23703			

224970_at_HG-U133B	NFIA	Hs.173933	Q12857	4774	1p31.3-p31.2	
224975_at_HG-U133B	NFIA	Hs.173933	AAH22264	4774	1p31.3-p31.2	
224976_at_HG-U133B	NFIA	Hs.173933	Q12857	4774	1p31.3-p31.2	
224994_at_HG-U133B	CAMK2D	Hs.111460	Q13557	817	4q25	
225003_at_HG-U133B	MBC3205	Hs.43621	Q96HM3	90585	19p13.2	
225010_at_HG-U133B						
225014_at_HG-U133B		Hs.235026	Q9BRT5			
225019_at_HG-U133B	CAMK2D	Hs.111460	Q13557	817	4q25	
225025_at_HG-U133B	IGSF8	Hs.332012	Q9BTG9	93185	1q23.1	
225051_at_HG-U133B		Hs.268024				
225055_at_HG-U133B	FLJ10120	Hs.339808	Q9NWC8	55073	17q21.32	
225064_at_HG-U133B		Hs.250535				
225065_x_at_HG-U133B		Hs.295362	AAH27986			
225073_at_HG-U133B	HSPC232	Hs.281428	Q96NB9	51535	12p11.23	
225080_at_HG-U133B	MYO1C	Hs.286226	O00159	4641	17p13	
225085_at_HG-U133B		Hs.96513	Q96D48			
225129_at_HG-U133B	MDS026	Hs.85752	Q9P1Y7	55844		10
225136_at_HG-U133B		Hs.18585				
225144_at_HG-U133B		Hs.28959				
225175_s_at_HG-U133B	CTL2	Hs.105509	Q8WY97	57153	19p13.1	
225230_at_HG-U133B	CEPT1	Hs.125031	Q9Y6K0	10390	1p12	
225246_at_HG-U133B	STIM2	Hs.278894	Q9P246	57620	4p15.2	
225250_at_HG-U133B	STIM2	Hs.278894	Q9P246	57620	4p15.2	
225270_at_HG-U133B						
225277_at_HG-U133B		Hs.9070	Q8WV10			
225285_at_HG-U133B						
225305_at_HG-U133B		Hs.27769				
225306_s_at_HG-U133B		Hs.27769				
225314_at_HG-U133B		Hs.95835				
225326_at_HG-U133B	KIAA1311	Hs.61441	Q9P2N5	54439		5
225327_at_HG-U133B	FLJ10980	Hs.29716	Q9NV24	56204	15q15.3	
225330_at_HG-U133B		Hs.104679	Q96FP4			
225331_at_HG-U133B		Hs.170307				
225344_at_HG-U133B						
225386_s_at_HG-U133B	LOC92906	Hs.91684	Q8WVV9	92906	2p22.3	
225406_at_HG-U133B	TSG	Hs.247302	Q9GZX9	57045	18p11.3	
225426_at_HG-U133B		Hs.356739				
225452_at_HG-U133B	PPARBP	Hs.15589	Q15648	5469	17q12	
225469_at_HG-U133B	KRAS2	Hs.351221	P01118	3845	12p12.1	
225510_at_HG-U133B	CHN1	Hs.22660	P15882	1123	2q31-q32.1	
225512_at_HG-U133B		Hs.23853	Q96NB8			
225547_at_HG-U133B		Hs.372680				

225553_at_HG-U133B		Hs.56847			
225563_at_HG-U133B		Hs.30348			
225565_at_HG-U133B		Hs.22315			
225592_at_HG-U133B	NRM	Hs.57222	Q9UN92	11270	6p21.31
225624_at_HG-U133B		Hs.194478	Q9H7K6		
225629_s_at_HG-U133B	KIAA1538	Hs.35096	BAA96062	57659	17p13.2
225635_s_at_HG-U133B		Hs.279607			
225640_at_HG-U133B		Hs.279607			
225653_at_HG-U133B		Hs.105664	Q9H6G8		
225660_at_HG-U133B	SEMA6A	Hs.263395	Q9H2E6	57556	5q23.1
225670_at_HG-U133B		Hs.18955			
225700_at_HG-U133B					
225713_at_HG-U133B	KIAA1898	Hs.22410	Q96PY9	114790	2q36.3
225735_at_HG-U133B					
225772_s_at_HG-U133B	MGC14288	Hs.181073	Q96I36	84987	12p11.1
225776_at_HG-U133B	BAZ2A	Hs.277401	Q9UIF9	11176	12q24.3-qter
225782_at_HG-U133B		Hs.339024			
225790_at_HG-U133B		Hs.339024			
225792_at_HG-U133B		Hs.299254			
225803_at_HG-U133B	FBXO32	Hs.61661	Q969P5	114907	8q24.13
225804_at_HG-U133B		Hs.284163	Q8WUJ1		
225889_at_HG-U133B		Hs.285833	Q96BG3		
225897_at_HG-U133B		Hs.330716			
225902_at_HG-U133B		Hs.35274			
225917_at_HG-U133B	DKFZp762B226	Hs.7041	BAA86522	55918	12q23.1
225927_at_HG-U133B	MAP3K1	Hs.170610	Q13233	4214	5q11.2
225959_s_at_HG-U133B	NIN283	Hs.320834	Q9H083	84937	16q22.3
226005_at_HG-U133B		Hs.296273			
226008_at_HG-U133B	HCA4	Hs.94011	AAM08357	145961	15q12
226013_at_HG-U133B		Hs.347459			
226014_at_HG-U133B	EIF3S5	Hs.7811	O00303	8665	2p16.1
226043_at_HG-U133B	AGS3	Hs.239370	Q96G60	26086	9q34.3
226060_at_HG-U133B	RFT1	Hs.334614	Q96J03	91869	3p21.31
226063_at_HG-U133B		Hs.4248	Q8WY83		
226066_at_HG-U133B					
226101_at_HG-U133B		Hs.374424			
226120_at_HG-U133B	LOC123016	Hs.55158	AAH26351	123016	14q31.3
226122_at_HG-U133B					
226147_s_at_HG-U133B		Hs.205126			
226156_at_HG-U133B	AKT2	Hs.326445	P31751	208	19q13.1-q13.2
226165_at_HG-U133B	E2F5	Hs.2331	Q15329	1875	8q21.13
226188_at_HG-U133B					

226190_at_HG-U133B		Hs.57776			
226210_s_at_HG-U133B		Hs.374572			
226236_at_HG-U133B		Hs.349092			
226244_at_HG-U133B		Hs.293815			
226247_at_HG-U133B		Hs.287830			
226250_at_HG-U133B		Hs.374454			
226252_at_HG-U133B		Hs.374454			
226258_at_HG-U133B		Hs.337603			
226291_at_HG-U133B	ALS2	Hs.27669	BAB13389	57679	2q33.2
226299_at_HG-U133B	pknbeta	Hs.44101	Q9UM03	29941	9q34.2
226301_at_HG-U133B	dJ55C23.6	Hs.347144		116843	6q22.3-q23.3
226324_s_at_HG-U133B	SLB	Hs.127401	Q9UG01	26160	2p23.3
226326_at_HG-U133B		Hs.11356			
226342_at_HG-U133B		Hs.236443			
226384_at_HG-U133B	HTPAP	Hs.169341	Q9BY45	84513	8p11.21
226408_at_HG-U133B	TEAD2	Hs.166556	Q15562	8463	19q13.3
226435_at_HG-U133B		Hs.301152			
226438_at_HG-U133B					
226448_at_HG-U133B		Hs.38516	Q96GI7		
226450_at_HG-U133B		Hs.98401			
226454_at_HG-U133B	LOC92979	Hs.65377	Q96GG2	92979	12q13.11
226496_at_HG-U133B		Hs.27774	AAH22434		
226499_at_HG-U133B		Hs.21812			
226508_at_HG-U133B		Hs.25328			
226531_at_HG-U133B	FLJ14466	Hs.55148	Q96BP7	84876	12q24.31
226538_at_HG-U133B	MAN2A1	Hs.63368	Q16706	4124	5q21-q22
226545_at_HG-U133B					
226546_at_HG-U133B		Hs.90286			
226550_at_HG-U133B		Hs.91389			
226560_at_HG-U133B		Hs.13234			
226590_at_HG-U133B		Hs.349208			
226607_at_HG-U133B	L3MBTL	Hs.119021	Q9UFX9	26013	20p13
226625_at_HG-U133B	TGFBR3	Hs.342874	Q03167	7049	1p33-p32
226634_at_HG-U133B		Hs.98613	AAH26167		
226635_at_HG-U133B		Hs.279607			
226641_at_HG-U133B		Hs.11571			
226646_at_HG-U133B	KLF2	Hs.107740	Q9Y5W3	10365	19p13.13-p13.11
226713_at_HG-U133B		Hs.55098			
226726_at_HG-U133B	LOC129642	Hs.356547	Q96KY4	129642	2p25.2
226734_at_HG-U133B		Hs.306915			
226735_at_HG-U133B		Hs.25119	Q9NZK9		
226741_at_HG-U133B	LOC51234	Hs.250905	Q96KX9	51234	15q13.1

226743_at_HG-U133B		Hs.235709			
226751_at_HG-U133B	DKFZP566K1924	Hs.26358	Q9UFZ0	25927	2p13.3
226783_at_HG-U133B		Hs.54982			
226795_at_HG-U133B		Hs.118913			
226818_at_HG-U133B		Hs.288581			
226841_at_HG-U133B		Hs.288581			
226844_at_HG-U133B		Hs.293849			
226876_at_HG-U133B		Hs.345588	Q96CJ4		
226878_at_HG-U133B		Hs.11135			
226905_at_HG-U133B		Hs.345588	Q96CJ4		
226936_at_HG-U133B		Hs.35962			
226939_at_HG-U133B		Hs.44833			
226989_at_HG-U133B		Hs.108972			
227030_at_HG-U133B		Hs.318893			
227038_at_HG-U133B		Hs.29567			
227039_at_HG-U133B	AKAP13	Hs.372326	Q8WXQ6	11214	15q24-q25
227041_at_HG-U133B		Hs.30977			
227046_at_HG-U133B	C17orf26	Hs.3402	Q8WZ81	201266	17q21.31
227047_x_at_HG-U133B	KIAA1538	Hs.35096	Q9P1Z0	57659	17p13.2
227056_at_HG-U133B	KIAA0141	Hs.63510	Q969R4	9812	5q31.3
227065_at_HG-U133B	COL5A2	Hs.82985	CAA75002	1290	2q14-q32
227121_at_HG-U133B		Hs.374267			
227145_at_HG-U133B	LOXL4	Hs.306814	Q96JB6	84171	10q24
227146_at_HG-U133B		Hs.309165			
227151_at_HG-U133B		Hs.32365	Q8WV41		
227152_at_HG-U133B		Hs.323822	Q9HCM1		
227167_s_at_HG-U133B		Hs.61426	Q9NYI4		
227173_s_at_HG-U133B	BACH2	Hs.88414	Q9BYV9	60468	6q15
227189_at_HG-U133B	KIAA1599	Hs.285714	Q9HCH3	57699	6p21.1
227198_at_HG-U133B		Hs.125019			
227206_at_HG-U133B		Hs.108593			
227212_s_at_HG-U133B		Hs.352417	AAH22374		
227224_at_HG-U133B		Hs.174104			
227230_s_at_HG-U133B	KIAA1211	Hs.205293	Q9ULK9	57482	4q11
227237_x_at_HG-U133B	KIAA1273	Hs.23413	Q9BUK4	57516	1p36.32
227242_s_at_HG-U133B		Hs.348805			
227243_s_at_HG-U133B					
227249_at_HG-U133B	NUDE1	Hs.263925	Q9NXR1	54820	16p13.11
227261_at_HG-U133B	KLF12	Hs.23510	Q9Y4X4	11278	13q22
227276_at_HG-U133B	TEM7R	Hs.33033	Q96E59	84898	10p12.1
227277_at_HG-U133B		Hs.33074			
227279_at_HG-U133B	MGC15737	Hs.39122	Q969E4	85012	Xq22.1

227299_at_HG-U133B	CCNI	Hs.79933	Q14094	10983	4q13.3
227326_at_HG-U133B		Hs.11924			
227336_at_HG-U133B	DTX1	Hs.124024	Q9BS04	1840	12q24.11
227353_at_HG-U133B		Hs.15284	AAH28076		
227367_at_HG-U133B		Hs.184067			
227375_at_HG-U133B	DKFZP566D1346	Hs.22612	AAH28840	81573	1p32.3-p31.3
227388_at_HG-U133B		Hs.26268			
227393_at_HG-U133B		Hs.288455			
227396_at_HG-U133B		Hs.374451			
227407_at_HG-U133B		Hs.356851			
227408_s_at_HG-U133B	MSTP043	Hs.306881	Q9H3E2	83891	4q35.1
227414_at_HG-U133B	DKFZp547E052	Hs.49359	BAB85031	84236	
227415_at_HG-U133B		Hs.47094			
227478_at_HG-U133B		Hs.128052			
227497_at_HG-U133B		Hs.196008			
227525_at_HG-U133B	LOC113263	Hs.18987	Q96FD0	113263	7p22.2
227527_at_HG-U133B		Hs.3640			
227533_at_HG-U133B		Hs.5415			
227556_at_HG-U133B	ATP1B1	Hs.78629	P05026	481	1q22-q25
227568_at_HG-U133B					
227584_at_HG-U133B		Hs.112461			
227587_at_HG-U133B	MGC15906	Hs.104938	Q969K0	84971	19p13.2
227606_s_at_HG-U133B	KIAA1373	Hs.16229	Q96FJ0	57559	10q23.33
227607_at_HG-U133B	KIAA1373	Hs.16229	Q96FJ0	57559	10q23.33
227627_at_HG-U133B	SGKL	Hs.279696	Q9P1Q7	23678	8q12.3-8q13.1
227646_at_HG-U133B	EBF	Hs.32425	Q9UH73	1879	5q34
227670_at_HG-U133B		Hs.50456	Q96N20		
227680_at_HG-U133B		Hs.348788			
227700_x_at_HG-U133B	FLJ10709	Hs.273357	Q96A50	55210	1p36.32
227701_at_HG-U133B					
227709_at_HG-U133B	RCN1	Hs.167791	AAH10120	5954	11p13
227729_at_HG-U133B		Hs.107265			
227744_s_at_HG-U133B	HNRPD	Hs.303627	Q14103	3184	4q21.1-q21.2
227749_at_HG-U133B		Hs.15085			
227767_at_HG-U133B	CSNK1G3	Hs.129206	Q9Y6M4	1456	5q23
227786_at_HG-U133B	TRAP25	Hs.336898	AAL89787	90390	8q24.11
227812_at_HG-U133B		Hs.48376			
227817_at_HG-U133B		Hs.352385			
227829_at_HG-U133B		Hs.86543	Q8WY62		
227867_at_HG-U133B		Hs.36723			
227900_at_HG-U133B		Hs.144139			
227936_at_HG-U133B		Hs.280858	Q8WUD2		

227988_s_at_HG-U133B	CHAC	Hs.53542	Q96RL7	23230	9q21
227998_at_HG-U133B	MGC17528	Hs.300893	Q96FQ6	140576	
227999_at_HG-U133B	LOC170394	Hs.157728	Q96F43	170394	10q26.3
228003_at_HG-U133B		Hs.95898			
228007_at_HG-U133B					
228024_at_HG-U133B	PAK1	Hs.62402	Q13153	5058	11q13-q14
228029_at_HG-U133B	KIAA1982	Hs.22969		170960	
228055_at_HG-U133B		Hs.104433			
228058_at_HG-U133B		Hs.105887	Q96DA0		
228083_at_HG-U133B		Hs.13768			
228092_at_HG-U133B		Hs.155924	Q96AG7		
228174_at_HG-U133B		Hs.356345			
228176_at_HG-U133B		Hs.55902			
228183_s_at_HG-U133B	MGC4189	Hs.334808	Q9BT00	84268	17p13.2
228193_s_at_HG-U133B	RGC32	Hs.76640	Q9UL69	28984	13q13.3
228211_at_HG-U133B		Hs.44367			
228242_at_HG-U133B		Hs.101624			
228266_s_at_HG-U133B	CGI-142	Hs.127842	Q9Y3E1	50810	15q11.2
228298_at_HG-U133B	LOC91523	Hs.258494	Q96B20	91523	12p11.21
228328_at_HG-U133B		Hs.7326			
228343_at_HG-U133B	POU2F2	Hs.1101	P09086	5452	19q13.31
228345_at_HG-U133B		Hs.34656			
228361_at_HG-U133B		Hs.231444	Q96ID7		
228377_at_HG-U133B	KIAA1384	Hs.88442	Q9P2G3	57565	18q12.1
228379_at_HG-U133B		Hs.356630			
228390_at_HG-U133B		Hs.184430			
228408_s_at_HG-U133B	FLJ10498	Hs.109045	Q9H831	55153	4q21.1
228410_at_HG-U133B	GAB3	Hs.102630	Q8WWW8	139716	Xq28
228424_at_HG-U133B	NAALADASEL	Hs.13967	Q9UQQ1	10004	11q12
228471_at_HG-U133B		Hs.145053			
228476_at_HG-U133B	KIAA1407	Hs.15370	Q9P2E0	57577	3q13.2
228485_s_at_HG-U133B	CDW92	Hs.179902	Q96KU3	23446	9q31.2
228496_s_at_HG-U133B	CRIM1	Hs.19280	Q9NZV1	51232	2p21
228497_at_HG-U133B	DKFZp761G0313	Hs.21710	AAH26358	55356	1p13.1
228518_at_HG-U133B	IGHG3	Hs.300697	P01860	3502	14q32.33
228551_at_HG-U133B					
228555_at_HG-U133B		Hs.32553			
228570_at_HG-U133B		Hs.5027			
228592_at_HG-U133B		Hs.86693			
228599_at_HG-U133B		Hs.86693			
228652_at_HG-U133B		Hs.109540			
228660_x_at_HG-U133B	SEMA4F	Hs.25887	O95754	10505	2p12

228693_at_HG-U133B		Hs.55098			
228708_at_HG-U133B		Hs.25318			
228737_at_HG-U133B	C20orf100	Hs.26608	Q96NM4	84969	20q13.11
228766_at_HG-U133B		Hs.325823			
228827_at_HG-U133B		Hs.90858			
228834_at_HG-U133B	TOB1	Hs.178137	P50616	10140	17q21
228904_at_HG-U133B		Hs.156044			
228916_at_HG-U133B		Hs.24380	Q96MI1		
228984_at_HG-U133B	KIAA1394	Hs.32156	Q9P2F3	57571	11q12.2
228988_at_HG-U133B	ZNF6	Hs.326801	Q9Y4J6	7552	Xq13-q21.1
229001_at_HG-U133B		Hs.39911	Q9H7J1		
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229061_s_at_HG-U133B	SLC25A13	Hs.9599	Q9UJS0	10165	7q21.3
229070_at_HG-U133B	MGC12335	Hs.97411	Q96IZ2	84830	6p22.3
229072_at_HG-U133B		Hs.26339			
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229194_at_HG-U133B		Hs.126695			
229232_at_HG-U133B		Hs.194071			
229253_at_HG-U133B	CTMP	Hs.293691	Q96AB5	117145	1q21
229280_s_at_HG-U133B					
229302_at_HG-U133B		Hs.40808			
229310_at_HG-U133B	KIAA1921	Hs.348392	Q96PW7	114818	2p23.3
229344_x_at_HG-U133B	KIAA1238	Hs.236463	Q9ULI2	57494	12p13.32
229362_at_HG-U133B		Hs.374508			
229368_s_at_HG-U133B	ZNF216	Hs.3776	O76080	7763	9q13-q21
229383_at_HG-U133B		Hs.107369			
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229513_at_HG-U133B					
229575_at_HG-U133B		Hs.122642			
229621_x_at_HG-U133B		Hs.348805			
229637_at_HG-U133B		Hs.25768			
229659_s_at_HG-U133B		Hs.205126			
229681_at_HG-U133B		Hs.17551			
229711_s_at_HG-U133B	MGC5370	Hs.332938	Q96J14	84825	12q13.2
229722_at_HG-U133B	HSPC072	Hs.87329		29075	20p11.23
229745_x_at_HG-U133B		Hs.134185	Q96B18		
229750_at_HG-U133B		Hs.143087			
229779_at_HG-U133B		Hs.119471			
229790_at_HG-U133B	TERF2	Hs.100030	AAH24890	7014	16q22.1
229817_at_HG-U133B	DKFZP434M098	Hs.93738	Q9UFL4	25863	

229833_at_HG-U133B		Hs.33728			
229844_at_HG-U133B		Hs.59368			
229848_at_HG-U133B	ZNF10	Hs.104115	AAH24182	7556	12q24.33
229872_s_at_HG-U133B	KIAA0493	Hs.36475		57234	1q21.3
229923_at_HG-U133B					
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230110_at_HG-U133B		Hs.210792			
230245_s_at_HG-U133B		Hs.181297			
230292_at_HG-U133B		Hs.25447	Q96DJ9		
230363_s_at_HG-U133B	SAC2	Hs.52463	Q9Y2H2	22876	10q26.13
230405_at_HG-U133B	RAD50	Hs.41587	O43254	10111	5q31
230441_at_HG-U133B		Hs.374272			
230489_at_HG-U133B	CD5	Hs.58685	AAH27901	921	11q13
230499_at_HG-U133B		Hs.121572			
230526_at_HG-U133B	FLJ20015	Hs.80618	Q96MU9	54459	17q25
230551_at_HG-U133B		Hs.107331			
230588_s_at_HG-U133B	MCPR	Hs.40137	Q9H8D0	64682	2q12.1
230636_s_at_HG-U133B	BTEB1	Hs.150557	Q13886	687	9q13
230648_at_HG-U133B		Hs.181297			
230650_at_HG-U133B		Hs.152460			
230659_at_HG-U133B	KIAA0212	Hs.154332	Q92611	9695	3p26.1
230689_at_HG-U133B		Hs.163426			
230713_at_HG-U133B		Hs.182185			
230743_at_HG-U133B		Hs.183096	Q96FJ8		
230753_at_HG-U133B		Hs.11594			
230768_at_HG-U133B		Hs.58753			
230775_s_at_HG-U133B	KIAA0610	Hs.118087	O60349	23111	13q13.1
230793_at_HG-U133B	FLJ20048	Hs.116470	Q9NXU7	55604	6p21.32
230795_at_HG-U133B	H4F2	Hs.55468	AAH19846	3022	1q21
230802_at_HG-U133B	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
230803_s_at_HG-U133B	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
230834_at_HG-U133B		Hs.114516			
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230917_at_HG-U133B		Hs.372303			
230939_at_HG-U133B		Hs.130352			
230960_at_HG-U133B		Hs.128292			
230983_at_HG-U133B		Hs.137319			
230986_at_HG-U133B		Hs.141120			
230988_at_HG-U133B		Hs.15155			
230997_at_HG-U133B		Hs.131816			
231002_s_at_HG-U133B	NUP88	Hs.172108	Q99567	4927	17p13

231050_at_HG-U133B	HRLP5	Hs.120869	Q96KN8	117245	11q13.2
231069_at_HG-U133B		Hs.295727			
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231101_at_HG-U133B	PPP2R5E	Hs.173328	Q16537	5529	7p11.2-p12
231118_at_HG-U133B		Hs.133081	Q96LS3		
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231215_at_HG-U133B		Hs.126962			
231241_at_HG-U133B		Hs.155635			
231259_s_at_HG-U133B	CCND2	Hs.75586	P30279	894	12p13
231269_at_HG-U133B	DJ467N11.1	Hs.143917		63921	6q16.1-q16.3
231277_x_at_HG-U133B		Hs.14822			
231310_at_HG-U133B		Hs.113170			
231332_at_HG-U133B		Hs.254986			
231406_at_HG-U133B		Hs.129568			
231418_at_HG-U133B	MS4A2	Hs.89751	AAH02807	931	11q12-q13.1
231472_at_HG-U133B		Hs.124087			
231538_at_HG-U133B	FLJ23499	Hs.17546	Q9H5F2	64776	11q13-q22
231552_at_HG-U133B		Hs.235240			
231567_s_at_HG-U133B	TSP-NY	Hs.97643	Q9BYZ5	84660	12q24.31
231647_s_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
231656_x_at_HG-U133B	OSBPL10	Hs.321622	Q9BTU5	114884	3p22.3
231736_x_at_HG-U133B	MGST1	Hs.355733	P10620	4257	12p12.3-p12.1
231775_at_HG-U133B	TNFRSF10A	Hs.249190	O00220	8797	8p21
231793_s_at_HG-U133B	CAMK2D	Hs.111460	Q13557	817	4q25
231794_at_HG-U133B	CTLA4	Hs.247824	Q96P43	1493	2q33
231837_at_HG-U133B	USP28	Hs.142856	Q96RU2	57646	11q23
231854_at_HG-U133B		Hs.120905			
231870_s_at_HG-U133B	LOC51068	Hs.181022	Q9Y2Z6	51068	
231873_at_HG-U133B		Hs.315284			
231887_s_at_HG-U133B	KIAA1274	Hs.300646	BAA86588	27143	10q22.3
231897_at_HG-U133B					
231926_at_HG-U133B					
231945_at_HG-U133B	KIAA1275	Hs.102796	Q96SK6	27145	6q14.2
231969_at_HG-U133B	DKFZp762K222	Hs.159200	Q9P2F5	56977	4q35.1
231981_at_HG-U133B					
231982_at_HG-U133B					
232027_at_HG-U133B					
232035_at_HG-U133B	H4FH	Hs.93758	AAH10926	8365	6p21.3
232060_at_HG-U133B					
232080_at_HG-U133B	KIAA1301	Hs.8707	Q9NPS9	57520	2q33.1
232112_at_HG-U133B		Hs.220745			
232125_at_HG-U133B		Hs.202577			

232127_at_HG-U133B					
232201_at_HG-U133B	NKD2	Hs.240951	Q969F2	85409	5p15.3
232204_at_HG-U133B	EBF	Hs.32425	Q9UH73	1879	5q34
232210_at_HG-U133B		Hs.206868			
232231_at_HG-U133B					
232234_at_HG-U133B	C20orf24	Hs.184062	Q9UI05	55969	20q11.22
232614_at_HG-U133B		Hs.171395			
232636_at_HG-U133B					
232641_at_HG-U133B					
232739_at_HG-U133B					
232841_at_HG-U133B					
232950_s_at_HG-U133B	NIR3	Hs.272759	Q9BZ72	57605	12q24.31
233072_at_HG-U133B	KIAA1857	Hs.163642	BAB47486	84628	9q34
233106_at_HG-U133B		Hs.367825			
233137_at_HG-U133B					
233138_at_HG-U133B		Hs.178533			
233177_s_at_HG-U133B	KIAA1184	Hs.100747	Q96IG7	64583	2q36.1
233195_at_HG-U133B					
233261_at_HG-U133B		Hs.293916			
233328_x_at_HG-U133B					
233483_at_HG-U133B		Hs.193857	Q9H7M0		
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233520_s_at_HG-U133B					
233555_s_at_HG-U133B					
233559_s_at_HG-U133B	FENS-1	Hs.44743	Q9H8N9	57590	2q36.3
233589_x_at_HG-U133B					
233613_x_at_HG-U133B		Hs.296737			
233813_at_HG-U133B					
233845_at_HG-U133B		Hs.283921	Q9UI64		
233955_x_at_HG-U133B	HSPC195	Hs.15093	AAH17439	51523	5q31.3
234005_x_at_HG-U133B	STK36	Hs.26996	Q9H9N9	27148	2q36.1
234032_at_HG-U133B					
234107_s_at_HG-U133B					
234132_at_HG-U133B					
234140_s_at_HG-U133B	STIM2	Hs.278894	Q9P246	57620	4p15.2
234362_s_at_HG-U133B	CTLA4	Hs.247824	O95653	1493	2q33
234584_s_at_HG-U133B	ATE1	Hs.355315	O95260	11101	10q26.3
234643_x_at_HG-U133B					
234660_s_at_HG-U133B	DIS3	Hs.323346	Q8WWI2	22894	13q21.33
234682_at_HG-U133B					
234725_s_at_HG-U133B	SEMA4B	Hs.9598	Q8WY86	10509	15q25
234726_s_at_HG-U133B					

234764_x_at_HG-U133B					
234839_at_HG-U133B					
234862_at_HG-U133B					
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235052_at_HG-U133B		Hs.50405			
235061_at_HG-U133B		Hs.291000	Q96NT4		
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235259_at_HG-U133B		Hs.97415	AAH23002		
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235353_at_HG-U133B	KIAA0746	Hs.49500	O94847	23231	4p15.31
235359_at_HG-U133B		Hs.162185			
235372_at_HG-U133B	FREB	Hs.266331	Q96PJ4	84824	1q23.1
235385_at_HG-U133B	FLJ20668	Hs.12920	Q9NWR0	55016	4q32.2
235400_at_HG-U133B	FREB	Hs.266331	AAM13980	84824	1q23.1
235401_s_at_HG-U133B	FREB	Hs.266331	AAM13980	84824	1q23.1
235414_at_HG-U133B		Hs.164102			
235421_at_HG-U133B		Hs.351250			
235422_at_HG-U133B	FALZ	Hs.99872	Q12830	2186	17q24
235428_at_HG-U133B		Hs.104480			
235444_at_HG-U133B		Hs.235860			
235446_at_HG-U133B		Hs.293702			
235459_at_HG-U133B		Hs.136316			
235483_at_HG-U133B		Hs.180711			
235502_at_HG-U133B		Hs.79204			
235521_at_HG-U133B	HOXA3	Hs.248074	O43365	3200	7p15-p14
235604_x_at_HG-U133B		Hs.256801			
235647_at_HG-U133B		Hs.293411			
235674_at_HG-U133B		Hs.13849			
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235823_at_HG-U133B		Hs.49892			
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236280_at_HG-U133B		Hs.176920			
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236301_at_HG-U133B		Hs.46645			
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236458_at_HG-U133B		Hs.163426			
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236908_at_HG-U133B		Hs.143905			
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238392_at_HG-U133B		Hs.145480			
238516_at_HG-U133B	BMPR2	Hs.53250	Q13161	659	2q33-q34
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238587_at_HG-U133B	MGC15437	Hs.55067	Q96IG9	84959	11q24.1
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239699_s_at_HG-U133B		Hs.144252			

239791_at_HG-U133B	HOXB6	Hs.98428	P17509	3216	17q21-q22
239824_s_at_HG-U133B	MGC10744	Hs.25092	Q96T82	84314	17p13.1
239835_at_HG-U133B	KIAA1842	Hs.116665	Q96JI5	84541	3p14
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243154_at_HG-U133B		Hs.86650			
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243798_at_HG-U133B		Hs.257490			
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244740_at_HG-U133B		Hs.23133	Q96HF5		
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266_s_at_HG-U133A	CD24	Hs.286124	AAH07674	934	6q21
32541_at_HG-U133A	PPP3CC	Hs.75206	P48454	5533	8p21.2
34210_at_HG-U133A	CDW52	Hs.276770	Q9BW46	1043	1p36
34689_at_HG-U133A	TREX1	Hs.278408	AAD48774	11277	3p21.3-p21.2
34726_at_HG-U133A	CACNB3	Hs.250712	P54284	784	12q13
35666_at_HG-U133A	SEMA3F	Hs.32981	Q13275	6405	3p21.3
35974_at_HG-U133A	LRMP	Hs.40202	Q12912	4033	12p12.3
36004_at_HG-U133A	IKBKG	Hs.43505	Q9Y6K9	8517	Xq28
36566_at_HG-U133A	CTNS	Hs.64837	O60931	1497	17p13
36612_at_HG-U133A	KIAA0280	Hs.75400	Q92567	23201	11q13.3
36920_at_HG-U133A	MTM1	Hs.75302	Q13496	4534	Xq28
37152_at_HG-U133A	PPARD	Hs.106415	Q03181	5467	6p21.2-p21.1
37424_at_HG-U133A	HCR	Hs.110746	AAK55759	54535	6p21.3
37831_at_HG-U133A	KIAA0545	Hs.129943	BAA25471	23094	19q13.13
38149_at_HG-U133A	KIAA0053	Hs.1528	P42331	9938	2p13.1
38269_at_HG-U133A	PKD2	Hs.91146	AAH25307	25865	19q13.2
38340_at_HG-U133A	HIP12	Hs.96731	O75146	9026	12q24
38487_at_HG-U133A	FLJ12442	Hs.84753	Q9H9Z8	64943	
39650_s_at_HG-U133A	KIAA0435	Hs.31438	O43162	9845	1q42.2
39835_at_HG-U133A	SBF1	Hs.112049	Q96GR9	6305	22q13.33
40148_at_HG-U133A	APBB2	Hs.324125	Q92870	323	4p14
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41220_at_HG-U133A	MSF	Hs.181002	Q96QF5	10801	17q25
41553_at_HG-U133A	C8orf1	Hs.40539	Q9Y236	734	8q21
41577_at_HG-U133A	PPP1R16B	Hs.45719	BAA74846	26051	20q11.23
41660_at_HG-U133A	CELSR1	Hs.252387	Q9BWQ5	9620	22q13.3
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44563_at_HG-U133A	FLJ10385	Hs.30922	Q9BUR4	55135	17p13.2
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45633_at_HG-U133A	FLJ13912	Hs.47125	Q9BRX5	64785	16q21
46142_at_HG-U133A	FLJ12681	Hs.58362	Q9H6G4	64788	16p13.3
49306_at_HG-U133A	AD037	Hs.296162	Q9H2L5	83937	10q11.23
49485_at_HG-U133A	PRDM4	Hs.21807	Q9UFA6	11108	12q23-q24.1
50221_at_HG-U133A		Hs.23391	P19484		
50277_at_HG-U133A	GGA1	Hs.238296	Q9UJY5	26088	22q13.31
51192_at_HG-U133A	SSH-3	Hs.29173	BAB85080	54961	11q12.2
54970_at_HG-U133A	DKFZP761I2123	Hs.77978	O94790	83637	7p15.1

55093_at_HG-U133A	KIAA1402	Hs.86392	Q9P2E5	54480	7q35
56256_at_HG-U133A	LOC51092	Hs.33724	Q9Y357	51092	11q23.3
56919_at_HG-U133A	KIAA1449	Hs.109778	AAH26353	57599	3p21.33
57588_at_HG-U133A	SLC24A3	Hs.12321	Q9HC58	57419	20p13
58780_s_at_HG-U133A	FLJ10357	Hs.22451	Q96G35	55701	14q11.1
59697_at_HG-U133A		Hs.21349			
635_s_at_HG-U133A	PPP2R5B	Hs.75199	Q15173	5526	11q12
64942_at_HG-U133A		Hs.7967			
74694_s_at_HG-U133A	FLJ23282	Hs.170253	Q9H5N1	79874	
77508_r_at_HG-U133A	FLJ23282	Hs.170253	Q9H5N1	79874	
90610_at_HG-U133A	LRRN1	Hs.125742	Q8WV85	4034	7q22
AFFX-M27830_5_at_HG-U133A					
AFFX-M27830_5_at_HG-U133B					
AFFX-M27830_M_at_HG-U133A					
AFFX-r2-Bs-dap-3_at_HG-U133A					
AFFX-r2-Ec-bioD-3_at_HG-U133A					

Table 43b: Full sequences descriptions of all genes identified with relevance to leukemia subtyping

ID	Gene Symbol	Gene Title	Sequence Description
1007_s_at_HG-U133A	DDR1	discoidin domain receptor family, member 1	U48705 /FEATURE=mRNA /DEFINITION=HSU48705 Human receptor tyrosine kinase DDR gene, complete cds
1729_at_HG-U133A	TRADD	TNFRSF1A-associated via death domain	L41690 /FEATURE= /DEFINITION=HUMTRADD Homo sapiens TNF receptor-1 associated protein (TRADD) mRNA, 3' end of cds
200008_s_at_HG-U133A	GDI2	GDP dissociation inhibitor 2	gb:D13988.1 /DEF=Human rab GDI mRNA, complete cds. /FEA=mRNA /PROD=human rab GDI /DB_XREF=gi:285974 /UG=Hs.56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2
200008_s_at_HG-U133B	GDI2	GDP dissociation inhibitor 2	gb:D13988.1 /DEF=Human rab GDI mRNA, complete cds. /FEA=mRNA /PROD=human rab GDI /DB_XREF=gi:285974 /UG=Hs.56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2
200023_s_at_HG-U133A	EIF3S5	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	gb:NM_003754.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) (EIF3S5), mRNA. /FEA=mRNA /GEN=EIF3S5 /PROD=eukaryotic translation initiation factor 3,subunit 5 (epsilon, 47kD) /DB_XREF=gi:4503518 /UG=Hs.7811 eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) /FL=gb:BC000490.1 gb:U94855.1 gb:NM_003754.1
200040_at_HG-U133A	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	gb:NM_006559.1 /DEF=Homo sapiens GAP-associated tyrosine phosphoprotein p62 (Sam68) (SAM68), mRNA. /FEA=mRNA /GEN=SAM68 /PROD=GAP-associated tyrosine phosphoprotein p62(Sam68) /DB_XREF=gi:5730026 /UG=Hs.119537 GAP-associated tyrosine phosphoprotein p62 (Sam68) /FL=gb:BC000717.1 gb:M88108.1 gb:NM_006559.1
200047_s_at_HG-U133A	YY1	YY1 transcription factor	gb:NM_003403.2 /DEF=Homo sapiens YY1 transcription factor (YY1), mRNA. /FEA=mRNA /GEN=YY1 /PROD=YY1 transcription factor /DB_XREF=gi:6042207 /UG=Hs.97496 YY1 transcription factor /FL=gb:M77698.1 gb:M76541.1 gb:NM_003403.2

200047_s_at_HG-U133B	YY1	YY1 transcription factor	gb:NM_003403.2 /DEF=Homo sapiens YY1 transcription factor (YY1), mRNA. /FEA=mRNA /GEN=YY1 /PROD=YY1 transcription factor /DB_XREF=gi:6042207 /UG=Hs.97496 YY1 transcription factor /FL=gb:M77698.1 gb:M76541.1 gb:NM_003403.2
200056_s_at_HG-U133A	C1D	nuclear DNA-binding protein	gb:NM_006333.1 /DEF=Homo sapiens nuclear DNA-binding protein (C1D), mRNA. /FEA=mRNA /GEN=C1D /PROD=nuclear DNA-binding protein /DB_XREF=gi:5453582 /UG=Hs.15164 nuclear DNA-binding protein /FL=gb:NM_006333.1
200068_s_at_HG-U133B	CANX	calnexin	gb:M94859.1 /DEF=Human calnexin mRNA, complete cds. /FEA=mRNA /PROD=calnexin /DB_XREF=gi:179831 /UG=Hs.155560 calnexin /FL=gb:NM_001746.1 gb:BC003552.1 gb:M94859.1 gb:M98452.1 gb:L10284.1 gb:L18887.1
200071_at_HG-U133A	SPF30	splicing factor 30, survival of motor neuron-related	Consensus includes gb:BF224259 /FEA=EST /DB_XREF=gi:11131523 /DB_XREF=est:7q85c09.x1 /CLONE=IMAGE:3705208 /UG=Hs.79968 splicing factor 30, survival of motor neuron-related /FL=gb:AF083385.1 gb:AF107463.1 gb:NM_005871.1
200072_s_at_HG-U133A	HNRPM	heterogeneous nuclear ribonucleoprotein M	gb:AF061832.1 /DEF=Homo sapiens M4 protein deletion mutant mRNA, complete cds. /FEA=mRNA /PROD=M4 protein deletion mutant /DB_XREF=gi:3126877 /UG=Hs.79024 heterogeneous nuclear ribonucleoprotein M /FL=gb:AF061832.1
200093_s_at_HG-U133A	HINT1	histidine triad nucleotide binding protein 1	Consensus includes gb:N32864 /FEA=EST /DB_XREF=gi:1153263 /DB_XREF=est:yw88d08.s1 /CLONE=IMAGE:259311 /UG=Hs.256697 histidine triad nucleotide-binding protein
200094_s_at_HG-U133A	EEF2	eukaryotic translation elongation factor 2	Consensus includes gb:AI004246 /FEA=EST /DB_XREF=gi:3213756 /DB_XREF=est:ou03g06.x1 /CLONE=IMAGE:1625242 /UG=Hs.75309 eukaryotic translation elongation factor 2
200598_s_at_HG-U133A	TRA1	tumor rejection antigen (gp96) 1	Consensus includes gb:AI582238 /FEA=EST /DB_XREF=gi:4568135 /DB_XREF=est:tq65c10.x1 /CLONE=IMAGE:2213682 /UG=Hs.82689 tumor

			rejection antigen (gp96) 1 /FL=gb:NM_003299.1
200608_s_at_HG-U133A	RAD21	RAD21 homolog (S. pombe)	gb:NM_006265.1 /DEF=Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA. /FEA=mRNA /GEN=RAD21 /PROD=RAD21 (S. pombe) homolog /DB_XREF=gi:5453993 /UG=Hs.81848 RAD21 (S. pombe) homolog /FL=gb:D38551.1 gb:NM_006265.1
200620_at_HG-U133A	C1orf8	chromosome 1 open reading frame 8	gb:NM_004872.1 /DEF=Homo sapiens chromosome 1 open reading frame 8 (C1ORF8), mRNA. /FEA=mRNA /GEN=C1ORF8 /PROD=chromosome 1 open reading frame 8 /DB_XREF=gi:4758571 /UG=Hs.11441 chromosome 1 open reading frame 8 /FL=gb:BC003106.1 gb:AF290615.1 gb:AF047439.1 gb:NM_004872.1
200625_s_at_HG-U133A	CAP	adenylyl cyclase-associated protein	gb:NM_006367.2 /DEF=Homo sapiens adenylyl cyclase-associated protein (CAP), mRNA. /FEA=mRNA /GEN=CAP /PROD=adenylyl cyclase-associated protein /DB_XREF=gi:10938021 /UG=Hs.104125 adenylyl cyclase-associated protein /FL=gb:NM_006367.2 gb:L12168.1 gb:M98474.1
200630_x_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	Consensus includes gb:AV702810 /FEA=EST /DB_XREF=gi:10719140 /DB_XREF=est:AV702810 /CLONE=ADBDGH01 /UG=Hs.145279 SET translocation (myeloid leukemia-associated) /FL=gb:U51924.1 gb:M93651.1 gb:NM_003011.1
200631_s_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	gb:NM_003011.1 /DEF=Homo sapiens SET translocation (myeloid leukemia-associated) (SET), mRNA. /FEA=mRNA /GEN=SET /PROD=SET translocation (myeloid leukemia-associated) /DB_XREF=gi:4506890 /UG=Hs.145279 SET translocation (myeloid leukemia-associated) /FL=gb:U51924.1 gb:M93651.1 gb:NM_003011.1
200646_s_at_HG-U133A	NUCB1	nucleobindin 1	gb:NM_006184.1 /DEF=Homo sapiens nucleobindin 1 (NUCB1), mRNA. /FEA=mRNA /GEN=NUCB1 /PROD=nucleobindin 1 /DB_XREF=gi:5453817 /UG=Hs.172609 nucleobindin 1 /FL=gb:BC002356.1 gb:M96824.1 gb:NM_006184.1
200649_at_HG-U133A	NUCB1	nucleobindin 1	gb:BC002356.1 /DEF=Homo sapiens, nucleobindin 1, clone MGC:8479,

			mRNA, complete cds. /FEA=mRNA /PROD=nucleobindin 1 /DB_XREF=gi:12803104 /UG=Hs.172609 nucleobindin 1 /FL=gb:BC002356.1 gb:M96824.1 gb:NM_006184.1
200650_s_at_HG-U133A	LDHA	lactate dehydrogenase A	gb:NM_005566.1 /DEF=Homo sapiens lactate dehydrogenase A (LDHA), mRNA. /FEA=mRNA /GEN=LDHA /PROD=LDHA /DB_XREF=gi:5031856 /UG=Hs.2795 lactate dehydrogenase A /FL=gb:BC001829.1 gb:NM_005566.1
200654_at_HG-U133A	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	gb:J02783.1 /DEF=Human thyroid hormone binding protein (p55) mRNA, complete cds. /FEA=mRNA /GEN=P4HB /DB_XREF=gi:339646 /UG=Hs.75655 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /FL=gb:J02783.1 gb:NM_000918.1
200655_s_at_HG-U133A	CALM1	calmodulin 1 (phosphorylase kinase, delta)	gb:NM_006888.1 /DEF=Homo sapiens calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA. /FEA=mRNA /GEN=CALM1 /PROD=calmodulin 1 (phosphorylase kinase, delta) /DB_XREF=gi:5901911 /UG=Hs.177656 calmodulin 1 (phosphorylase kinase, delta) /FL=gb:M27319.1 gb:NM_006888.1
200656_s_at_HG-U133A	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	gb:NM_000918.1 /DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA. /FEA=mRNA /GEN=P4HB /PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), beta polypeptide(protein disulfide isomerase; thyroid hormone bindingprotein p55) /DB_XREF=gi:4505566 /UG=Hs.75655 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /FL=gb:J02783.1 gb:NM_000918.1
200659_s_at_HG-U133A	PHB	prohibitin	gb:NM_002634.2 /DEF=Homo sapiens prohibitin (PHB), mRNA. /FEA=mRNA /GEN=PHB /PROD=prohibitin /DB_XREF=gi:6031190 /UG=Hs.75323 prohibitin /FL=gb:NM_002634.2
200661_at_HG-U133A	PPGB	protective protein for beta-galactosidase	gb:NM_000308.1 /DEF=Homo sapiens protective protein for beta-

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		(galactosialidosis)	galactosidase (galactosialidosis) (PPGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase /DB_XREF=gi:4505988 /UG=Hs.118126 protective protein for beta-galactosidase (galactosialidosis) /FL=gb:BC000597.1 gb:M22960.1 gb:NM_000308.1
200665_s_at_HG-U133A	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	gb:NM_003118.1 /DEF=Homo sapiens secreted protein, acidic, cysteine-rich (osteonectin) (SPARC), mRNA. /FEA=mRNA /GEN=SPARC /PROD=secreted protein, acidic, cysteine-rich(osteonectin) /DB_XREF=gi:4507170 /UG=Hs.111779 secreted protein, acidic, cysteine-rich (osteonectin) /FL=gb:BC004974.1 gb:J03040.1 gb:NM_003118.1
200673_at_HG-U133A	LAPTM4A	lysosomal-associated protein transmembrane 4 alpha	gb:NM_014713.2 /DEF=Homo sapiens lysosomal-associated protein transmembrane 4 alpha (MBNT), mRNA. /FEA=mRNA /GEN=MBNT /PROD=lysosomal-associated protein transmembrane 4alpha /DB_XREF=gi:13518239 /UG=Hs.111894 lysosomal-associated protein transmembrane 4 alpha /FL=gb:BC000421.1 gb:BC003158.1 gb:NM_014713.2 gb:D14696.1
200675_at_HG-U133A	CD81	CD81 antigen (target of antiproliferative antibody 1)	gb:NM_004356.1 /DEF=Homo sapiens CD81 antigen (target of antiproliferative antibody 1) (CD81), mRNA. /FEA=mRNA /GEN=CD81 /PROD=CD81 antigen (target of antiproliferativeantibody 1) /DB_XREF=gi:4757943 /UG=Hs.54457 CD81 antigen (target of antiproliferative antibody 1) /FL=gb:BC002978.1 gb:M33680.1 gb:NM_004356.1
200679_x_at_HG-U133A	HMG1	high-mobility group (nonhistone chromosomal) protein 1	Consensus includes gb:BE311760 /FEA=EST /DB_XREF=gi:9148272 /DB_XREF=est:601143587F1 /CLONE=IMAGE:3507284 /UG=Hs.274472 high-mobility group (nonhistone chromosomal) protein 1 /FL=gb:BC003378.1 gb:NM_002128.1 gb:D63874.1
200707_at_HG-U133A	PRKCSH	protein kinase C substrate 80K-H	gb:NM_002743.1 /DEF=Homo sapiens protein kinase C substrate 80K-H (PRKCSH), mRNA. /FEA=mRNA /GEN=PRKCSH /PROD=protein kinase C substrate 80K-H /DB_XREF=gi:4506076 /UG=Hs.1432 protein kinase C substrate 80K-H /FL=gb:J03075.1 gb:NM_002743.1 gb:AF144075.1

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200742_s_at_HG-U133A	CLN2	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)	Consensus includes gb:BG231932 /FEA=EST /DB_XREF=gi:12727071 /DB_XREF=est:naf34b12.x1 /CLONE=IMAGE:4142926 /UG=Hs.20478 ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) /FL=gb:AF017456.1 gb:NM_000391.2
200743_s_at_HG-U133A	CLN2	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)	gb:NM_000391.2 /DEF=Homo sapiens ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) (CLN2), mRNA. /FEA=mRNA /GEN=CLN2 /PROD=ceroid-lipofuscinosis, neuronal 2, lateinfantile (Jansky-Bielschowsky disease) /DB_XREF=gi:5597012 /UG=Hs.20478 ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) /FL=gb:AF017456.1 gb:NM_000391.2
200765_x_at_HG-U133A	CTNNA1	catenin (cadherin-associated protein), alpha 1 (102kD)	gb:NM_001903.1 /DEF=Homo sapiens catenin (cadherin-associated protein), alpha 1 (102kD) (CTNNA1), mRNA. /FEA=mRNA /GEN=CTNNA1 /PROD=catenin (cadherin-associated protein), alpha 1(102kD) /DB_XREF=gi:4503126 /UG=Hs.178452 catenin (cadherin-associated protein), alpha 1 (102kD) /FL=gb:L23805.1 gb:NM_001903.1
200770_s_at_HG-U133A	LAMC1	laminin, gamma 1 (formerly LAMB2)	gb:J03202.1 /DEF=Human laminin B2 chain mRNA, complete cds. /FEA=mRNA /GEN=LAMB2 /DB_XREF=gi:186916 /UG=Hs.214982 laminin, gamma 1 (formerly LAMB2) /FL=gb:J03202.1 gb:NM_002293.2
200825_s_at_HG-U133A	ORP150	oxygen regulated protein (150kD)	gb:NM_006389.2 /DEF=Homo sapiens oxygen regulated protein (150kD) (ORP150), mRNA. /FEA=mRNA /GEN=ORP150 /PROD=oxygen regulated protein precursor /DB_XREF=gi:13699861 /UG=Hs.277704 oxygen regulated protein (150kD) /FL=gb:NM_006389.2 gb:U65785.1
200829_x_at_HG-U133A	ZNF207	zinc finger protein 207	gb:NM_003457.1 /DEF=Homo sapiens zinc finger protein 207 (ZNF207), mRNA. /FEA=mRNA /GEN=ZNF207 /PROD=zinc finger protein 207 /DB_XREF=gi:4508016 /UG=Hs.62112 zinc finger protein 207 /FL=gb:AF046001.1 gb:NM_003457.1
200832_s_at_HG-U133A	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	gb:AB032261.1 /DEF=Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds. /FEA=mRNA /GEN=Scd /PROD=stearoyl-CoA desaturase

			/DB_XREF=gi:7415720 /UG=Hs.119597 stearoyl-CoA desaturase (delta-9-desaturase) /FL=gb:AF097514.1 gb:NM_005063.1 gb:AB032261.1
200867_at_HG-U133A			Consensus includes gb:AL031685 /DEF=Human DNA sequence from clone RP5-963K23 on chromosome 20q13.11-13.2 Contains a KRT18 (Keratin type I, Cytoskeletal 18 (Cytokeratin 18, CK18,CYK18)) pseudogene, a gene for a novel protein, the gene for spermatogenesis associated protein PD1 (KIAA0... /FEA=mRNA_2 /DB_XREF=gi:9368423 /UG=Hs.10590 zinc finger protein 313 /FL=gb:AF265215.1 gb:NM_018683.1
200872_at_HG-U133A	S100A10	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	gb:NM_002966.1 /DEF=Homo sapiens S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA. /FEA=mRNA /GEN=S100A10 /PROD=S100 calcium-binding protein A10 /DB_XREF=gi:4506760 /UG=Hs.119301 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) /FL=gb:M81457.1 gb:M38591.1 gb:NM_002966.1
200890_s_at_HG-U133A	SSR1	signal sequence receptor, alpha (translocon-associated protein alpha)	Consensus includes gb:AW006345 /FEA=EST /DB_XREF=gi:5855123 /DB_XREF=est:wt04d05.x1 /CLONE=IMAGE:2506473 /UG=Hs.250773 signal sequence receptor, alpha (translocon-associated protein alpha) /FL=gb:AF156965.1 gb:NM_003144.2
200906_s_at_HG-U133A			Consensus includes gb:AK025843.1 /DEF=Homo sapiens cDNA: FLJ22190 fis, clone HRC01053. /FEA=mRNA /DB_XREF=gi:10438481 /UG=Hs.194431 palladin /FL=gb:AF077041.1 gb:AF151909.1 gb:NM_016081.1
200907_s_at_HG-U133A	KIAA0992	palladin	Consensus includes gb:AU157932 /FEA=EST /DB_XREF=gi:11019453 /DB_XREF=est:AU157932 /CLONE=PLACE1010217 /UG=Hs.194431 palladin /FL=gb:AF077041.1 gb:AF151909.1 gb:NM_016081.1
200917_s_at_HG-U133A	SRPR	signal recognition particle receptor ('docking protein')	Consensus includes gb:BG474541 /FEA=EST /DB_XREF=gi:13406818 /DB_XREF=est:602517313F1 /CLONE=IMAGE:4649162 /UG=Hs.75730 signal recognition particle receptor (docking protein) /FL=gb:BC001162.1 gb:NM_003139.1

200931_s_at_HG-U133A	VCL	vinculin	gb:NM_014000.1 /DEF=Homo sapiens vinculin (VCL), transcript variant meta-VCL, mRNA. /FEA=mRNA /GEN=VCL /PROD=VCL isoform meta-VCL /DB_XREF=gi:7669549 /UG=Hs.75350 vinculin /FL=gb:NM_014000.1
200935_at_HG-U133A	CALR	calreticulin	gb:NM_004343.2 /DEF=Homo sapiens calreticulin (CALR), mRNA. /FEA=mRNA /GEN=CALR /PROD=calreticulin precursor /DB_XREF=gi:5921996 /UG=Hs.16488 calreticulin /FL=gb:BC002500.1 gb:M84739.1 gb:M32294.1 gb:NM_004343.2
200951_s_at_HG-U133A	CCND2	cyclin D2	Consensus includes gb:AW026491 /FEA=EST /DB_XREF=gi:5880021 /DB_XREF=est:wv14b06.x1 /CLONE=IMAGE:2529491 /UG=Hs.75586 cyclin D2 /FL=gb:M90813.1 gb:D13639.1 gb:NM_001759.1
200952_s_at_HG-U133A	CCND2	cyclin D2	Consensus includes gb:AI635187 /FEA=EST /DB_XREF=gi:4686517 /DB_XREF=est:tz22b10.x1 /CLONE=IMAGE:2289307 /UG=Hs.75586 cyclin D2 /FL=gb:M90813.1 gb:D13639.1 gb:NM_001759.1
200953_s_at_HG-U133A	CCND2	cyclin D2	gb:NM_001759.1 /DEF=Homo sapiens cyclin D2 (CCND2), mRNA. /FEA=mRNA /GEN=CCND2 /PROD=cyclin D2 /DB_XREF=gi:4502616 /UG=Hs.75586 cyclin D2 /FL=gb:M90813.1 gb:D13639.1 gb:NM_001759.1
200967_at_HG-U133A	PPIB	peptidylprolyl isomerase B (cyclophilin B)	gb:NM_000942.1 /DEF=Homo sapiens peptidylprolyl isomerase B (cyclophilin B) (PPIB), mRNA. /FEA=mRNA /GEN=PPIB /PROD=peptidylprolyl isomerase B (cyclophilin B) /DB_XREF=gi:4758949 /UG=Hs.699 peptidylprolyl isomerase B (cyclophilin B) /FL=gb:BC001125.1 gb:M60857.1 gb:M63573.1 gb:NM_000942.1
200968_s_at_HG-U133A	PPIB	peptidylprolyl isomerase B (cyclophilin B)	gb:NM_000942.1 /DEF=Homo sapiens peptidylprolyl isomerase B (cyclophilin B) (PPIB), mRNA. /FEA=mRNA /GEN=PPIB /PROD=peptidylprolyl isomerase B (cyclophilin B) /DB_XREF=gi:4758949 /UG=Hs.699 peptidylprolyl isomerase B (cyclophilin B) /FL=gb:BC001125.1 gb:M60857.1 gb:M63573.1 gb:NM_000942.1
200984_s_at_HG-U133A	CD59	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16,	Consensus includes gb:X16447.1 /DEF=Human mRNA for CD59, an LY-6-like protein regulating complement membrane attack. /FEA=mRNA

		EJ30, EL32 and G344)	/PROD=precursor polypeptide (AA -25 to 103) /DB_XREF=gi:29805 /UG=Hs.119663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /FL=gb:NM_000611.1 gb:M34671.1
200985_s_at_HG-U133A	CD59	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	gb:NM_000611.1 /DEF=Homo sapiens CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA. /FEA=mRNA /GEN=CD59 /PROD=CD59 antigen p18-20 (antigen identified bymonoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /DB_XREF=gi:10835164 /UG=Hs.119663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /FL=gb:NM_000611.1 gb:M34671.1
200986_at_HG-U133A	SERPING1	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	gb:NM_000062.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), mRNA. /FEA=mRNA /GEN=SERPING1 /PROD=complement component 1 inhibitor precursor /DB_XREF=gi:4557378 /UG=Hs.151242 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 /FL=gb:M13690.1 gb:M13656.1 gb:NM_000062.1
200996_at_HG-U133A	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	gb:NM_005721.2 /DEF=Homo sapiens ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA. /FEA=mRNA /GEN=ACTR3 /PROD=ARP3 (actin-related protein 3, yeast) homolog /DB_XREF=gi:7262289 /UG=Hs.5321 ARP3 (actin-related protein 3, yeast) homolog /FL=gb:AF006083.1 gb:NM_005721.2
200998_s_at_HG-U133A	CKAP4	cytoskeleton-associated protein 4	Consensus includes gb:AW029619 /FEA=EST /DB_XREF=gi:5888375 /DB_XREF=est:wx14e05.x1 /CLONE=IMAGE:2543648 /UG=Hs.74368 transmembrane protein (63kD), endoplasmic reticulumGolgi intermediate compartment /FL=gb:NM_006825.1
201004_at_HG-U133A	SSR4	signal sequence receptor, delta (translocon-associated protein delta)	gb:NM_006280.1 /DEF=Homo sapiens signal sequence receptor, delta (translocon-associated protein delta) (SSR4), mRNA. /FEA=mRNA /GEN=SSR4 /PROD=signal sequence receptor, delta /DB_XREF=gi:5454089

			/UG=Hs.102135 signal sequence receptor, delta (translocon-associated protein delta) /FL=gb:BC003371.1 gb:NM_006280.1
201005_at_HG-U133A	CD9	CD9 antigen (p24)	gb:NM_001769.1 /DEF=Homo sapiens CD9 antigen (p24) (CD9), mRNA. /FEA=mRNA /GEN=CD9 /PROD=CD9 antigen (p24) /DB_XREF=gi:4502692 /UG=Hs.1244 CD9 antigen (p24) /FL=gb:M38690.1 gb:NM_001769.1 gb:L34068.1
201008_s_at_HG-U133A	TXNIP	thioredoxin interacting protein	Consensus includes gb:AA812232 /FEA=EST /DB_XREF=gi:2881843 /DB_XREF=est:ob84h09.s1 /CLONE=IMAGE:1338113 /UG=Hs.179526 upregulated by 1,25-dihydroxyvitamin D-3 /FL=gb:NM_006472.1 gb:S73591.1
201012_at_HG-U133A	ANXA1	annexin A1	gb:NM_000700.1 /DEF=Homo sapiens annexin A1 (ANXA1), mRNA. /FEA=mRNA /GEN=ANXA1 /PROD=annexin I /DB_XREF=gi:4502100 /UG=Hs.78225 annexin A1 /FL=gb:BC001275.1 gb:NM_000700.1
201015_s_at_HG-U133A	JUP	junction plakoglobin	gb:NM_021991.1 /DEF=Homo sapiens junction plakoglobin (JUP), transcript variant 2, mRNA. /FEA=mRNA /GEN=JUP /PROD=junction plakoglobin, isoform 1 /DB_XREF=gi:12056467 /UG=Hs.2340 junction plakoglobin /FL=gb:NM_021991.1 gb:BC000441.1
201029_s_at_HG-U133A	MIC2	antigen identified by monoclonal antibodies 12E7, F21 and O13	gb:NM_002414.1 /DEF=Homo sapiens antigen identified by monoclonal antibodies 12E7, F21 and O13 (MIC2), mRNA. /FEA=mRNA /GEN=MIC2 /PROD=antigen identified by monoclonal antibodies12E7, F21 and O13 /DB_XREF=gi:4505182 /UG=Hs.177543 antigen identified by monoclonal antibodies 12E7, F21 and O13 /FL=gb:BC002584.1 gb:BC003147.1 gb:M16279.1 gb:U82164.1 gb:NM_002414.1
201034_at_HG-U133A	ADD3	adducin 3 (gamma)	Consensus includes gb:BE545756 /FEA=EST /DB_XREF=gi:9774401 /DB_XREF=est:601076920F1 /CLONE=IMAGE:3462940 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:BC000306.1 gb:NM_005327.1
201061_s_at_HG-U133A	EPB72	erythrocyte membrane protein band 7.2 (stomatin)	gb:M81635.1 /DEF=Homo sapiens erythrocyte membrane protein mRNA, complete cds. /FEA=mRNA /GEN=stomatin peptide /PROD=stomatin peptide

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			/DB_XREF=gi:181183 /UG=Hs.160483 erythrocyte membrane protein band 7.2 (stomatin) /FL=gb:M81635.1 gb:NM_004099.1
201069_at_HG-U133A	MMP2	matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)	gb:NM_004530.1 /DEF=Homo sapiens matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) (MMP2), mRNA. /FEA=mRNA /GEN=MMP2 /PROD=matrix metalloproteinase 2 preproprotein /DB_XREF=gi:11342665 /UG=Hs.111301 matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) /FL=gb:NM_004530.1 gb:BC002576.1
201079_at_HG-U133A	SYNGR2	synaptogyrin 2	gb:NM_004710.1 /DEF=Homo sapiens synaptogyrin 2 (SYNGR2), mRNA. /FEA=mRNA /GEN=SYNGR2 /PROD=synaptogyrin 2 /DB_XREF=gi:4759201 /UG=Hs.5097 synaptogyrin 2 /FL=gb:BC000407.1 gb:NM_004710.1
201105_at_HG-U133A	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	gb:NM_002305.2 /DEF=Homo sapiens lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA. /FEA=mRNA /GEN=LGALS1 /PROD=beta-galactosidase binding lectin precursor /DB_XREF=gi:6006015 /UG=Hs.227751 lectin, galactoside-binding, soluble, 1 (galectin 1) /FL=gb:BC001693.1 gb:J04456.1 gb:NM_002305.2
201125_s_at_HG-U133A	ITGB5	integrin, beta 5	gb:NM_002213.1 /DEF=Homo sapiens integrin, beta 5 (ITGB5), mRNA. /FEA=mRNA /GEN=ITGB5 /PROD=integrin, beta 5 /DB_XREF=gi:4504772 /UG=Hs.149846 integrin, beta 5 /FL=gb:M35011.1 gb:J05633.1 gb:NM_002213.1
201137_s_at_HG-U133A	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	gb:NM_002121.1 /DEF=Homo sapiens major histocompatibility complex, class II, DP beta 1 (HLA-DPB1), mRNA. /FEA=mRNA /GEN=HLA-DPB1 /PROD=major histocompatibility complex, class II, DPbeta 1 /DB_XREF=gi:4504404 /UG=Hs.814 major histocompatibility complex, class II, DP beta 1 /FL=gb:J03041.1 gb:M57466.1 gb:M83664.1 gb:NM_002121.1 gb:M28200.1 gb:M28202.1
201152_s_at_HG-U133A	MBNL	muscleblind-like (Drosophila)	Consensus includes gb:N31913 /FEA=EST /DB_XREF=gi:1152312 /DB_XREF=est:yy21f10.s1 /CLONE=IMAGE:271915 /UG=Hs.28578 muscleblind

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			(Drosophila)-like /FL=gb:NM_021038.1 gb:AB007888.1
201153_s_at_HG-U133A	MBNL	muscleblind-like (Drosophila)	gb:NM_021038.1 /DEF=Homo sapiens muscleblind (Drosophila)-like (MBNL), mRNA. /FEA=mRNA /GEN=MBNL /PROD=muscleblind (Drosophila)-like /DB_XREF=gi:10518339 /UG=Hs.28578 muscleblind (Drosophila)-like /FL=gb:NM_021038.1 gb:AB007888.1
201162_at_HG-U133A	IGFBP7	insulin-like growth factor binding protein 7	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:L19182.1 gb:NM_001553.1
201163_s_at_HG-U133A	IGFBP7	insulin-like growth factor binding protein 7	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:L19182.1 gb:NM_001553.1
201164_s_at_HG-U133A	PUM1	pumilio homolog 1 (Drosophila)	Consensus includes gb:BG474429 /FEA=EST /DB_XREF=gi:13406706 /DB_XREF=est:602517152F1 /CLONE=IMAGE:4648765 /UG=Hs.153834 pumilio (Drosophila) homolog 1 /FL=gb:AF315592.1 gb:NM_014676.1
201189_s_at_HG-U133A	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	gb:NM_002224.1 /DEF=Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA. /FEA=mRNA /GEN=ITPR3 /PROD=inositol 1,4,5-triphosphate receptor, type 3 /DB_XREF=gi:4504794 /UG=Hs.77515 inositol 1,4,5-triphosphate receptor, type 3 /FL=gb:D26351.1 gb:NM_002224.1 gb:U01062.1
201200_at_HG-U133A	CREG	cellular repressor of E1A-stimulated genes	gb:NM_003851.1 /DEF=Homo sapiens cellular repressor of E1A-stimulated genes (CREG), mRNA. /FEA=mRNA /GEN=CREG /PROD=cellular repressor of E1A-stimulated genes /DB_XREF=gi:4503036 /UG=Hs.5710 cellular repressor of E1A-stimulated genes /FL=gb:AF084523.1 gb:NM_003851.1
201247_at_HG-U133A	SREBF2	sterol regulatory element binding transcription factor 2	Consensus includes gb:BE513151 /FEA=EST /DB_XREF=gi:9720362 /DB_XREF=est:601171940F1 /CLONE=IMAGE:3545697 /UG=Hs.108689 sterol regulatory element binding transcription factor 2 /FL=gb:U02031.1

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			gb:NM_004599.1
201263_at_HG-U133A	TARS	threonyl-tRNA synthetase	gb:NM_003191.1 /DEF=Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. /FEA=mRNA /GEN=TARS /PROD=threonyl-tRNA synthetase /DB_XREF=gi:4507366 /UG=Hs.84131 threonyl-tRNA synthetase /FL=gb:BC000517.1 gb:M63180.1 gb:NM_003191.1
201278_at_HG-U133A	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	Consensus includes gb:N21202 /FEA=EST /DB_XREF=gi:1126372 /DB_XREF=est:yx41e12.s1 /CLONE=IMAGE:264334 /UG=Hs.81988 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein) /FL=gb:U39050.1 gb:U53446.1 gb:BC003064.1 gb:NM_001343.1
201281_at_HG-U133A	ADRM1	adhesion regulating molecule 1	gb:NM_007002.1 /DEF=Homo sapiens cell membrane glycoprotein, 110000M(r) (surface antigen) (GP110), mRNA. /FEA=mRNA /GEN=GP110 /PROD=cell membrane glycoprotein, 110000M(r) (surfaceantigen) /DB_XREF=gi:5901959 /UG=Hs.90107 cell membrane glycoprotein, 110000M(r) (surface antigen) /FL=gb:NM_007002.1 gb:D64154.1
201324_at_HG-U133A	EMP1	epithelial membrane protein 1	gb:NM_001423.1 /DEF=Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /FEA=mRNA /GEN=EMP1 /PROD=epithelial membrane protein 1 /DB_XREF=gi:4503558 /UG=Hs.79368 epithelial membrane protein 1 /FL=gb:U77085.1 gb:U43916.1 gb:NM_001423.1
201334_s_at_HG-U133A	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	Consensus includes gb:AB002380.1 /DEF=Human mRNA for KIAA0382 gene, partial cds. /FEA=mRNA /GEN=KIAA0382 /DB_XREF=gi:2224704 /UG=Hs.6582 Rho guanine exchange factor (GEF) 12 /FL=gb:AF180681.1 gb:NM_015313.1
201338_x_at_HG-U133A	GTF3A	general transcription factor IIIA	gb:NM_002097.1 /DEF=Homo sapiens general transcription factor IIIA (GTF3A), mRNA. /FEA=mRNA /GEN=GTF3A /PROD=general transcription factor IIIA /DB_XREF=gi:4753158 /UG=Hs.75113 general transcription factor IIIA /FL=gb:D32257.1 gb:NM_002097.1
201352_at_HG-U133A	YME1L1	YME1-like 1 (S. cerevisiae)	gb:NM_014263.1 /DEF=Homo sapiens YME1 (S.cerevisiae)-like 1 (YME1L1), mRNA. /FEA=mRNA /GEN=YME1L1 /PROD=YME1 (S.cerevisiae)-like 1

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			/DB_XREF=gi:7657688 /UG=Hs.206521 YME1 (S.cerevisiae)-like 1 /FL=gb:AF070656.1 gb:NM_014263.1
201358_s_at_HG-U133A	COPB	coatomer protein complex, subunit beta	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /GEN=COPB /PROD=coatomer protein complex, subunit beta /DB_XREF=gi:7705368 /UG=Hs.3059 coatomer protein complex, subunit beta /FL=gb:AF084457.1 gb:AL136593.1 gb:NM_016451.1
201359_at_HG-U133A	COPB	coatomer protein complex, subunit beta	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /GEN=COPB /PROD=coatomer protein complex, subunit beta /DB_XREF=gi:7705368 /UG=Hs.3059 coatomer protein complex, subunit beta /FL=gb:AF084457.1 gb:AL136593.1 gb:NM_016451.1
201360_at_HG-U133A	CST3	cystatin C (amyloid angiopathy and cerebral hemorrhage)	gb:NM_000099.1 /DEF=Homo sapiens cystatin C (amyloid angiopathy and cerebral hemorrhage) (CST3), mRNA. /FEA=mRNA /GEN=CST3 /PROD=cystatin C (amyloid angiopathy and cerebralhemorrhage) /DB_XREF=gi:4503106 /UG=Hs.135084 cystatin C (amyloid angiopathy and cerebral hemorrhage) /FL=gb:NM_000099.1
201362_at_HG-U133A	NS1-BP	NS1-binding protein	gb:AF205218.1 /DEF=Homo sapiens NS1-binding protein-like protein mRNA, complete cds. /FEA=mRNA /PROD=NS1-binding protein-like protein /DB_XREF=gi:12003206 /UG=Hs.197298 NS1-binding protein /FL=gb:AF205218.1 gb:AB020657.1 gb:AF161553.1 gb:NM_016389.1
201377_at_HG-U133A	KIAA0144	KIAA0144 gene product	gb:NM_014847.1 /DEF=Homo sapiens KIAA0144 gene product (KIAA0144), mRNA. /FEA=mRNA /GEN=KIAA0144 /PROD=KIAA0144 gene product /DB_XREF=gi:7661941 /UG=Hs.8127 KIAA0144 gene product /FL=gb:D63478.1 gb:NM_014847.1
201396_s_at_HG-U133A	SGT	small glutamine-rich tetratricopeptide repeat (TPR)-containing	gb:NM_003021.2 /DEF=Homo sapiens small glutamine-rich tetratricopeptide repeat (TPR)-containing (SGT), mRNA. /FEA=mRNA /GEN=SGT /PROD=small glutamine-rich tetratricopeptide /DB_XREF=gi:13259553 /UG=Hs.203910 small glutamine-rich tetratricopeptide repeat (TPR)-containing /FL=gb:BC000390.1 gb:NM_003021.2 gb:BC005165.1 gb:AL050156.1

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201416_at_HG-U133A	SOX4	SRY (sex determining region Y)-box 4	Consensus includes gb:BG528420 /FEA=EST /DB_XREF=gi:13519957 /DB_XREF=est:602579853F1 /CLONE=IMAGE:4719060 /UG=Hs.83484 SRY (sex determining region Y)-box 4 /FL=gb:NM_003107.1
201417_at_HG-U133A			Consensus includes gb:AL136179 /DEF=Human DNA sequence from clone RP3-322L4 on chromosome 6. Contains the SOX4 gene for SRY (sex determining region Y)-box 4, a pseudogene similar to predicted fly, worm and yeast genes, ESTs, STSs, GSSs and four CpG islands /FEA=mRNA /DB_XREF=gi:8649149 /UG=Hs.83484 SRY (sex determining region Y)-box 4 /FL=gb:NM_003107.1
201425_at_HG-U133A	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	gb:NM_000690.1 /DEF=Homo sapiens aldehyde dehydrogenase 2, mitochondrial (ALDH2), mRNA. /FEA=mRNA /GEN=ALDH2 /PROD=aldehyde dehydrogenase 2, mitochondrial /DB_XREF=gi:4502032 /UG=Hs.195432 aldehyde dehydrogenase 2 family (mitochondrial) /FL=gb:BC002967.1 gb:NM_000690.1
201433_s_at_HG-U133A	PTDSS1	phosphatidylserine synthase 1	gb:NM_014754.1 /DEF=Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /FEA=mRNA /GEN=PTDSS1 /PROD=phosphatidylserine synthase 1 /DB_XREF=gi:7662646 /UG=Hs.77329 phosphatidylserine synthase 1 /FL=gb:BC004192.1 gb:BC004390.1 gb:D14694.1 gb:NM_014754.1
201437_s_at_HG-U133A	EIF4E	eukaryotic translation initiation factor 4E	gb:NM_001968.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), mRNA. /FEA=mRNA /GEN=EIF4E /PROD=eukaryotic translation initiation factor 4E /DB_XREF=gi:4503534 /UG=Hs.79306 eukaryotic translation initiation factor 4E /FL=gb:M15353.1 gb:NM_001968.1
201462_at_HG-U133A	KIAA0193	KIAA0193 gene product	gb:NM_014766.1 /DEF=Homo sapiens KIAA0193 gene product (KIAA0193), mRNA. /FEA=mRNA /GEN=KIAA0193 /PROD=KIAA0193 gene product /DB_XREF=gi:7661983 /UG=Hs.75137 KIAA0193 gene product /FL=gb:D83777.1 gb:NM_014766.1
201463_s_at_HG-U133A	TALDO1	transaldolase 1	gb:NM_006755.1 /DEF=Homo sapiens transaldolase 1 (TALDO1), mRNA. /FEA=mRNA /GEN=TALDO1 /PROD=transaldolase 1 /DB_XREF=gi:5803186

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			/UG=Hs.77290 transaldolase 1 /FL=gb:L19437.2 gb:NM_006755.1
201482_at_HG-U133A	QSCN6	quiescin Q6	gb:NM_002826.2 /DEF=Homo sapiens quiescin Q6 (QSCN6), mRNA. /FEA=mRNA /GEN=QSCN6 /PROD=quiescin Q6 /DB_XREF=gi:13325074 /UG=Hs.77266 quiescin Q6 /FL=gb:L42379.1 gb:U97276.2 gb:NM_002826.2
201485_s_at_HG-U133A	RCN2	reticulocalbin 2, EF-hand calcium binding domain	gb:BC004892.1 /DEF=Homo sapiens, reticulocalbin 2, EF-hand calcium binding domain, clone MGC:1650, mRNA, complete cds. /FEA=mRNA /PROD=reticulocalbin 2, EF-hand calcium bindingdomain /DB_XREF=gi:13436151 /UG=Hs.79088 reticulocalbin 2, EF-hand calcium binding domain /FL=gb:BC004892.1 gb:NM_002902.1
201486_at_HG-U133A	RCN2	reticulocalbin 2, EF-hand calcium binding domain	gb:NM_002902.1 /DEF=Homo sapiens reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA. /FEA=mRNA /GEN=RCN2 /PROD=reticulocalbin 2, EF-hand calcium bindingdomain /DB_XREF=gi:4506456 /UG=Hs.79088 reticulocalbin 2, EF-hand calcium binding domain /FL=gb:BC004892.1 gb:NM_002902.1
201496_x_at_HG-U133A	MYH11	myosin, heavy polypeptide 11, smooth muscle	Consensus includes gb:S67238.1 /DEF=smooth muscle myosin heavy chain isoform SM2 human, umbilical cord, fetal aorta, mRNA Partial, 1078 nt. /FEA=mRNA /GEN=smooth muscle myosin heavy chain isoform SM2 /PROD=smooth muscle myosin heavy chain isoform SM2 /DB_XREF=gi:452982 /UG=Hs.78344 myosin, heavy polypeptide 11, smooth muscle /FL=gb:NM_022844.1
201497_x_at_HG-U133A	MYH11	myosin, heavy polypeptide 11, smooth muscle	gb:NM_022844.1 /DEF=Homo sapiens myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM2, mRNA. /FEA=mRNA /GEN=MYH11 /PROD=smooth muscle myosin heavy chain 11, isoformSM2 /DB_XREF=gi:13124874 /UG=Hs.78344 myosin, heavy polypeptide 11, smooth muscle /FL=gb:NM_022844.1
201506_at_HG-U133A	TGFBI	transforming growth factor, beta-induced, 68kD	gb:NM_000358.1 /DEF=Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA. /FEA=mRNA /GEN=TGFBI /PROD=transforming growth factor, beta-induced, 68kD /DB_XREF=gi:4507466

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			/UG=Hs.118787 transforming growth factor, beta-induced, 68kD /FL=gb:BC000097.1 gb:BC004972.1 gb:M77349.1 gb:NM_000358.1
201530_x_at_HG-U133A	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	gb:NM_001416.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA. /FEA=mRNA /GEN=EIF4A1 /PROD=eukaryotic translation initiation factor 4A,isoform 1 /DB_XREF=gi:4503528 /UG=Hs.129673 eukaryotic translation initiation factor 4A, isoform 1 /FL=gb:NM_001416.1
201537_s_at_HG-U133A	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	gb:BC002682.1 /DEF=Homo sapiens, dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related), clone MGC:3615, mRNA, complete cds. /FEA=mRNA /PROD=dual specificity phosphatase 3 (vaccinia virusphosphatase VH1-related) /DB_XREF=gi:12803692 /UG=Hs.181046 dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) /FL=gb:BC002682.1 gb:L05147.1 gb:NM_004090.1
201540_at_HG-U133A	FHL1	four and a half LIM domains 1	gb:NM_001449.1 /DEF=Homo sapiens four and a half LIM domains 1 (FHL1), mRNA. /FEA=mRNA /GEN=FHL1 /PROD=four and a half LIM domains 1 /DB_XREF=gi:4503720 /UG=Hs.239069 four and a half LIM domains 1 /FL=gb:U29538.1 gb:U60115.1 gb:NM_001449.1
201548_s_at_HG-U133A	PLU-1	putative DNA/chromatin binding motif	Consensus includes gb:W02593 /FEA=EST /DB_XREF=gi:1274571 /DB_XREF=est:za51e06.r1 /CLONE=IMAGE:296098 /UG=Hs.143323 putative DNAchromatin binding motif /FL=gb:NM_006618.1
201564_s_at_HG-U133A	SNL	singed-like (fascin homolog, sea urchin) (Drosophila)	gb:NM_003088.1 /DEF=Homo sapiens singed (Drosophila)-like (sea urchin fascin homolog like) (SNL), mRNA. /FEA=mRNA /GEN=SNL /PROD=singed (Drosophila)-like (sea urchin fascinhomolog like) /DB_XREF=gi:4507114 /UG=Hs.118400 singed (Drosophila)-like (sea urchin fascin homolog like) /FL=gb:BC000521.1 gb:NM_003088.1 gb:U03057.1 gb:U09873.1
201585_s_at_HG-U133A	SFPQ	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Consensus includes gb:BG035151 /FEA=EST /DB_XREF=gi:12428997 /DB_XREF=est:602324851F1 /CLONE=IMAGE:4412917 /UG=Hs.180610 splicing factor prolineglutamine rich (polypyrimidine tract-binding protein-

			associated) /FL=gb:NM_005066.1
201592_at_HG-U133A	EIF3S3	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	gb:NM_003756.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S3), mRNA. /FEA=mRNA /GEN=EIF3S3 /PROD=eukaryotic translation initiation factor 3,subunit 3 (gamma, 40kD) /DB_XREF=gi:4503514 /UG=Hs.58189 eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) /FL=gb:BC000386.1 gb:U54559.1 gb:NM_003756.1
201595_s_at_HG-U133A	HT010	uncharacterized hypothalamus protein HT010	gb:NM_018471.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HT010 (HT010), mRNA. /FEA=mRNA /GEN=HT010 /PROD=uncharacterized hypothalamus protein HT010 /DB_XREF=gi:8923807 /UG=Hs.6375 uncharacterized hypothalamus protein HT010 /FL=gb:AF220184.1 gb:NM_018471.1
201596_x_at_HG-U133A	KRT18	keratin 18	gb:NM_000224.1 /DEF=Homo sapiens keratin 18 (KRT18), mRNA. /FEA=mRNA /GEN=KRT18 /PROD=keratin 18 /DB_XREF=gi:4557887 /UG=Hs.65114 keratin 18 /FL=gb:BC000698.1 gb:BC000180.2 gb:BC004253.1 gb:M26326.1 gb:NM_000224.1
201602_s_at_HG-U133A	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	Consensus includes gb:BE737620 /FEA=EST /DB_XREF=gi:10151612 /DB_XREF=est:601572895F1 /CLONE=IMAGE:3839831 /UG=Hs.16533 myosin phosphatase, target subunit 1 /FL=gb:NM_002480.1
201640_x_at_HG-U133A	CLPTM1	cleft lip and palate associated transmembrane protein 1	gb:NM_001294.1 /DEF=Homo sapiens cleft lip and palate associated transmembrane protein 1 (CLPTM1), mRNA. /FEA=mRNA /GEN=CLPTM1 /PROD=cleft lip and palate associated transmembraneprotein 1 /DB_XREF=gi:4502896 /UG=Hs.106671 cleft lip and palate associated transmembrane protein 1 /FL=gb:AF037339.1 gb:NM_001294.1
201644_at_HG-U133A	TSTA3	tissue specific transplantation antigen P35B	gb:NM_003313.2 /DEF=Homo sapiens tissue specific transplantation antigen P35B (TSTA3), mRNA. /FEA=mRNA /GEN=TSTA3 /PROD=tissue specific transplantation antigen P35B /DB_XREF=gi:6598326 /UG=Hs.264428 tissue specific transplantation antigen P35B /FL=gb:BC001941.1 gb:U58766.1 gb:NM_003313.2

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201652_at_HG-U133A	COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	gb:NM_006837.1 /DEF=Homo sapiens COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5 (COPS5), mRNA. /FEA=mRNA /GEN=COPS5 /PROD=COP9 (constitutive photomorphogenic,Arabidopsis, homolog) subunit 5 /DB_XREF=gi:5803045 /UG=Hs.198767 COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5 /FL=gb:BC001187.1 gb:BC001859.1 gb:U65928.1 gb:U70734.1 gb:NM_006837.1
201753_s_at_HG-U133A	ADD3	adducin 3 (gamma)	gb:NM_019903.1 /DEF=Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, mRNA. /FEA=mRNA /GEN=ADD3 /PROD=adducin 3, isoform b /DB_XREF=gi:9951926 /UG=Hs.324470 adducin 3 (gamma) /FL=gb:D67031.1 gb:NM_019903.1
201761_at_HG-U133A	MTHFD2	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	gb:NM_006636.2 /DEF=Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MTHFD2 /PROD=methylene tetrahydrofolate dehydrogenase (NAD+dependent), methenyltetrahydrofolate cyclohydrolase,precursor /DB_XREF=gi:13699869 /UG=Hs.154672 methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase /FL=gb:NM_006636.2
201810_s_at_HG-U133A	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	Consensus includes gb:AL562152 /FEA=EST /DB_XREF=gi:12910291 /DB_XREF=est:AL562152 /CLONE=CS0DC001YK23 (3 prime) /UG=Hs.109150 SH3-domain binding protein 5 (BTK-associated) /FL=gb:AB005047.1 gb:NM_004844.1
201811_x_at_HG-U133A	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	gb:NM_004844.1 /DEF=Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA. /FEA=mRNA /GEN=SH3BP5 /PROD=SH3-domain binding protein 5 (BTK-associated) /DB_XREF=gi:4759057 /UG=Hs.109150 SH3-domain binding protein 5 (BTK-associated) /FL=gb:AB005047.1 gb:NM_004844.1

201812_s_at_HG-U133A	LOC54543	6.2 kd protein	gb:NM_019059.1 /DEF=Homo sapiens 6.2 kd protein (LOC54543), mRNA. /FEA=mRNA /GEN=LOC54543 /PROD=6.2 kd protein /DB_XREF=gi:9506858 /UG=Hs.112318 6.2 kd protein /FL=gb:BC001732.1 gb:AF150733.1 gb:NM_019059.1
201813_s_at_HG-U133A	KIAA0210	KIAA0210 gene product	Consensus includes gb:AI654161 /FEA=EST /DB_XREF=gi:4738140 /DB_XREF=est:ty62e04.x1 /CLONE=IMAGE:2283678 /UG=Hs.115740 KIAA0210 gene product /FL=gb:D86965.1 gb:NM_014744.1
201825_s_at_HG-U133A	LOC51097	CGI-49 protein	Consensus includes gb:AL572542 /FEA=EST /DB_XREF=gi:12930912 /DB_XREF=est:AL572542 /CLONE=CS0DI008YC09 (3 prime) /UG=Hs.238126 CGI-49 protein /FL=gb:AF151807.1 gb:NM_016002.1
201828_x_at_HG-U133A	CXX1	CAAX box 1	gb:NM_003928.1 /DEF=Homo sapiens CAAX box 1 (CXX1), mRNA. /FEA=mRNA /GEN=CXX1 /PROD=CAAX box 1 /DB_XREF=gi:4503180 /UG=Hs.250708 CAAX box 1 /FL=gb:BC002385.1 gb:BC002410.1 gb:AF038168.1 gb:AF052096.1 gb:NM_003928.1
201829_at_HG-U133A	NET1	neuroepithelial cell transforming gene 1	Consensus includes gb:AW263232 /FEA=EST /DB_XREF=gi:6640048 /DB_XREF=est:xn79e03.x1 /CLONE=IMAGE:2700700 /UG=Hs.25155 neuroepithelial cell transforming gene 1 /FL=gb:NM_005863.1 gb:U02081.1
201830_s_at_HG-U133A	NET1	neuroepithelial cell transforming gene 1	gb:NM_005863.1 /DEF=Homo sapiens neuroepithelial cell transforming gene 1 (NET1), mRNA. /FEA=mRNA /GEN=NET1 /PROD=neuroepithelial cell transforming gene 1 /DB_XREF=gi:5031938 /UG=Hs.25155 neuroepithelial cell transforming gene 1 /FL=gb:NM_005863.1 gb:U02081.1
201851_at_HG-U133A	SH3GL1	SH3-domain GRB2-like 1	gb:NM_003025.1 /DEF=Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), mRNA. /FEA=mRNA /GEN=SH3GL1 /PROD=SH3-domain GRB2-like 1 /DB_XREF=gi:4506928 /UG=Hs.97616 SH3-domain GRB2-like 1 /FL=gb:BC001270.1 gb:U65999.1 gb:NM_003025.1
201853_s_at_HG-U133A	CDC25B	cell division cycle 25B	gb:NM_021873.1 /DEF=Homo sapiens cell division cycle 25B (CDC25B), transcript variant 3, mRNA. /FEA=mRNA /GEN=CDC25B /PROD=cell division cycle 25B, isoform 3 /DB_XREF=gi:11641412 /UG=Hs.153752 cell division

			cycle 25B /FL=gb:NM_021873.1
201858_s_at_HG-U133A	PRG1	proteoglycan 1, secretory granule	gb:J03223.1 /DEF=Human secretory granule proteoglycan peptide core mRNA, complete cds. /FEA=mRNA /GEN=PRG1 /DB_XREF=gi:190419 /UG=Hs.1908 proteoglycan 1, secretory granule /FL=gb:J03223.1 gb:NM_002727.1
201874_at_HG-U133A	FLJ21047	hypothetical protein FLJ21047	Consensus includes gb:BF978611 /FEA=EST /DB_XREF=gi:12345826 /DB_XREF=est:602149061F1 /CLONE=IMAGE:4307822 /UG=Hs.14891 hypothetical protein FLJ21047 /FL=gb:NM_024569.1
201889_at_HG-U133A	GS3786	predicted osteoblast protein	gb:NM_014888.1 /DEF=Homo sapiens predicted osteoblast protein (GS3786), mRNA. /FEA=mRNA /GEN=GS3786 /PROD=predicted osteoblast protein /DB_XREF=gi:7661713 /UG=Hs.29882 predicted osteoblast protein /FL=gb:D87120.1 gb:NM_014888.1
201922_at_HG-U133A	YR-29	hypothetical protein YR-29	gb:NM_014886.1 /DEF=Homo sapiens hypothetical protein (YR-29), mRNA. /FEA=mRNA /GEN=YR-29 /PROD=hypothetical protein /DB_XREF=gi:7662676 /UG=Hs.8170 hypothetical protein /FL=gb:AF077615.1 gb:BC005288.1 gb:NM_014886.1
201923_at_HG-U133A	PRDX4	peroxiredoxin 4	gb:NM_006406.1 /DEF=Homo sapiens thioredoxin peroxidase (antioxidant enzyme) (AOE372), mRNA. /FEA=mRNA /GEN=AOE372 /PROD=thioredoxin peroxidase /DB_XREF=gi:5453548 /UG=Hs.83383 thioredoxin peroxidase (antioxidant enzyme) /FL=gb:BC003609.1 gb:NM_006406.1 gb:U25182.1
201962_s_at_HG-U133A	SBB103	hypothetical SBBI03 protein	gb:NM_005785.1 /DEF=Homo sapiens hypothetical SBBI03 protein (SBB103), mRNA. /FEA=mRNA /GEN=SBB103 /PROD=hypothetical SBBI03 protein /DB_XREF=gi:5032070 /UG=Hs.153639 hypothetical SBBI03 protein /FL=gb:AF077599.1 gb:NM_005785.1
201968_s_at_HG-U133A	PGM1	phosphoglucomutase 1	gb:NM_002633.1 /DEF=Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /FEA=mRNA /GEN=PGM1 /PROD=phosphoglucomutase 1 /DB_XREF=gi:4505764 /UG=Hs.1869 phosphoglucomutase 1 /FL=gb:BC001756.1 gb:M83088.1 gb:NM_002633.1

201974_s_at_HG-U133A	LOC51622	CGI-43 protein	gb:NM_015622.1 /DEF=Homo sapiens CGI-43 protein (LOC51622), mRNA. /FEA=mRNA /GEN=LOC51622 /PROD=DKFZP586I1023 protein /DB_XREF=gi:11056021 /UG=Hs.289112 CGI-43 protein /FL=gb:NM_015622.1 gb:AF151801.1
201985_at_HG-U133A	KIAA0196	KIAA0196 gene product	gb:NM_014846.1 /DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. /FEA=mRNA /GEN=KIAA0196 /PROD=KIAA0196 gene product /DB_XREF=gi:7661987 /UG=Hs.8294 KIAA0196 gene product /FL=gb:D83780.1 gb:NM_014846.1
201988_s_at_HG-U133A	CREBL2	cAMP responsive element binding protein-like 2	Consensus includes gb:BF438056 /FEA=EST /DB_XREF=gi:11450573 /DB_XREF=est:7q66e01.x1 /CLONE=IMAGE:3703369 /UG=Hs.13313 cAMP responsive element binding protein-like 2 /FL=gb:AF039081.1 gb:NM_001310.1
201998_at_HG-U133A	SIAT1	sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase)	Consensus includes gb:AI743792 /FEA=EST /DB_XREF=gi:5112080 /DB_XREF=est:wg53h11.x1 /CLONE=IMAGE:2368869 /UG=Hs.2554 sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase) /FL=gb:NM_003032.1
202016_at_HG-U133A	MEST	mesoderm specific transcript homolog (mouse)	gb:NM_002402.1 /DEF=Homo sapiens mesoderm specific transcript (mouse) homolog (MEST), mRNA. /FEA=mRNA /GEN=MEST /PROD=mesoderm specific transcript (mouse) homolog /DB_XREF=gi:4505154 /UG=Hs.79284 mesoderm specific transcript (mouse) homolog /FL=gb:BC002413.1 gb:D78611.1 gb:D87367.1 gb:NM_002402.1
202018_s_at_HG-U133A	LTF	lactotransferrin	gb:NM_002343.1 /DEF=Homo sapiens lactotransferrin (LTF), mRNA. /FEA=mRNA /GEN=LTF /PROD=lactotransferrin /DB_XREF=gi:4505042 /UG=Hs.105938 lactotransferrin /FL=gb:AF332168.1 gb:M93150.1 gb:M83202.1 gb:NM_002343.1
202028_s_at_HG-U133A	RPL38	ribosomal protein L38	Consensus includes gb:BC000603.1 /DEF=Homo sapiens, ribosomal protein L38, clone MGC:1637, mRNA, complete cds. /FEA=mRNA /PROD=ribosomal protein L38 /DB_XREF=gi:12653644 /UG=Hs.2017 ribosomal protein L38

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			/FL=gb:BC000603.1 gb:NM_000999.1
202052_s_at_HG-U133A	RAI14	retinoic acid induced 14	gb:NM_015577.1 /DEF=Homo sapiens novel retinal pigment epithelial gene (NORPEG), mRNA. /FEA=mRNA /GEN=NORPEG /PROD=DKFZP564G013 protein /DB_XREF=gi:13470085 /UG=Hs.15165 novel retinal pigment epithelial gene /FL=gb:NM_015577.1 gb:AF155135.1
202074_s_at_HG-U133A	OPTN	optineurin	gb:NM_021980.1 /DEF=Homo sapiens tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein (FIP2), mRNA. /FEA=mRNA /GEN=FIP2 /PROD=tumor necrosis factor alpha-inducible cellularprotein containing leucine zipper domains; Huntingtininteracting protein L; transcrption factorIIIA-interacting protein /DB_XREF=gi:11415041 /UG=Hs.278898 tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein /FL=gb:NM_021980.1
202080_s_at_HG-U133A	KIAA1042	KIAA1042 protein	gb:NM_014965.1 /DEF=Homo sapiens KIAA1042 protein (KIAA1042), mRNA. /FEA=mRNA /GEN=KIAA1042 /PROD=KIAA1042 protein /DB_XREF=gi:7662457 /UG=Hs.6705 KIAA1042 protein /FL=gb:AB028965.1 gb:NM_014965.1
202085_at_HG-U133A	TJP2	tight junction protein 2 (zona occludens 2)	gb:NM_004817.1 /DEF=Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2), mRNA. /FEA=mRNA /GEN=TJP2 /PROD=tight junction protein 2 (zona occludens 2) /DB_XREF=gi:4759341 /UG=Hs.75608 tight junction protein 2 (zona occludens 2) /FL=gb:NM_004817.1 gb:L27476.1
202095_s_at_HG-U133A	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	gb:NM_001168.1 /DEF=Homo sapiens baculoviral IAP repeat-containing 5 (survivin) (BIRC5), mRNA. /FEA=mRNA /GEN=BIRC5 /PROD=baculoviral IAP repeat-containing protein 5 /DB_XREF=gi:4502144 /UG=Hs.1578 baculoviral IAP repeat-containing 5 (survivin) /FL=gb:NM_001168.1 gb:AF077350.1
202101_s_at_HG-U133A	RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding	gb:NM_002881.1 /DEF=Homo sapiens v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA. /FEA=mRNA

		protein)	/GEN=RALB /PROD=v-ral simian leukemia viral oncogene homolog B /DB_XREF=gi:4506404 /UG=Hs.250811 v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) /FL=gb:M35416.1 gb:NM_002881.1
202113_s_at_HG-U133A	SNX2	sorting nexin 2	gb:AF043453.1 /DEF=Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. /FEA=mRNA /GEN=SNX2 /PROD=sorting nexin 2 /DB_XREF=gi:2827433 /UG=Hs.11183 sorting nexin 2 /FL=gb:BC003382.1 gb:AF043453.1 gb:AF065482.1 gb:NM_003100.1
202123_s_at_HG-U133A	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	gb:NM_005157.2 /DEF=Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 1 (ABL1), transcript variant a, mRNA. /FEA=mRNA /GEN=ABL1 /PROD=v-abl Abelson murine leukemia viral oncogenehomolog 1 isoform a /DB_XREF=gi:6382056 /UG=Hs.146355 v-abl Abelson murine leukemia viral oncogene homolog 1 /FL=gb:M14752.1 gb:NM_005157.2
202137_s_at_HG-U133A	BS69	adenovirus 5 E1A binding protein	gb:NM_006624.1 /DEF=Homo sapiens adenovirus 5 E1A binding protein (BS69), mRNA. /FEA=mRNA /GEN=BS69 /PROD=adenovirus 5 E1A binding protein /DB_XREF=gi:5729745 /UG=Hs.301449 adenovirus 5 E1A binding protein /FL=gb:NM_006624.1
202148_s_at_HG-U133A	PYCR1	pyrroline-5-carboxylate reductase 1	gb:NM_006907.1 /DEF=Homo sapiens pyrroline-5-carboxylate reductase 1 (PYCR1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=PYCR1 /PROD=pyrroline-5-carboxylate reductase 1 /DB_XREF=gi:5902035 /UG=Hs.79217 pyrroline-5-carboxylate reductase 1 /FL=gb:M77836.1 gb:NM_006907.1
202150_s_at_HG-U133A	HEF1	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)	gb:U64317.1 /DEF=Human Crk-associated substrate related protein Cas-L mRNA, complete cds. /FEA=mRNA /PROD=Crk-associated substrate related protein Cas-L /DB_XREF=gi:1490786 /UG=Hs.80261 enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) /FL=gb:L43821.1 gb:U64317.1 gb:NM_006403.1
202156_s_at_HG-	CUGBP2	CUG triplet repeat, RNA binding protein	Consensus includes gb:N36839 /FEA=EST /DB_XREF=gi:1157981

U133A		2	/DB_XREF=est:yy35f07.s1 /CLONE=IMAGE:273253 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1
202206_at_HG-U133A	ARL7	ADP-ribosylation factor-like 7	Consensus includes gb:AW450363 /FEA=EST /DB_XREF=gi:6991139 /DB_XREF=est:UI-H-BI3-akn-d-02-0-UI.s1 /CLONE=IMAGE:2734875 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM_005737.2
202249_s_at_HG-U133A	H326	H326	Consensus includes gb:AU146233 /FEA=EST /DB_XREF=gi:11007754 /DB_XREF=est:AU146233 /CLONE=HEMBA1007223 /UG=Hs.110707 H326 /FL=gb:U06631.1 gb:NM_015726.1
202254_at_HG-U133A	KIAA0440	KIAA0440 protein	Consensus includes gb:AB007900.1 /DEF=Homo sapiens KIAA0440 mRNA, partial cds. /FEA=mRNA /GEN=KIAA0440 /DB_XREF=gi:2662160 /UG=Hs.172180 KIAA0440 protein /FL=gb:AF090990.1 gb:NM_015556.1
202262_x_at_HG-U133A	DDAH2	dimethylarginine dimethylaminohydrolase 2	gb:NM_013974.1 /DEF=Homo sapiens dimethylarginine dimethylaminohydrolase 2 (DDAH2), mRNA. /FEA=mRNA /GEN=DDAH2 /PROD=dimethylarginine dimethylaminohydrolase 2 /DB_XREF=gi:7524353 /UG=Hs.247362 dimethylarginine dimethylaminohydrolase 2 /FL=gb:BC001435.1 gb:AF070667.1 gb:NM_013974.1
202265_at_HG-U133A	BMI1	B lymphoma Mo-MLV insertion region (mouse)	gb:NM_005180.1 /DEF=Homo sapiens murine leukemia viral (bmi-1) oncogene homolog (BMI1), mRNA. /FEA=mRNA /GEN=BMI1 /PROD=murine leukemia viral (bmi-1) oncogene homolog /DB_XREF=gi:4885094 /UG=Hs.431 murine leukemia viral (bmi-1) oncogene homolog /FL=gb:L13689.1 gb:NM_005180.1
202283_at_HG-U133A	SERPINF1	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	gb:NM_002615.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 (SERPINF1), mRNA. /FEA=mRNA /GEN=SERPINF1 /PROD=serine (or cysteine) proteinase inhibitor, cladeF (alpha-2 antiplasmin, pigment epithelium derivedfactor), member 1 /DB_XREF=gi:4505708 /UG=Hs.173594

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			serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 /FL=gb:M90439.1 gb:BC000522.1 gb:M76979.1 gb:NM_002615.1
202288_at_HG-U133A	FRAP1	FK506 binding protein 12-rapamycin associated protein 1	gb:U88966.1 /DEF=Human protein rapamycin associated protein (FRAP2) gene, complete cds. /FEA=mRNA /GEN=FRAP2 /PROD=rapamycin associated protein FRAP2 /DB_XREF=gi:3282238 /UG=Hs.250723 FK506 binding protein 12-rapamycin associated protein 1 /FL=gb:U88966.1 gb:NM_004958.1 gb:L34075.1
202328_s_at_HG-U133A	PKD1	polycystic kidney disease 1 (autosomal dominant)	gb:NM_000296.1 /DEF=Homo sapiens polycystic kidney disease 1 (autosomal dominant) (PKD1), mRNA. /FEA=mRNA /GEN=PKD1 /PROD=polycystic kidney disease 1 (autosomaldominant) /DB_XREF=gi:4505832 /UG=Hs.75813 polycystic kidney disease 1 (autosomal dominant) /FL=gb:NM_000296.1 gb:U24497.1 gb:L33243.1
202332_at_HG-U133A	CSNK1E	casein kinase 1, epsilon	gb:NM_001894.1 /DEF=Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA. /FEA=mRNA /GEN=CSNK1E /PROD=casein kinase 1, epsilon /DB_XREF=gi:4503092 /UG=Hs.79658 casein kinase 1, epsilon /FL=gb:NM_001894.1 gb:AB024597.1 gb:L37043.1
202340_x_at_HG-U133A	NR4A1	nuclear receptor subfamily 4, group A, member 1	gb:NM_002135.1 /DEF=Homo sapiens nuclear receptor subfamily 4, group A, member 1 (NR4A1), mRNA. /FEA=mRNA /GEN=NR4A1 /PROD=nuclear receptor subfamily 4, group A, member 1 /DB_XREF=gi:4504440 /UG=Hs.1119 nuclear receptor subfamily 4, group A, member 1 /FL=gb:L13740.1 gb:NM_002135.1
202370_s_at_HG-U133A	CBFB	core-binding factor, beta subunit	gb:NM_001755.1 /DEF=Homo sapiens core-binding factor, beta subunit (CBFB), transcript variant 2, mRNA. /FEA=mRNA /GEN=CBFB /PROD=core-binding factor, beta subunit, isoform 2 /DB_XREF=gi:13124872 /UG=Hs.179881 core-binding factor, beta subunit /FL=gb:NM_001755.1
202371_at_HG-U133A	FLJ21174	hypothetical protein FLJ21174	gb:NM_024863.1 /DEF=Homo sapiens hypothetical protein FLJ21174 (FLJ21174), mRNA. /FEA=mRNA /GEN=FLJ21174 /PROD=hypothetical protein

			FLJ21174 /DB_XREF=gi:13376293 /UG=Hs.194329 hypothetical protein FLJ21174 /FL=gb:AF271783.1 gb:NM_024863.1
202377_at_HG-U133A	HSOBRGRP	leptin receptor gene-related protein	Consensus includes gb:AW026535 /FEA=EST /DB_XREF=gi:5880065 /DB_XREF=est:wv14f10.x1 /CLONE=IMAGE:2529547 /UG=Hs.23581 leptin receptor gene-related protein /FL=gb:NM_017526.1
202382_s_at_HG-U133A	GNPI	glucosamine-6-phosphate isomerase	gb:NM_005471.1 /DEF=Homo sapiens glucosamine-6-phosphate isomerase (GNPI), mRNA. /FEA=mRNA /GEN=GNPI /PROD=glucosamine-6-phosphate isomerase /DB_XREF=gi:13027377 /UG=Hs.278500 glucosamine-6-phosphate isomerase /FL=gb:NM_005471.1 gb:AF029914.1 gb:AF048826.1 gb:D31766.1
202391_at_HG-U133A	BASP1	brain abundant, membrane attached signal protein 1	gb:NM_006317.1 /DEF=Homo sapiens brain acid-soluble protein 1 (BASP1), mRNA. /FEA=mRNA /GEN=BASP1 /PROD=brain acid-soluble protein 1 /DB_XREF=gi:5453749 /UG=Hs.79516 brain abundant, membrane attached signal protein 1 /FL=gb:BC000518.1 gb:AF039656.1 gb:NM_006317.1
202406_s_at_HG-U133A	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	gb:NM_003252.2 /DEF=Homo sapiens TIA1 cytotoxic granule-associated RNA-binding protein-like 1 (TIAL1), transcript variant 1, mRNA. /FEA=mRNA /GEN=TIAL1 /PROD=TIA1 cytotoxic granule-associated RNA-bindingprotein-like 1, isoform 1 /DB_XREF=gi:13435392 /UG=Hs.182741 TIA1 cytotoxic granule-associated RNA-binding protein-like 1 /FL=gb:NM_003252.2 gb:M96954.1
202413_s_at_HG-U133A	USP1	ubiquitin specific protease 1	gb:NM_003368.1 /DEF=Homo sapiens ubiquitin specific protease 1 (USP1), mRNA. /FEA=mRNA /GEN=USP1 /PROD=ubiquitin specific protease 1 /DB_XREF=gi:4507850 /UG=Hs.35086 ubiquitin specific protease 1 /FL=gb:AB014458.1 gb:AF117386.1 gb:NM_003368.1 gb:AL117575.1
202421_at_HG-U133A	IGSF3	immunoglobulin superfamily, member 3	Consensus includes gb:AB007935.1 /DEF=Homo sapiens mRNA for KIAA0466 protein, partial cds. /FEA=mRNA /GEN=KIAA0466 /PROD=KIAA0466 protein /DB_XREF=gi:3413893 /UG=Hs.81234 immunoglobulin superfamily, member 3 /FL=gb:AF031174.1 gb:NM_001542.1
202441_at_HG-U133A	KEO4	similar to Caenorhabditis elegans protein C42C1.9	Consensus includes gb:AL568449 /FEA=EST /DB_XREF=gi:12922799 /DB_XREF=est:AL568449 /CLONE=CS0DE001YC12 (3 prime) /UG=Hs.285818

			similar to Caenorhabditis elegans protein C42C1.9 /FL=gb:AF064093.1 gb:NM_006459.1
202443_x_at_HG-U133A	NOTCH2	Notch homolog 2 (Drosophila)	Consensus includes gb:AA291203 /FEA=EST /DB_XREF=gi:1939386 /DB_XREF=est:zt38h02.s1 /CLONE=IMAGE:724659 /UG=Hs.8121 Notch (Drosophila) homolog 2 /FL=gb:AF315356.1 gb:NM_024408.1
202477_s_at_HG-U133A	GCP2	gamma-tubulin complex protein 2	gb:NM_006659.1 /DEF=Homo sapiens gamma-tubulin complex protein 2 (GCP2), mRNA. /FEA=mRNA /GEN=GCP2 /PROD=gamma-tubulin complex protein 2 /DB_XREF=gi:5729839 /UG=Hs.13386 gamma-tubulin complex protein 2 /FL=gb:BC005011.1 gb:AF042379.1 gb:NM_006659.1
202479_s_at_HG-U133A	GS3955	GS3955 protein	gb:BC002637.1 /DEF=Homo sapiens, GS3955 protein, clone MGC:3860, mRNA, complete cds. /FEA=mRNA /PROD=GS3955 protein /DB_XREF=gi:12803604 /UG=Hs.155418 GS3955 protein /FL=gb:NM_021643.1 gb:BC002637.1 gb:D87119.1
202481_at_HG-U133A	SDR1	short-chain dehydrogenase/reductase 1	gb:NM_004753.1 /DEF=Homo sapiens short-chain dehydrogenasereductase 1 (SDR1), mRNA. /FEA=mRNA /GEN=SDR1 /PROD=short-chain dehydrogenasereductase 1 /DB_XREF=gi:4759083 /UG=Hs.17144 short-chain dehydrogenasereductase 1 /FL=gb:BC002730.1 gb:AF061741.1 gb:NM_004753.1
202503_s_at_HG-U133A	KIAA0101	KIAA0101 gene product	gb:NM_014736.1 /DEF=Homo sapiens KIAA0101 gene product (KIAA0101), mRNA. /FEA=mRNA /GEN=KIAA0101 /PROD=KIAA0101 gene product /DB_XREF=gi:7661905 /UG=Hs.81892 KIAA0101 gene product /FL=gb:D14657.1 gb:NM_014736.1
202519_at_HG-U133A	MONDOA	Mlx interactor	gb:NM_014938.1 /DEF=Homo sapiens KIAA0867 protein (MONDOA), mRNA. /FEA=mRNA /GEN=MONDOA /PROD=MondoA protein /DB_XREF=gi:7662347 /UG=Hs.52081 KIAA0867 protein /FL=gb:AB020674.1 gb:NM_014938.1
202524_s_at_HG-U133A	KIAA0275	KIAA0275 gene product	gb:NM_014767.1 /DEF=Homo sapiens KIAA0275 gene product (KIAA0275), mRNA. /FEA=mRNA /GEN=KIAA0275 /PROD=KIAA0275 gene product /DB_XREF=gi:7662035 /UG=Hs.74583 KIAA0275 gene product

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			/FL=gb:D87465.1 gb:NM_014767.1
202530_at_HG-U133A	MAPK14	mitogen-activated protein kinase 14	gb:NM_001315.1 /DEF=Homo sapiens mitogen-activated protein kinase 14 (MAPK14), mRNA. /FEA=mRNA /GEN=MAPK14 /PROD=mitogen-activated protein kinase 14 /DB_XREF=gi:4503068 /UG=Hs.79107 mitogen-activated protein kinase 14 /FL=gb:NM_001315.1 gb:L35263.1
202535_at_HG-U133A	FADD	Fas (TNFRSF6)-associated via death domain	gb:NM_003824.1 /DEF=Homo sapiens Fas (TNFRSF6)-associated via death domain (FADD), mRNA. /FEA=mRNA /GEN=FADD /PROD=Fas (TNFRSF6)-associated via death domain /DB_XREF=gi:4505228 /UG=Hs.86131 Fas (TNFRSF6)-associated via death domain /FL=gb:BC000334.1 gb:NM_003824.1 gb:U24231.1
202545_at_HG-U133A	PRKCD	protein kinase C, delta	gb:NM_006254.1 /DEF=Homo sapiens protein kinase C, delta (PRKCD), mRNA. /FEA=mRNA /GEN=PRKCD /PROD=protein kinase C, delta /DB_XREF=gi:5453969 /UG=Hs.155342 protein kinase C, delta /FL=gb:L07860.1 gb:L07861.1 gb:D10495.1 gb:NM_006254.1
202551_s_at_HG-U133A	CRIM1	cysteine-rich motor neuron 1	Consensus includes gb:BG546884 /FEA=EST /DB_XREF=gi:13545549 /DB_XREF=est:602574066F1 /CLONE=IMAGE:4702049 /UG=Hs.19280 cysteine-rich motor neuron 1 /FL=gb:NM_016441.1 gb:AF167706.1
202552_s_at_HG-U133A	CRIM1	cysteine-rich motor neuron 1	gb:NM_016441.1 /DEF=Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /FEA=mRNA /GEN=CRIM1 /PROD=cysteine-rich motor neuron 1 /DB_XREF=gi:10092638 /UG=Hs.19280 cysteine-rich motor neuron 1 /FL=gb:NM_016441.1 gb:AF167706.1
202572_s_at_HG-U133A	KIAA0964	KIAA0964 protein	gb:NM_014902.1 /DEF=Homo sapiens KIAA0964 protein (KIAA0964), mRNA. /FEA=mRNA /GEN=KIAA0964 /PROD=KIAA0964 protein /DB_XREF=gi:7662411 /UG=Hs.177425 KIAA0964 protein /FL=gb:AB023181.1 gb:NM_014902.1
202580_x_at_HG-U133A	FOXM1	forkhead box M1	gb:NM_021953.1 /DEF=Homo sapiens forkhead box M1 (FOXM1), mRNA. /FEA=mRNA /GEN=FOXM1 /PROD=forkhead box M1 /DB_XREF=gi:11386144 /UG=Hs.239 forkhead box M1 /FL=gb:NM_021953.1 gb:U83113.1 gb:L16783.1

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202589_at_HG-U133A	TYMS	thymidylate synthetase	gb:NM_001071.1 /DEF=Homo sapiens thymidylate synthetase (TYMS), mRNA. /FEA=mRNA /GEN=TYMS /PROD=thymidylate synthetase /DB_XREF=gi:4507750 /UG=Hs.82962 thymidylate synthetase /FL=gb:BC002567.1 gb:NM_001071.1
202600_s_at_HG-U133A	NRIP1	nuclear receptor interacting protein 1	Consensus includes gb:AI824012 /FEA=EST /DB_XREF=gi:5444683 /DB_XREF=est:wj29e06.x1 /CLONE=IMAGE:2404258 /UG=Hs.155017 nuclear receptor interacting protein 1 /FL=gb:NM_003489.1
202606_s_at_HG-U133A	TLK1	tousled-like kinase 1	gb:NM_012290.1 /DEF=Homo sapiens tousled-like kinase 1 (TLK1), mRNA. /FEA=mRNA /GEN=TLK1 /PROD=tousled-like kinase 1 /DB_XREF=gi:6912719 /UG=Hs.18895 tousled-like kinase 1 /FL=gb:AB004885.1 gb:NM_012290.1 gb:AF246219.1
202619_s_at_HG-U133A	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Consensus includes gb:AI754404 /FEA=EST /DB_XREF=gi:5132668 /DB_XREF=est:cr24g06.x1 /CLONE=HBMSC_cr24g06 /UG=Hs.41270 procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 /FL=gb:U84573.1 gb:NM_000935.1
202625_at_HG-U133A	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	Consensus includes gb:AI356412 /FEA=EST /DB_XREF=gi:4108033 /DB_XREF=est:qz26h02.x1 /CLONE=IMAGE:2028051 /UG=Hs.80887 v-yes-1 Yamaguchi sarcoma viral related oncogene homolog /FL=gb:NM_002350.1
202626_s_at_HG-U133A	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	gb:NM_002350.1 /DEF=Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA. /FEA=mRNA /GEN=LYN /PROD=v-yes-1 Yamaguchi sarcoma viral related oncogenehomolog /DB_XREF=gi:4505054 /UG=Hs.80887 v-yes-1 Yamaguchi sarcoma viral related oncogene homolog /FL=gb:NM_002350.1
202655_at_HG-U133A	ARMET	arginine-rich, mutated in early stage tumors	gb:NM_006010.1 /DEF=Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA. /FEA=mRNA /GEN=ARMET /PROD=arginine-rich protein /DB_XREF=gi:5174392 /UG=Hs.75412 arginine-rich, mutated in early stage tumors /FL=gb:M83751.1 gb:NM_006010.1
202705_at_HG-U133A	CCNB2	cyclin B2	gb:NM_004701.2 /DEF=Homo sapiens cyclin B2 (CCNB2), mRNA.

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			/FEA=mRNA /GEN=CCNB2 /PROD=cyclin B2 /DB_XREF=gi:10938017 /UG=Hs.194698 cyclin B2 /FL=gb:NM_004701.2 gb:AF002822.1 gb:AB020981.1 gb:AL080146.1
202709_at_HG-U133A	FMOD	fibromodulin	gb:NM_002023.2 /DEF=Homo sapiens fibromodulin (FMOD), mRNA. /FEA=mRNA /GEN=FMOD /PROD=fibromodulin precursor /DB_XREF=gi:5016093 /UG=Hs.230 fibromodulin /FL=gb:NM_002023.2
202718_at_HG-U133A	IGFBP2	insulin-like growth factor binding protein 2 (36kD)	gb:NM_000597.1 /DEF=Homo sapiens insulin-like growth factor binding protein 2 (36kD) (IGFBP2), mRNA. /FEA=mRNA /GEN=IGFBP2 /PROD=insulin-like growth factor binding protein 2(36kD) /DB_XREF=gi:10835156 /UG=Hs.162 insulin-like growth factor binding protein 2 (36kD) /FL=gb:NM_000597.1 gb:BC004312.1 gb:M35410.1
202723_s_at_HG-U133A	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	Consensus includes gb:AW117498 /FEA=EST /DB_XREF=gi:6086082 /DB_XREF=est:xd92e10.x1 /CLONE=IMAGE:2605098 /UG=Hs.170133 forkhead box O1A (rhabdomyosarcoma) /FL=gb:AF032885.1 gb:U02310.1 gb:NM_002015.2
202729_s_at_HG-U133A	LTBP1	latent transforming growth factor beta binding protein 1	gb:NM_000627.1 /DEF=Homo sapiens latent transforming growth factor beta binding protein 1 (LTBP1), mRNA. /FEA=mRNA /GEN=LTBP1 /PROD=latent transforming growth factor beta bindingprotein 1 precursor /DB_XREF=gi:4557730 /UG=Hs.241257 latent transforming growth factor beta binding protein 1 /FL=gb:M34057.1 gb:NM_000627.1
202746_at_HG-U133A			Consensus includes gb:AL021786 /DEF=Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs /FEA=mRNA /DB_XREF=gi:2853186 /UG=Hs.17109 integral membrane protein 2A /FL=gb:AF038953.1 gb:NM_004867.1
202747_s_at_HG-U133A	ITM2A	integral membrane protein 2A	gb:NM_004867.1 /DEF=Homo sapiens integral membrane protein 2A (ITM2A), mRNA. /FEA=mRNA /GEN=ITM2A /PROD=integral membrane protein 2A /DB_XREF=gi:4758223 /UG=Hs.17109 integral membrane protein 2A

			/FL=gb:AF038953.1 gb:NM_004867.1
202761_s_at_HG-U133A	SYNE-2	synaptic nuclei expressed gene 2	gb:NM_015180.1 /DEF=Homo sapiens synaptic nuclei expressed gene 2; KIAA1011 protein (KIAA1011), mRNA. /FEA=mRNA /GEN=KIAA1011 /PROD=KIAA1011 protein /DB_XREF=gi:11056019 /UG=Hs.57749 synaptic nuclei expressed gene 2; KIAA1011 protein /FL=gb:NM_015180.1 gb:AL080133.1
202819_s_at_HG-U133A	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A)	gb:NM_003198.1 /DEF=Homo sapiens transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A) (TCEB3), mRNA. /FEA=mRNA /GEN=TCEB3 /PROD=elongin A /DB_XREF=gi:4507388 /UG=Hs.155202 transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A) /FL=gb:BC002883.1 gb:NM_003198.1 gb:L47345.1
202822_at_HG-U133A	LPP	LIM domain containing preferred translocation partner in lipoma	Consensus includes gb:BF221852 /FEA=EST /DB_XREF=gi:11129029 /DB_XREF=est:7p37f11.x1 /CLONE=IMAGE:3648141 /UG=Hs.180398 LIM domain-containing preferred translocation partner in lipoma /FL=gb:NM_005578.1
202823_at_HG-U133A	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)	Consensus includes gb:N89607 /FEA=EST /DB_XREF=gi:1442934 /DB_XREF=est:zb08h02.s1 /CLONE=IMAGE:301491 /UG=Hs.184693 transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C) /FL=gb:NM_005648.1 gb:L34587.1
202853_s_at_HG-U133A	RYK	RYK receptor-like tyrosine kinase	gb:NM_002958.1 /DEF=Homo sapiens RYK receptor-like tyrosine kinase (RYK), mRNA. /FEA=mRNA /GEN=RYK /PROD=RYK receptor-like tyrosine kinase precursor /DB_XREF=gi:11863158 /UG=Hs.79350 RYK receptor-like tyrosine kinase /FL=gb:NM_002958.1
202862_at_HG-U133A	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	gb:NM_000137.1 /DEF=Homo sapiens fumarylacetoacetate (FAH), mRNA. /FEA=mRNA /GEN=FAH /PROD=fumarylacetoacetase /DB_XREF=gi:4557586 /UG=Hs.73875 fumarylacetoacetate /FL=gb:BC002527.1 gb:M55150.1 gb:NM_000137.1
202863_at_HG-U133A	SP100	nuclear antigen Sp100	gb:NM_003113.1 /DEF=Homo sapiens nuclear antigen Sp100 (SP100),

			mRNA. /FEA=mRNA /GEN=SP100 /PROD=nuclear antigen Sp100 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Sp100 /FL=gb:M60618.1 gb:NM_003113.1
202880_s_at_HG-U133A	PSCD1	pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1)	gb:NM_004762.1 /DEF=Homo sapiens pleckstrin homology, Sec7 and coiledcoil domains 1(cytohesin 1) (PSCD1), transcript variant 1, mRNA. /FEA=mRNA /GEN=PSCD1 /PROD=cytohesin 1, isoform 1 /DB_XREF=gi:4758963 /UG=Hs.1050 pleckstrin homology, Sec7 and coiledcoil domains 1(cytohesin 1) /FL=gb:M85169.1 gb:NM_004762.1 gb:NM_017456.1
202883_s_at_HG-U133A	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Consensus includes gb:T79584 /FEA=EST /DB_XREF=gi:698093 /DB_XREF=est:yd71a11.s1 /CLONE=IMAGE:113660 /UG=Hs.108705 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /FL=gb:NM_002716.1 gb:AF163473.1 gb:M65254.1 gb:AF087438.1
202926_at_HG-U133A	NAG	neuroblastoma-amplified protein	gb:NM_015909.1 /DEF=Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA. /FEA=mRNA /GEN=LOC51594 /PROD=neuroblastoma-amplified protein /DB_XREF=gi:7706239 /UG=Hs.15430 neuroblastoma-amplified protein /FL=gb:AF056195.1 gb:NM_015909.1
202944_at_HG-U133A	NAGA	N-acetylgalactosaminidase, alpha-	gb:NM_000262.1 /DEF=Homo sapiens N-acetylgalactosaminidase, alpha- (NAGA), mRNA. /FEA=mRNA /GEN=NAGA /PROD=alpha-N-acetylgalactosaminidase precursor /DB_XREF=gi:4557780 /UG=Hs.75372 N-acetylgalactosaminidase, alpha- /FL=gb:BC000095.1 gb:M62783.1 gb:M38083.1 gb:NM_000262.1
202945_at_HG-U133A	FPGS	folylpolyglutamate synthase	gb:NM_004957.1 /DEF=Homo sapiens folylpolyglutamate synthase (FPGS), mRNA. /FEA=mRNA /GEN=FPGS /PROD=folylpolyglutamate synthase /DB_XREF=gi:4826727 /UG=Hs.754 folylpolyglutamate synthase /FL=gb:M98045.1 gb:NM_004957.1
202956_at_HG-U133A	BIG1	brefeldin A-inhibited guanine nucleotide-exchange protein 1	gb:NM_006421.2 /DEF=Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA. /FEA=mRNA /GEN=BIG1 /PROD=brefeldin A-inhibited guaninenucleotide-exchange protein 1

			/DB_XREF=gi:6715588 /UG=Hs.94631 brefeldin A-inhibited guanine nucleotide-exchange protein 1 /FL=gb:AF084520.1 gb:AF111162.1 gb:NM_006421.2
202973_x_at_HG-U133A	KIAA0914	KIAA0914 gene product	gb:NM_014883.1 /DEF=Homo sapiens KIAA0914 gene product (KIAA0914), mRNA. /FEA=mRNA /GEN=KIAA0914 /PROD=KIAA0914 gene product /DB_XREF=gi:7662375 /UG=Hs.177664 KIAA0914 gene product /FL=gb:AB020721.1 gb:NM_014883.1
203005_at_HG-U133A	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	gb:NM_002342.1 /DEF=Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3 (LTBR), mRNA. /FEA=mRNA /GEN=LTBR /PROD=lymphotoxin B receptor /DB_XREF=gi:4505038 /UG=Hs.1116 lymphotoxin beta receptor (TNFR superfamily, member 3 /FL=gb:L04270.1 gb:NM_002342.1
203007_x_at_HG-U133A			gb:AF077198.1 /DEF=Homo sapiens lysophospholipase mRNA, complete cds. /FEA=mRNA /PROD=lysophospholipase /DB_XREF=gi:4679009 /UG=Hs.12540 lysophospholipase I /FL=gb:AF081281.1 gb:AF077198.1 gb:NM_006330.1 gb:AF291053.1
203020_at_HG-U133A	KIAA0471	KIAA0471 gene product	gb:NM_014857.1 /DEF=Homo sapiens KIAA0471 gene product (KIAA0471), mRNA. /FEA=mRNA /GEN=KIAA0471 /PROD=KIAA0471 gene product /DB_XREF=gi:7662143 /UG=Hs.242271 KIAA0471 gene product /FL=gb:AB007940.1 gb:NM_014857.1
203021_at_HG-U133A	SLPI	secretory leukocyte protease inhibitor (antileukoproteinase)	gb:NM_003064.1 /DEF=Homo sapiens secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA. /FEA=mRNA /GEN=SLPI /PROD=secretory leukocyte protease inhibitor(antileukoproteinase) /DB_XREF=gi:4507064 /UG=Hs.251754 secretory leukocyte protease inhibitor (antileukoproteinase) /FL=gb:NM_003066.1 gb:AF114471.1 gb:NM_003064.1
203026_at_HG-U133A	KIAA0354	KIAA0354 gene product	gb:NM_014872.1 /DEF=Homo sapiens KIAA0354 gene product (KIAA0354), mRNA. /FEA=mRNA /GEN=KIAA0354 /PROD=KIAA0354 gene product /DB_XREF=gi:7662073 /UG=Hs.3682 KIAA0354 gene product

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			/FL=gb:AB002352.1 gb:NM_014872.1
203037_s_at_HG-U133A	KIAA0429	KIAA0429 gene product	gb:NM_014751.1 /DEF=Homo sapiens KIAA0429 gene product (KIAA0429), mRNA. /FEA=mRNA /GEN=KIAA0429 /PROD=KIAA0429 gene product /DB_XREF=gi:7662113 /UG=Hs.77694 KIAA0429 gene product /FL=gb:AB007889.1 gb:NM_014751.1
203041_s_at_HG-U133A	LAMP2	lysosomal-associated membrane protein 2	gb:J04183.1 /DEF=Homo sapiens lysosomal membrane glycoprotein-2 (LAMP2), complete cds. /FEA=mRNA /GEN=LAMP2 /PROD=lysosomal membrane glycoprotein-2 /DB_XREF=gi:186929 /UG=Hs.8262 lysosomal-associated membrane protein 2 /FL=gb:J04183.1 gb:NM_002294.1
203053_at_HG-U133A	BCAS2	breast carcinoma amplified sequence 2	gb:NM_005872.1 /DEF=Homo sapiens breast carcinoma amplified sequence 2 (BCAS2), mRNA. /FEA=mRNA /GEN=BCAS2 /PROD=breast carcinoma amplified sequence 2 /DB_XREF=gi:5031652 /UG=Hs.22960 breast carcinoma amplified sequence 2 /FL=gb:BC005285.1 gb:AF081788.1 gb:AB020623.1 gb:NM_005872.1
203057_s_at_HG-U133A	PRDM2	PR domain containing 2, with ZNF domain	Consensus includes gb:AV724783 /FEA=EST /DB_XREF=gi:10829513 /DB_XREF=est:AV724783 /CLONE=HTBCEG11 /UG=Hs.26719 zinc-finger DNA-binding protein /FL=gb:D45132.1 gb:NM_015866.1
203074_at_HG-U133A	ANXA8	annexin A8	gb:NM_001630.1 /DEF=Homo sapiens annexin A8 (ANXA8), mRNA. /FEA=mRNA /GEN=ANXA8 /PROD=annexin VIII /DB_XREF=gi:4502112 /UG=Hs.87268 annexin A8 /FL=gb:BC004376.1 gb:M81844.1 gb:NM_001630.1
203092_at_HG-U133A	TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	gb:AF026030.1 /DEF=Homo sapiens putative mitochondrial inner membrane protein import receptor (hTIM44) mRNA, nuclear gene encoding mitochondrial protein, complete cds. /FEA=mRNA /GEN=hTIM44 /PROD=putative mitochondrial inner membrane proteinimport receptor /DB_XREF=gi:4103601 /UG=Hs.123178 translocase of inner mitochondrial membrane 44 (yeast) homolog /FL=gb:AF026030.1 gb:NM_006351.1
203104_at_HG-U133A	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral	gb:NM_005211.1 /DEF=Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog

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		(v-fms) oncogene homolog	(CSF1R), mRNA. /FEA=mRNA /GEN=CSF1R /PROD=colony stimulating factor 1 receptor, formerlyMcDonough feline sarcoma viral (v-fms) oncogene homolog /DB_XREF=gi:4885158 /UG=Hs.174142 colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog /FL=gb:NM_005211.1
203110_at_HG-U133A	PTK2B	protein tyrosine kinase 2 beta	gb:U43522.1 /DEF=Human cell adhesion kinase beta (CAKbeta) mRNA, complete cds. /FEA=mRNA /GEN=CAKbeta /PROD=cell adhesion kinase beta /DB_XREF=gi:1165218 /UG=Hs.20313 protein tyrosine kinase 2 beta /FL=gb:L49207.1 gb:U43522.1 gb:NM_004103.1 gb:U33284.1
203133_at_HG-U133A	SEC61B	protein translocation complex beta	gb:NM_006808.1 /DEF=Homo sapiens protein translocation complex beta (SEC61B), mRNA. /FEA=mRNA /GEN=SEC61B /PROD=protein translocation complex beta /DB_XREF=gi:5803164 /UG=Hs.77028 protein translocation complex beta /FL=gb:BC001734.1 gb:L25085.1 gb:NM_006808.1
203143_s_at_HG-U133A	KIAA0040	KIAA0040 gene product	Consensus includes gb:T79953 /FEA=EST /DB_XREF=gi:698462 /DB_XREF=est:yd85c11.s1 /CLONE=IMAGE:115028 /UG=Hs.158282 KIAA0040 gene product /FL=gb:D25539.1 gb:NM_014656.1
203177_x_at_HG-U133A	TFAM	transcription factor A, mitochondrial	gb:NM_003201.1 /DEF=Homo sapiens transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1), mRNA. /FEA=mRNA /GEN=TCF6L1 /PROD=transcription factor 6-like 1 (mitochondrialtranscription factor 1-like) /DB_XREF=gi:4507400 /UG=Hs.75133 transcription factor 6-like 1 (mitochondrial transcription factor 1-like) /FL=gb:M62810.1 gb:NM_003201.1
203188_at_HG-U133A	B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6	gb:NM_006876.1 /DEF=Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase (BETA3GNTI), mRNA. /FEA=mRNA /GEN=BETA3GNTI /PROD=i-beta-1,3-N-acetylglucosaminyltransferase /DB_XREF=gi:5802983 /UG=Hs.8526 i-beta-1,3-N-acetylglucosaminyltransferase /FL=gb:AF029893.1 gb:NM_006876.1
203217_s_at_HG-U133A	SIAT9	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-	gb:NM_003896.1 /DEF=Homo sapiens sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9),

		sialyltransferase; GM3 synthase)	mRNA. /FEA=mRNA /GEN=SIAT9 /PROD=sialyltransferase 9 (CMP-NeuAc:lactosylceramidealpha-2,3-sialyltransferase; GM3 synthase) /DB_XREF=gi:4506954 /UG=Hs.225939 sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /FL=gb:AB018356.1 gb:NM_003896.1 gb:AF119415.1
203233_at_HG-U133A	IL4R	interleukin 4 receptor	gb:NM_000418.1 /DEF=Homo sapiens interleukin 4 receptor (IL4R), mRNA. /FEA=mRNA /GEN=IL4R /PROD=interleukin 4 receptor precursor /DB_XREF=gi:4557668 /UG=Hs.75545 interleukin 4 receptor /FL=gb:NM_000418.1
203241_at_HG-U133A	UVRAG	UV radiation resistance associated gene	gb:NM_003369.1 /DEF=Homo sapiens UV radiation resistance associated gene (UVRAG), mRNA. /FEA=mRNA /GEN=UVRAG /PROD=UV radiation resistance associated gene /DB_XREF=gi:4507860 /UG=Hs.13137 UV radiation resistance associated gene /FL=gb:NM_003369.1 gb:AB012958.1
203288_at_HG-U133A	KIAA0355	KIAA0355 gene product	gb:NM_014686.1 /DEF=Homo sapiens KIAA0355 gene product (KIAA0355), mRNA. /FEA=mRNA /GEN=KIAA0355 /PROD=KIAA0355 gene product /DB_XREF=gi:7662075 /UG=Hs.186840 KIAA0355 gene product /FL=gb:AB002353.1 gb:NM_014686.1
203345_s_at_HG-U133A	M96	putative DNA binding protein	Consensus includes gb:AI566096 /FEA=EST /DB_XREF=gi:4524548 /DB_XREF=est:tn53d02.x1 /CLONE=IMAGE:2172099 /UG=Hs.31016 putative DNA binding protein /FL=gb:AF072814.1 gb:NM_007358.1
203355_s_at_HG-U133A	KIAA0942	KIAA0942 protein	gb:NM_015310.1 /DEF=Homo sapiens KIAA0942 protein (KIAA0942), mRNA. /FEA=mRNA /GEN=KIAA0942 /PROD=KIAA0942 protein /DB_XREF=gi:7662395 /UG=Hs.6763 KIAA0942 protein /FL=gb:AF243495.2 gb:NM_015310.1
203367_at_HG-U133A	DUSP14	dual specificity phosphatase 14	gb:NM_007026.1 /DEF=Homo sapiens MKP-1 like protein tyrosine phosphatase (MKP-L), mRNA. /FEA=mRNA /GEN=MKP-L /PROD=MKP-1 like protein tyrosine phosphatase /DB_XREF=gi:5902001 /UG=Hs.91448 MKP-1 like protein tyrosine phosphatase /FL=gb:BC000370.1 gb:BC001894.1

			gb:BC004448.1 gb:AF038844.1 gb:NM_007026.1 gb:AF120032.1
203370_s_at_HG-U133A	ENIGMA	enigma (LIM domain protein)	gb:NM_005451.2 /DEF=Homo sapiens enigma (LIM domain protein) (ENIGMA), mRNA. /FEA=mRNA /GEN=ENIGMA /PROD=enigma protein /DB_XREF=gi:11496884 /UG=Hs.102948 enigma (LIM domain protein) /FL=gb:NM_005451.2 gb:BC001093.1 gb:AF265209.1
203372_s_at_HG-U133A	STATI2	STAT induced STAT inhibitor-2	gb:AB004903.1 /DEF=Homo sapiens mRNA for STAT induced STAT inhibitor-2, complete cds. /FEA=mRNA /PROD=STAT induced STAT inhibitor-2 /DB_XREF=gi:2443360 /UG=Hs.110776 STAT induced STAT inhibitor-2 /FL=gb:AB004903.1 gb:AB006966.1 gb:AF037989.1 gb:AF020590.1 gb:NM_003877.1
203373_at_HG-U133A	STATI2	STAT induced STAT inhibitor-2	gb:NM_003877.1 /DEF=Homo sapiens STAT induced STAT inhibitor-2 (STATI2), mRNA. /FEA=mRNA /GEN=STATI2 /PROD=STAT induced STAT inhibitor-2 /DB_XREF=gi:4507262 /UG=Hs.110776 STAT induced STAT inhibitor-2 /FL=gb:AB004903.1 gb:AB006966.1 gb:AF037989.1 gb:AF020590.1 gb:NM_003877.1
203380_x_at_HG-U133A	SFRS5	splicing factor, arginine/serine-rich 5	gb:NM_006925.1 /DEF=Homo sapiens splicing factor, argininesserine-rich 5 (SFRS5), mRNA. /FEA=mRNA /GEN=SFRS5 /PROD=splicing factor, argininesserine-rich 5 /DB_XREF=gi:5902077 /UG=Hs.166975 splicing factor, argininesserine-rich 5 /FL=gb:U30827.1 gb:NM_006925.1
203385_at_HG-U133A	DGKA	diacylglycerol kinase, alpha (80kD)	gb:NM_001345.1 /DEF=Homo sapiens diacylglycerol kinase, alpha (80kD) (DGKA), mRNA. /FEA=mRNA /GEN=DGKA /PROD=diacylglycerol kinase, alpha (80kD) /DB_XREF=gi:11415023 /UG=Hs.172690 diacylglycerol kinase, alpha (80kD) /FL=gb:NM_001345.1 gb:AF064770.1
203386_at_HG-U133A	KIAA0603	KIAA0603 gene product	Consensus includes gb:AI650848 /FEA=EST /DB_XREF=gi:4734827 /DB_XREF=est:wa95d04.x1 /CLONE=IMAGE:2303911 /UG=Hs.173802 KIAA0603 gene product /FL=gb:AB011175.1 gb:NM_014832.1
203387_s_at_HG-U133A	KIAA0603	KIAA0603 gene product	gb:NM_014832.1 /DEF=Homo sapiens KIAA0603 gene product (KIAA0603), mRNA. /FEA=mRNA /GEN=KIAA0603 /PROD=KIAA0603 gene product

			/DB_XREF=gi:7662197 /UG=Hs.173802 KIAA0603 gene product /FL=gb:AB011175.1 gb:NM_014832.1
203394_s_at_HG-U133A	HRY	hairy homolog (Drosophila)	Consensus includes gb:BE973687 /FEA=EST /DB_XREF=gi:10587023 /DB_XREF=est:601680868F1 /CLONE=IMAGE:3951041 /UG=Hs.250666 hairy (Drosophila)-homolog /FL=gb:AF264785.1 gb:NM_005524.2
203535_at_HG-U133A	S100A9	S100 calcium binding protein A9 (calgranulin B)	gb:NM_002965.2 /DEF=Homo sapiens S100 calcium-binding protein A9 (calgranulin B) (S100A9), mRNA. /FEA=mRNA /GEN=S100A9 /PROD=S100 calcium-binding protein A9 /DB_XREF=gi:9845520 /UG=Hs.112405 S100 calcium-binding protein A9 (calgranulin B) /FL=gb:M26311.1 gb:NM_002965.2
203544_s_at_HG-U133A	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	gb:NM_003473.1 /DEF=Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA. /FEA=mRNA /GEN=STAM /PROD=signal transducing adaptor molecule (SH3 domainand ITAM motif) 1 /DB_XREF=gi:4507248 /UG=Hs.153487 signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 /FL=gb:U43899.1 gb:NM_003473.1
203556_at_HG-U133A	KIAA0854	KIAA0854 protein	gb:NM_014943.1 /DEF=Homo sapiens KIAA0854 protein (KIAA0854), mRNA. /FEA=mRNA /GEN=KIAA0854 /PROD=KIAA0854 protein /DB_XREF=gi:7662341 /UG=Hs.30209 KIAA0854 protein /FL=gb:AB020661.1 gb:NM_014943.1
203593_at_HG-U133A	CD2AP	CD2-associated protein	gb:NM_012120.1 /DEF=Homo sapiens CD2-associated protein (CD2AP), mRNA. /FEA=mRNA /GEN=CD2AP /PROD=CD2-associated protein /DB_XREF=gi:11321633 /UG=Hs.265561 CD2-associated protein /FL=gb:NM_012120.1 gb:AF146277.1 gb:AF164377.1
203602_s_at_HG-U133A	ZNF151	zinc finger protein 151 (pHZ-67)	gb:NM_003443.1 /DEF=Homo sapiens zinc finger protein 151 (pHZ-67) (ZNF151), mRNA. /FEA=mRNA /GEN=ZNF151 /PROD=zinc finger protein 151 (pHZ-67) /DB_XREF=gi:4507996 /UG=Hs.33532 zinc finger protein 151 (pHZ-67) /FL=gb:NM_003443.1
203607_at_HG-U133A	SAC2	Sac domain-containing inositol phosphatase 2	gb:NM_014937.1 /DEF=Homo sapiens KIAA0966 protein (KIAA0966), mRNA. /FEA=mRNA /GEN=KIAA0966 /PROD=KIAA0966 protein

			/DB_XREF=gi:7662413 /UG=Hs.52463 KIAA0966 protein /FL=gb:AF113227.1 gb:AB023183.1 gb:NM_014937.1
203645_s_at_HG-U133A	CD163	CD163 antigen	gb:NM_004244.1 /DEF=Homo sapiens CD163 antigen (CD163), mRNA. /FEA=mRNA /GEN=CD163 /PROD=CD163 antigen /DB_XREF=gi:4758721 /UG=Hs.74076 CD163 antigen /FL=gb:NM_004244.1
203679_at_HG-U133A	IL1RL1LG	putative T1/ST2 receptor binding protein	gb:NM_006858.1 /DEF=Homo sapiens putative T1ST2 receptor binding protein (IL1RL1LG), mRNA. /FEA=mRNA /GEN=IL1RL1LG /PROD=putative T1ST2 receptor binding protein /DB_XREF=gi:5803039 /UG=Hs.54411 putative T1ST2 receptor binding protein /FL=gb:U41804.1 gb:BC002443.1 gb:NM_006858.1
203685_at_HG-U133A	BCL2	B-cell CLL/lymphoma 2	gb:NM_000633.1 /DEF=Homo sapiens B-cell CLLlymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha, mRNA. /FEA=mRNA /GEN=BCL2 /PROD=B-cell lymphoma protein 2 alpha /DB_XREF=gi:4557354 /UG=Hs.79241 B-cell CLLlymphoma 2 /FL=gb:M13994.1 gb:NM_000633.1
203725_at_HG-U133A	GADD45A	growth arrest and DNA-damage-inducible, alpha	gb:NM_001924.2 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA. /FEA=mRNA /GEN=GADD45A /PROD=growth arrest and DNA-damage-inducible, alpha /DB_XREF=gi:9790904 /UG=Hs.80409 growth arrest and DNA-damage-inducible, alpha /FL=gb:M60974.1 gb:NM_001924.2
203729_at_HG-U133A	EMP3	epithelial membrane protein 3	gb:NM_001425.1 /DEF=Homo sapiens epithelial membrane protein 3 (EMP3), mRNA. /FEA=mRNA /GEN=EMP3 /PROD=epithelial membrane protein 3 /DB_XREF=gi:4503562 /UG=Hs.9999 epithelial membrane protein 3 /FL=gb:U52101.1 gb:U87947.1 gb:NM_001425.1
203731_s_at_HG-U133A	ZFP95	zinc finger protein 95 homolog (mouse)	gb:NM_014569.1 /DEF=Homo sapiens zinc finger protein homologous to Zfp95 in mouse (ZFP95), mRNA. /FEA=mRNA /GEN=ZFP95 /PROD=zinc finger protein homologous to Zfp95 inmouse /DB_XREF=gi:11036641 /UG=Hs.110839 zinc finger protein homologous to Zfp95 in mouse

			/FL=gb:NM_014569.1 gb:AB023232.1
203753_at_HG-U133A	TCF4	transcription factor 4	gb:NM_003199.1 /DEF=Homo sapiens transcription factor 4 (TCF4), mRNA. /FEA=mRNA /GEN=TCF4 /PROD=transcription factor 4, isoform b /DB_XREF=gi:4507398 /UG=Hs.326198 transcription factor 4 /FL=gb:M74719.1 gb:NM_003199.1
203757_s_at_HG-U133A	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	gb:BC005008.1 /DEF=Homo sapiens, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds. /FEA=mRNA /PROD=carcinoembryonic antigen-related cell adhesionmolecule 6 (non-specific cross reacting antigen) /DB_XREF=gi:13477106 /UG=Hs.73848 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /FL=gb:BC005008.1 gb:M18216.1 gb:M29541.1 gb:NM_002483.1
203787_at_HG-U133A	SSBP2	single-stranded DNA binding protein 2	gb:NM_012446.1 /DEF=Homo sapiens single-stranded-DNA-binding protein (SSBP2), mRNA. /FEA=mRNA /GEN=SSBP2 /PROD=single-stranded-DNA-binding protein /DB_XREF=gi:7106422 /UG=Hs.169833 single-stranded-DNA-binding protein /FL=gb:AL080076.1 gb:AF161465.1 gb:NM_012446.1
203795_s_at_HG-U133A	BCL7A	B-cell CLL/lymphoma 7A	gb:NM_020993.1 /DEF=Homo sapiens B-cell CLLlymphoma 7A (BCL7A), mRNA. /FEA=mRNA /GEN=BCL7A /PROD=B-cell CLLlymphoma 7A /DB_XREF=gi:10337612 /UG=Hs.211563 B-cell CLLlymphoma 7A /FL=gb:NM_020993.1
203796_s_at_HG-U133A	BCL7A	B-cell CLL/lymphoma 7A	Consensus includes gb:AI950380 /FEA=EST /DB_XREF=gi:5742690 /DB_XREF=est:wp10g03.x1 /CLONE=IMAGE:2464468 /UG=Hs.211563 B-cell CLLlymphoma 7A /FL=gb:NM_020993.1
203808_at_HG-U133A	AKT2	v-akt murine thymoma viral oncogene homolog 2	Consensus includes gb:M95936.1 /DEF=Human protein-serinethreonine (AKT2) mRNA, complete cds. /FEA=mRNA /GEN=AKT2 /PROD=protein serinethreonine kinase /DB_XREF=gi:178325 /UG=Hs.326445 v-akt murine thymoma viral oncogene homolog 2 /FL=gb:M95936.1 gb:NM_001626.2
203818_s_at_HG-	SF3A3	splicing factor 3a, subunit 3, 60kD	gb:NM_006802.1 /DEF=Homo sapiens splicing factor 3a, subunit 3, 60kD

U133A			(SF3A3), mRNA. /FEA=mRNA /GEN=SF3A3 /PROD=splicing factor 3a, subunit 3, 60kD /DB_XREF=gi:5803166 /UG=Hs.77897 splicing factor 3a, subunit 3, 60kD /FL=gb:BC002395.1 gb:U08815.1 gb:NM_006802.1
203857_s_at_HG-U133A	PDIR	for protein disulfide isomerase-related	gb:NM_006810.1 /DEF=Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA. /FEA=mRNA /GEN=PDIR /PROD=for protein disulfide isomerase-related /DB_XREF=gi:5803120 /UG=Hs.76901 for protein disulfide isomerase-related /FL=gb:D49490.1 gb:NM_006810.1
203859_s_at_HG-U133A	PALM	paralemmin	gb:NM_002579.1 /DEF=Homo sapiens paralemmin (PALM), mRNA. /FEA=mRNA /GEN=PALM /PROD=paralemmin /DB_XREF=gi:4557041 /UG=Hs.78482 paralemmin /FL=gb:NM_002579.1
203881_s_at_HG-U133A	DMD	dystrophin (muscular dystrophy, Duchenne and Becker types)	gb:NM_004010.1 /DEF=Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427p2, mRNA. /FEA=mRNA /GEN=DMD /PROD=dystrophin Dp427p2 isoform /DB_XREF=gi:5032314 /UG=Hs.169470 dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 /FL=gb:NM_004010.1
203897_at_HG-U133A	LOC57149	hypothetical protein A-211C6.1	Consensus includes gb:BE963444 /FEA=EST /DB_XREF=gi:11766863 /DB_XREF=est:601657224R1 /CLONE=IMAGE:3866357 /UG=Hs.28607 hypothetical protein A-211C6.1 /FL=gb:NM_020424.1
203904_x_at_HG-U133A	KAI1	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	gb:NM_002231.2 /DEF=Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1), mRNA. /FEA=mRNA /GEN=KAI1 /PROD=kangai 1 /DB_XREF=gi:13259537 /UG=Hs.323949 kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) /FL=gb:BC000726.1 gb:BC001821.1 gb:NM_002231.2 gb:U20770.1

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203910_at_HG-U133A	PARG1	PTPL1-associated RhoGAP 1	gb:NM_004815.1 /DEF=Homo sapiens PTPL1-associated RhoGAP 1 (PARG1), mRNA. /FEA=mRNA /GEN=PARG1 /PROD=PTPL1-associated RhoGAP 1 /DB_XREF=gi:4758881 /UG=Hs.70983 PTPL1-associated RhoGAP 1 /FL=gb:U90920.1 gb:NM_004815.1
203932_at_HG-U133A	HLA-DMB	major histocompatibility complex, class II, DM beta	gb:NM_002118.1 /DEF=Homo sapiens major histocompatibility complex, class II, DM beta (HLA-DMB), mRNA. /FEA=mRNA /GEN=HLA-DMB /PROD=major histocompatibility complex, class II, DMbeta /DB_XREF=gi:4504398 /UG=Hs.1162 major histocompatibility complex, class II, DM beta /FL=gb:NM_002118.1 gb:U15085.1
203936_s_at_HG-U133A	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	gb:NM_004994.1 /DEF=Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA. /FEA=mRNA /GEN=MMP9 /PROD=matrix metalloproteinase 9 preproprotein /DB_XREF=gi:4826835 /UG=Hs.151738 matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) /FL=gb:J05070.1 gb:NM_004994.1
203939_at_HG-U133A	NT5E	5'-nucleotidase, ecto (CD73)	gb:NM_002526.1 /DEF=Homo sapiens 5 nucleotidase (CD73) (NT5), mRNA. /FEA=mRNA /GEN=NT5 /PROD=5 nucleotidase /DB_XREF=gi:4505466 /UG=Hs.153952 5 nucleotidase (CD73) /FL=gb:NM_002526.1
203948_s_at_HG-U133A	MPO	myeloperoxidase	gb:J02694.1 /DEF=Human myeloperoxidase mRNA, complete cds. /FEA=mRNA /GEN=MPO /PROD=myeloperoxidase /DB_XREF=gi:189039 /UG=Hs.1817 myeloperoxidase /FL=gb:M19507.1 gb:J02694.1 gb:NM_000250.1
203949_at_HG-U133A	MPO	myeloperoxidase	gb:NM_000250.1 /DEF=Homo sapiens myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MPO /PROD=myeloperoxidase /DB_XREF=gi:4557758 /UG=Hs.1817 myeloperoxidase /FL=gb:M19507.1 gb:J02694.1 gb:NM_000250.1
203973_s_at_HG-U133A	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	gb:NM_005195.1 /DEF=Homo sapiens CCAATenhancer binding protein (CEBP), delta (CEBPD), mRNA. /FEA=mRNA /GEN=CEBPD

			/PROD=CCAATenhancer binding protein (CEBP), delta /DB_XREF=gi:4885130 /UG=Hs.76722 CCAATenhancer binding protein (CEBP), delta /FL=gb:M83667.1 gb:NM_005195.1
204000_at_HG-U133A	GNB5	guanine nucleotide binding protein (G protein), beta 5	gb:NM_016194.1 /DEF=Homo sapiens hypothetical protein (DKFZp586O1922), mRNA. /FEA=mRNA /GEN=DKFZp586O1922 /PROD=hypothetical protein /DB_XREF=gi:7705366 /UG=Hs.155090 hypothetical protein /FL=gb:AL117471.1 gb:NM_016194.1
204030_s_at_HG-U133A	SCHIP1	schwannomin interacting protein 1	gb:NM_014575.1 /DEF=Homo sapiens schwannomin interacting protein 1 (SCHIP-1), mRNA. /FEA=mRNA /GEN=SCHIP-1 /PROD=schwannomin interacting protein 1 /DB_XREF=gi:7657539 /UG=Hs.61490 schwannomin interacting protein 1 /FL=gb:AF145713.1 gb:NM_014575.1
204044_at_HG-U133A	QPRT	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	gb:NM_014298.2 /DEF=Homo sapiens quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating)) (QPRT), mRNA. /FEA=mRNA /GEN=QPRT /PROD=quinolinate phosphoribosyltransferase /DB_XREF=gi:9257236 /UG=Hs.8935 quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating)) /FL=gb:D78177.1 gb:BC005060.1 gb:NM_014298.2
204057_at_HG-U133A	ICSBP1	interferon consensus sequence binding protein 1	Consensus includes gb:AI073984 /FEA=EST /DB_XREF=gi:3400628 /DB_XREF=est:oy66c05.x1 /CLONE=IMAGE:1670792 /UG=Hs.14453 interferon consensus sequence binding protein 1 /FL=gb:M91196.1 gb:NM_002163.1
204069_at_HG-U133A	MEIS1	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)	gb:NM_002398.1 /DEF=Homo sapiens Meis1 (mouse) homolog (MEIS1), mRNA. /FEA=mRNA /GEN=MEIS1 /PROD=Meis1 homolog /DB_XREF=gi:4505150 /UG=Hs.170177 Meis1 (mouse) homolog /FL=gb:U85707.1 gb:NM_002398.1
204075_s_at_HG-U133A	KIAA0562	KIAA0562 gene product	gb:NM_014704.1 /DEF=Homo sapiens KIAA0562 gene product (KIAA0562), mRNA. /FEA=mRNA /GEN=KIAA0562 /PROD=KIAA0562 gene product /DB_XREF=gi:7662179 /UG=Hs.200595 KIAA0562 gene product /FL=gb:AB011134.1 gb:NM_014704.1

204082_at_HG-U133A	PBX3	pre-B-cell leukemia transcription factor 3	gb:NM_006195.1 /DEF=Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /FEA=mRNA /GEN=PBX3 /PROD=pre-B-cell leukemia transcription factor 3 /DB_XREF=gi:5453851 /UG=Hs.294101 pre-B-cell leukemia transcription factor 3 /FL=gb:NM_006195.1
204101_at_HG-U133A	MTM1	myotubular myopathy 1	gb:NM_000252.1 /DEF=Homo sapiens myotubular myopathy 1 (MTM1), mRNA. /FEA=mRNA /GEN=MTM1 /PROD=myotubularin /DB_XREF=gi:4557895 /UG=Hs.75302 myotubular myopathy 1 /FL=gb:U46024.1 gb:NM_000252.1
204112_s_at_HG-U133A	HNMT	histamine N-methyltransferase	gb:NM_006895.1 /DEF=Homo sapiens histamine N-methyltransferase (HNMT), mRNA. /FEA=mRNA /GEN=HNMT /PROD=histamine N-methyltransferase /DB_XREF=gi:5901969 /UG=Hs.81182 histamine N-methyltransferase /FL=gb:U08092.1 gb:D16224.1 gb:NM_006895.1
204116_at_HG-U133A	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	gb:NM_000206.1 /DEF=Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA. /FEA=mRNA /GEN=IL2RG /PROD=interleukin 2 receptor, gamma chain, precursor /DB_XREF=gi:4557881 /UG=Hs.84 interleukin 2 receptor, gamma (severe combined immunodeficiency) /FL=gb:NM_000206.1
204118_at_HG-U133A	CD48	CD48 antigen (B-cell membrane protein)	gb:NM_001778.1 /DEF=Homo sapiens CD48 antigen (B-cell membrane protein) (CD48), mRNA. /FEA=mRNA /GEN=CD48 /PROD=CD48 antigen (B-cell membrane protein) /DB_XREF=gi:4502674 /UG=Hs.901 CD48 antigen (B-cell membrane protein) /FL=gb:M59904.1 gb:M37766.1 gb:NM_001778.1
204150_at_HG-U133A	STAB1	stabilin 1	gb:NM_015136.1 /DEF=Homo sapiens KIAA0246 protein (KIAA0246), mRNA. /FEA=mRNA /GEN=KIAA0246 /PROD=KIAA0246 protein /DB_XREF=gi:12225239 /UG=Hs.301989 KIAA0246 protein /FL=gb:NM_015136.1
204163_at_HG-U133A	EMILIN	elastin microfibril interface located protein	gb:NM_007046.1 /DEF=Homo sapiens elastin microfibril interface located protein (EMILIN), mRNA. /FEA=mRNA /GEN=EMILIN /PROD=elastin microfibril interface located protein /DB_XREF=gi:5901943 /UG=Hs.63348

			elastin microfibril interface located protein /FL=gb:AF088916.1 gb:NM_007046.1
204174_at_HG-U133A	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	gb:NM_001629.1 /DEF=Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA. /FEA=mRNA /GEN=ALOX5AP /PROD=arachidonate 5-lipoxygenase-activating protein /DB_XREF=gi:4502058 /UG=Hs.100194 arachidonate 5-lipoxygenase-activating protein /FL=gb:NM_001629.1
204192_at_HG-U133A	CD37	CD37 antigen	gb:NM_001774.1 /DEF=Homo sapiens CD37 antigen (CD37), mRNA. /FEA=mRNA /GEN=CD37 /PROD=CD37 antigen /DB_XREF=gi:4502662 /UG=Hs.153053 CD37 antigen /FL=gb:NM_001774.1
204199_at_HG-U133A	RALGPS1A	Ral guanine nucleotide exchange factor RalGPS1A	gb:NM_014636.1 /DEF=Homo sapiens Ral guanine nucleotide exchange factor RalGPS1A (RalGPS1A), mRNA. /FEA=mRNA /GEN=RalGPS1A /PROD=Ral guanine nucleotide exchange factor RalGPS1A /DB_XREF=gi:7662069 /UG=Hs.170307 Ral guanine nucleotide exchange factor RalGPS1A /FL=gb:AB002349.1 gb:NM_014636.1
204205_at_HG-U133A	MDS019	phorbolin-like protein MDS019	gb:NM_021822.1 /DEF=Homo sapiens phorbolin-like protein MDS019 (MDS019), mRNA. /FEA=mRNA /GEN=MDS019 /PROD=phorbolin-like protein MDS019 /DB_XREF=gi:13399303 /UG=Hs.250619 phorbolin-like protein MDS019 /FL=gb:AF182420.1 gb:NM_021822.1
204208_at_HG-U133A	RNGTT	RNA guanylyltransferase and 5'-phosphatase	gb:NM_003800.1 /DEF=Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), mRNA. /FEA=mRNA /GEN=RNGTT /PROD=RNA guanylyltransferase and 5-phosphatase /DB_XREF=gi:4506562 /UG=Hs.27345 RNA guanylyltransferase and 5-phosphatase /FL=gb:AF025654.1 gb:AB012142.1 gb:AB009022.1 gb:NM_003800.1
204214_s_at_HG-U133A	RAB32	RAB32, member RAS oncogene family	gb:NM_006834.1 /DEF=Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA. /FEA=mRNA /GEN=RAB32 /PROD=RAB32, member RAS oncogene family /DB_XREF=gi:5803132 /UG=Hs.32217 RAB32, member RAS oncogene family /FL=gb:U71127.1 gb:NM_006834.1

204215_at_HG-U133A	MGC4175	hypothetical protein MGC4175	gb:NM_024315.1 /DEF=Homo sapiens hypothetical protein MGC4175 (MGC4175), mRNA. /FEA=mRNA /GEN=MGC4175 /PROD=hypothetical protein MGC4175 /DB_XREF=gi:13236556 /UG=Hs.322404 hypothetical protein MGC4175 /FL=gb:BC002837.1 gb:NM_024315.1
204225_at_HG-U133A	HDAC4	histone deacetylase 4	gb:NM_006037.2 /DEF=Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /FEA=mRNA /GEN=HDAC4 /PROD=histone deacetylase 4 /DB_XREF=gi:13259519 /UG=Hs.91400 histone deacetylase 4 /FL=gb:NM_006037.2 gb:AF132607.1
204227_s_at_HG-U133A	TK2	thymidine kinase 2, mitochondrial	gb:NM_004614.1 /DEF=Homo sapiens thymidine kinase 2, mitochondrial (TK2), mRNA. /FEA=mRNA /GEN=TK2 /PROD=thymidine kinase 2, mitochondrial /DB_XREF=gi:10281329 /UG=Hs.274701 thymidine kinase 2, mitochondrial /FL=gb:NM_004614.1 gb:U77088.1
204249_s_at_HG-U133A	LMO2	LIM domain only 2 (rhombotin-like 1)	gb:NM_005574.2 /DEF=Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), mRNA. /FEA=mRNA /GEN=LMO2 /PROD=LIM domain only 2 /DB_XREF=gi:6633806 /UG=Hs.184585 LIM domain only 2 (rhombotin-like 1) /FL=gb:NM_005574.2
204269_at_HG-U133A	PIM2	pim-2 oncogene	gb:NM_006875.1 /DEF=Homo sapiens pim-2 oncogene (PIM2), mRNA. /FEA=mRNA /GEN=PIM2 /PROD=pim-2 oncogene /DB_XREF=gi:5803124 /UG=Hs.80205 pim-2 oncogene /FL=gb:U77735.1 gb:NM_006875.1
204285_s_at_HG-U133A	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	Consensus includes gb:AI857639 /FEA=EST /DB_XREF=gi:5511255 /DB_XREF=est:wk95g09.x1 /CLONE=IMAGE:2423200 /UG=Hs.96 phorbol-12-myristate-13-acetate-induced protein 1 /FL=gb:NM_021127.1
204306_s_at_HG-U133A	CD151	CD151 antigen	gb:NM_004357.1 /DEF=Homo sapiens CD151 antigen (CD151), mRNA. /FEA=mRNA /GEN=CD151 /PROD=CD151 antigen /DB_XREF=gi:4757941 /UG=Hs.75564 CD151 antigen /FL=gb:BC001374.1 gb:D29963.1 gb:NM_004357.1 gb:U14650.1
204319_s_at_HG-U133A	RGS10	regulator of G-protein signalling 10	gb:NM_002925.2 /DEF=Homo sapiens regulator of G-protein signalling 10 (RGS10), mRNA. /FEA=mRNA /GEN=RGS10 /PROD=regulator of G-protein

			signaling 10 /DB_XREF=gi:11184225 /UG=Hs.82280 regulator of G-protein signalling 10 /FL=gb:NM_002925.2 gb:AF045229.1
204328_at_HG-U133A	LAK-4P	expressed in activated T/LAK lymphocytes	gb:NM_007267.2 /DEF=Homo sapiens expressed in activated TLAK lymphocytes (LAK-4P), mRNA. /FEA=mRNA /GEN=LAK-4P /PROD=expressed in activated TLAK lymphocytes /DB_XREF=gi:7305226 /UG=Hs.16165 expressed in activated TLAK lymphocytes /FL=gb:AB002405.2 gb:NM_007267.2
204348_s_at_HG-U133A	AK3	adenylate kinase 3	gb:NM_013410.1 /DEF=Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=AK3 /PROD=adenylate kinase 3 /DB_XREF=gi:8051578 /UG=Hs.274691 adenylate kinase 3 /FL=gb:NM_013410.1
204351_at_HG-U133A	S100P	S100 calcium binding protein P	gb:NM_005980.1 /DEF=Homo sapiens S100 calcium-binding protein P (S100P), mRNA. /FEA=mRNA /GEN=S100P /PROD=S100 calcium-binding protein P /DB_XREF=gi:5174662 /UG=Hs.2962 S100 calcium-binding protein P /FL=gb:NM_005980.1
204352_at_HG-U133A	TRAF5	TNF receptor-associated factor 5	gb:NM_004619.1 /DEF=Homo sapiens TNF receptor-associated factor 5 (TRAF5), mRNA. /FEA=mRNA /GEN=TRAF5 /PROD=TNF receptor-associated factor 5 /DB_XREF=gi:11321602 /UG=Hs.29736 TNF receptor-associated factor 5 /FL=gb:NM_004619.1 gb:AB000509.1
204401_at_HG-U133A	KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	gb:NM_002250.1 /DEF=Homo sapiens potassium intermediatesmall conductance calcium-activated channel, subfamily N, member 4 (KCNN4), mRNA. /FEA=mRNA /GEN=KCNN4 /PROD=potassium intermediatesmall conductancecalcium-activated channel, subfamily N, member 4 /DB_XREF=gi:4504858 /UG=Hs.10082 potassium intermediatesmall conductance calcium-activated channel, subfamily N, member 4 /FL=gb:AF000972.1 gb:AF033021.1 gb:AF022150.1 gb:AF022797.1 gb:NM_002250.1
204422_s_at_HG-	FGF2	fibroblast growth factor 2 (basic)	gb:NM_002006.1 /DEF=Homo sapiens fibroblast growth factor 2 (basic)

U133A			(FGF2), mRNA. /FEA=mRNA /GEN=FGF2 /PROD=fibroblast growth factor 2 (basic) /DB_XREF=gi:4503698 /UG=Hs.284244 fibroblast growth factor 2 (basic) /FL=gb:M27968.1 gb:NM_002006.1
204425_at_HG-U133A	ARHGAP4	Rho GTPase activating protein 4	gb:NM_001666.1 /DEF=Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA. /FEA=mRNA /GEN=ARHGAP4 /PROD=Rho GTPase activating protein 4 /DB_XREF=gi:11386132 /UG=Hs.3109 Rho GTPase activating protein 4 /FL=gb:NM_001666.1
204446_s_at_HG-U133A	ALOX5	arachidonate 5-lipoxygenase	gb:NM_000698.1 /DEF=Homo sapiens arachidonate 5-lipoxygenase (ALOX5), mRNA. /FEA=mRNA /GEN=ALOX5 /PROD=arachidonate 5-lipoxygenase /DB_XREF=gi:4502056 /UG=Hs.89499 arachidonate 5-lipoxygenase /FL=gb:J03600.1 gb:J03571.1 gb:NM_000698.1
204484_at_HG-U133A	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	gb:NM_002646.1 /DEF=Homo sapiens phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B), mRNA. /FEA=mRNA /GEN=PIK3C2B /PROD=phosphoinositide-3-kinase, class 2, betapolypeptide /DB_XREF=gi:11136637 /UG=Hs.132463 phosphoinositide-3-kinase, class 2, beta polypeptide /FL=gb:NM_002646.1
204495_s_at_HG-U133A	DKFZP434H132	DKFZP434H132 protein	gb:NM_015492.1 /DEF=Homo sapiens DKFZP434H132 protein (DKFZP434H132), mRNA. /FEA=mRNA /GEN=DKFZP434H132 /PROD=DKFZP434H132 protein /DB_XREF=gi:7661575 /UG=Hs.17936 DKFZP434H132 protein /FL=gb:BC000540.1 gb:NM_015492.1
204501_at_HG-U133A	NOV	nephroblastoma overexpressed gene	gb:NM_002514.1 /DEF=Homo sapiens nephroblastoma overexpressed gene (NOV), mRNA. /FEA=mRNA /GEN=NOV /PROD=nephroblastoma overexpressed gene /DB_XREF=gi:4505422 /UG=Hs.235935 nephroblastoma overexpressed gene /FL=gb:NM_002514.1
204511_at_HG-U133A	KIAA0793	KIAA0793 gene product	gb:NM_014808.1 /DEF=Homo sapiens KIAA0793 gene product (KIAA0793), mRNA. /FEA=mRNA /GEN=KIAA0793 /PROD=KIAA0793 gene product /DB_XREF=gi:7662309 /UG=Hs.301283 KIAA0793 gene product /FL=gb:AB018336.1 gb:NM_014808.1

204512_at_HG-U133A	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	gb:NM_002114.1 /DEF=Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA. /FEA=mRNA /GEN=HIVEP1 /PROD=human immunodeficiency virus type lenhancer-binding protein 1 /DB_XREF=gi:4504388 /UG=Hs.306 human immunodeficiency virus type I enhancer-binding protein 1 /FL=gb:M32019.1 gb:NM_002114.1
204562_at_HG-U133A	IRF4	interferon regulatory factor 4	gb:NM_002460.1 /DEF=Homo sapiens interferon regulatory factor 4 (IRF4), mRNA. /FEA=mRNA /GEN=IRF4 /PROD=interferon regulatory factor 4 /DB_XREF=gi:4505286 /UG=Hs.82132 interferon regulatory factor 4 /FL=gb:U52682.1 gb:NM_002460.1
204563_at_HG-U133A	SELL	selectin L (lymphocyte adhesion molecule 1)	gb:NM_000655.2 /DEF=Homo sapiens selectin L (lymphocyte adhesion molecule 1) (SELL), mRNA. /FEA=mRNA /GEN=SELL /PROD=selectin L /DB_XREF=gi:5713320 /UG=Hs.82848 selectin L (lymphocyte adhesion molecule 1) /FL=gb:M25280.1 gb:NM_000655.2
204604_at_HG-U133A	PFTK1	PFTAIRE protein kinase 1	gb:NM_012395.1 /DEF=Homo sapiens PFTAIRE protein kinase 1 (PFTK1), mRNA. /FEA=mRNA /GEN=PFTK1 /PROD=PFTAIRE protein kinase 1 /DB_XREF=gi:6912583 /UG=Hs.57856 PFTAIRE protein kinase 1 /FL=gb:AB020641.1 gb:NM_012395.1
204638_at_HG-U133A	ACP5	acid phosphatase 5, tartrate resistant	gb:NM_001611.2 /DEF=Homo sapiens acid phosphatase 5, tartrate resistant (ACP5), mRNA. /FEA=mRNA /GEN=ACP5 /PROD=tartrate resistant acid phosphatase 5 precursor /DB_XREF=gi:6138970 /UG=Hs.1211 acid phosphatase 5, tartrate resistant /FL=gb:J04430.1 gb:NM_001611.2
204647_at_HG-U133A	HOMER-3	Homer, neuronal immediate early gene, 3	gb:NM_004838.1 /DEF=Homo sapiens Homer, neuronal immediate early gene, 3 (HOMER-3), mRNA. /FEA=mRNA /GEN=HOMER-3 /PROD=Homer, neuronal immediate early gene, 3 /DB_XREF=gi:4758549 /UG=Hs.166146 Homer, neuronal immediate early gene, 3 /FL=gb:AF093265.1 gb:NM_004838.1
204661_at_HG-U133A	CDW52	CDW52 antigen (CAMPATH-1 antigen)	gb:NM_001803.1 /DEF=Homo sapiens CDW52 antigen (CAMPATH-1 antigen) (CDW52), mRNA. /FEA=mRNA /GEN=CDW52 /PROD=CDW52 antigen

			(CAMPATH-1 antigen) /DB_XREF=gi:4502760 /UG=Hs.276770 CDW52 antigen (CAMPATH-1 antigen) /FL=gb:BC000644.1 gb:NM_001803.1
204663_at_HG-U133A	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	gb:NM_006680.1 /DEF=Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), mRNA. /FEA=mRNA /GEN=ME3 /PROD=malic enzyme 3, NADP(+)-dependent,mitochondrial /DB_XREF=gi:5729919 /UG=Hs.2838 malic enzyme 3, NADP(+)-dependent, mitochondrial /FL=gb:NM_006680.1
204670_x_at_HG-U133A	HLA-DRB5	major histocompatibility complex, class II, DR beta 5	gb:NM_002125.1 /DEF=Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /FEA=mRNA /GEN=HLA-DRB5 /PROD=major histocompatibility complex, class II, DRbeta 5 /DB_XREF=gi:4504412 /UG=Hs.308026 major histocompatibility complex, class II, DR beta 5 /FL=gb:M11867.1 gb:M20430.1 gb:NM_002125.1
204672_s_at_HG-U133A	ANKRD6	ankyrin repeat domain 6	gb:NM_014942.1 /DEF=Homo sapiens KIAA0957 protein (KIAA0957), mRNA. /FEA=mRNA /GEN=KIAA0957 /PROD=KIAA0957 protein /DB_XREF=gi:7662405 /UG=Hs.30991 KIAA0957 protein /FL=gb:AB023174.1 gb:NM_014942.1
204674_at_HG-U133A	LRMP	lymphoid-restricted membrane protein	gb:NM_006152.1 /DEF=Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA. /FEA=mRNA /GEN=LRMP /PROD=lymphoid-restricted membrane protein /DB_XREF=gi:5453723 /UG=Hs.40202 lymphoid-restricted membrane protein /FL=gb:U10485.1 gb:NM_006152.1
204703_at_HG-U133A	TG737	Probe hTg737 (polycystic kidney disease, autosomal recessive, in)	gb:NM_006531.1 /DEF=Homo sapiens Probe hTg737 (polycystic kidney disease, autosomal recessive, in) (TG737), mRNA. /FEA=mRNA /GEN=TG737 /PROD=Tg737 protein /DB_XREF=gi:5729799 /UG=Hs.2291 Probe hTg737 (polycystic kidney disease, autosomal recessive, in) /FL=gb:NM_006531.1 gb:U20362.1
204731_at_HG-U133A	TGFBR3	transforming growth factor, beta receptor III (betaglycan, 300kD)	gb:NM_003243.1 /DEF=Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kD) (TGFBR3), mRNA. /FEA=mRNA /GEN=TGFBR3 /PROD=transforming growth factor, beta receptor III(betaglycan, 300kD) /DB_XREF=gi:4507470 /UG=Hs.79059 transforming

			growth factor, beta receptor III (betaglycan, 300kD) /FL=gb:NM_003243.1 gb:L07594.1
204776_at_HG-U133A	THBS4	thrombospondin 4	gb:NM_003248.1 /DEF=Homo sapiens thrombospondin 4 (THBS4), mRNA. /FEA=mRNA /GEN=THBS4 /PROD=thrombospondin 4 /DB_XREF=gi:4507488 /UG=Hs.75774 thrombospondin 4 /FL=gb:NM_003248.1
204793_at_HG-U133A	KIAA0443	KIAA0443 gene product	gb:NM_014710.1 /DEF=Homo sapiens KIAA0443 gene product (KIAA0443), mRNA. /FEA=mRNA /GEN=KIAA0443 /PROD=KIAA0443 gene product /DB_XREF=gi:7662129 /UG=Hs.113082 KIAA0443 gene product /FL=gb:AB007903.1 gb:NM_014710.1
204798_at_HG-U133A	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	gb:NM_005375.1 /DEF=Homo sapiens v-myb avian myeloblastosis viral oncogene homolog (MYB), mRNA. /FEA=mRNA /GEN=MYB /PROD=v-myb avian myeloblastosis viral oncogenehomolog /DB_XREF=gi:4885496 /UG=Hs.1334 v-myb avian myeloblastosis viral oncogene homolog /FL=gb:M15024.1 gb:AF104863.1 gb:NM_005375.1
204811_s_at_HG-U133A	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	gb:NM_006030.1 /DEF=Homo sapiens calcium channel, voltage-dependent, alpha 2delta subunit 2 (CACNA2D2), mRNA. /FEA=mRNA /GEN=CACNA2D2 /PROD=calcium channel, voltage-dependent, alpha2delta subunit 2 /DB_XREF=gi:5174402 /UG=Hs.127436 calcium channel, voltage-dependent, alpha 2delta subunit 2 /FL=gb:AF040709.1 gb:NM_006030.1
204858_s_at_HG-U133A	ECGF1	endothelial cell growth factor 1 (platelet-derived)	gb:NM_001953.2 /DEF=Homo sapiens endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA. /FEA=mRNA /GEN=ECGF1 /PROD=endothelial cell growth factor 1(platelet-derived) /DB_XREF=gi:7669488 /UG=Hs.73946 endothelial cell growth factor 1 (platelet-derived) /FL=gb:NM_001953.2
204882_at_HG-U133A	KIAA0053	KIAA0053 gene product	gb:NM_014882.1 /DEF=Homo sapiens KIAA0053 gene product (KIAA0053), mRNA. /FEA=mRNA /GEN=KIAA0053 /PROD=KIAA0053 gene product /DB_XREF=gi:7661881 /UG=Hs.1528 KIAA0053 gene product /FL=gb:D29642.1 gb:NM_014882.1

204891_s_at_HG-U133A	LCK	lymphocyte-specific protein tyrosine kinase	gb:NM_005356.1 /DEF=Homo sapiens lymphocyte-specific protein tyrosine kinase (LCK), mRNA. /FEA=mRNA /GEN=LCK /PROD=lymphocyte-specific protein tyrosine kinase /DB_XREF=gi:4885448 /UG=Hs.1765 lymphocyte-specific protein tyrosine kinase /FL=gb:M36881.1 gb:U07236.1 gb:NM_005356.1
204922_at_HG-U133A	FLJ22531	hypothetical protein FLJ22531	gb:NM_024650.1 /DEF=Homo sapiens hypothetical protein FLJ22531 (FLJ22531), mRNA. /FEA=mRNA /GEN=FLJ22531 /PROD=hypothetical protein FLJ22531 /DB_XREF=gi:13375894 /UG=Hs.55613 hypothetical protein FLJ22531 /FL=gb:NM_024650.1
204951_at_HG-U133A	ARHH	ras homolog gene family, member H	gb:NM_004310.1 /DEF=Homo sapiens ras homolog gene family, member H (ARHH), mRNA. /FEA=mRNA /GEN=ARHH /PROD=ras homolog gene family, member H /DB_XREF=gi:4757769 /UG=Hs.109918 ras homolog gene family, member H /FL=gb:NM_004310.1
204992_s_at_HG-U133A	PFN2	profilin 2	gb:NM_002628.1 /DEF=Homo sapiens profilin 2 (PFN2), mRNA. /FEA=mRNA /GEN=PFN2 /PROD=profilin 2 /DB_XREF=gi:4505750 /UG=Hs.91747 profilin 2 /FL=gb:L10678.1 gb:NM_002628.1
205019_s_at_HG-U133A	VIPR1	vasoactive intestinal peptide receptor 1	gb:NM_004624.1 /DEF=Homo sapiens vasoactive intestinal peptide receptor 1 (VIPR1), mRNA. /FEA=mRNA /GEN=VIPR1 /PROD=vasoactive intestinal peptide receptor 1 /DB_XREF=gi:4759307 /UG=Hs.198726 vasoactive intestinal peptide receptor 1 /FL=gb:NM_004624.1
205040_at_HG-U133A	ORM1	orosomucoid 1	gb:NM_000607.1 /DEF=Homo sapiens orosomucoid 1 (ORM1), mRNA. /FEA=mRNA /GEN=ORM1 /PROD=orosomucoid 1 precursor /DB_XREF=gi:9257231 /UG=Hs.572 orosomucoid 1 /FL=gb:M13692.1 gb:NM_000607.1
205041_s_at_HG-U133A	ORM1	orosomucoid 1	gb:NM_000607.1 /DEF=Homo sapiens orosomucoid 1 (ORM1), mRNA. /FEA=mRNA /GEN=ORM1 /PROD=orosomucoid 1 precursor /DB_XREF=gi:9257231 /UG=Hs.572 orosomucoid 1 /FL=gb:M13692.1 gb:NM_000607.1

205049_s_at_HG-U133A	CD79A	CD79A antigen (immunoglobulin-associated alpha)	gb:NM_001783.1 /DEF=Homo sapiens CD79A antigen (immunoglobulin-associated alpha) (CD79A), transcript variant 1, mRNA. /FEA=mRNA /GEN=CD79A /PROD=CD79A antigen, isoform 1 precursor /DB_XREF=gi:4502684 /UG=Hs.79630 CD79A antigen (immunoglobulin-associated alpha) /FL=gb:M80462.1 gb:M86921.1 gb:M74721.1 gb:NM_001783.1
205051_s_at_HG-U133A	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	gb:NM_000222.1 /DEF=Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), mRNA. /FEA=mRNA /GEN=KIT /PROD=v-kit Hardy-Zuckerman 4 feline sarcoma viraloncogene homolog precursor /DB_XREF=gi:4557694 /UG=Hs.81665 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog /FL=gb:NM_000222.1
205055_at_HG-U133A	ITGAE	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	gb:NM_002208.3 /DEF=Homo sapiens integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) (ITGAE), mRNA. /FEA=mRNA /GEN=ITGAE /PROD=integrin, alpha E (antigen CD103, human mucosallymphocyte antigen 1; alpha polypeptide) /DB_XREF=gi:6007850 /UG=Hs.851 integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) /FL=gb:L25851.2 gb:NM_002208.3
205059_s_at_HG-U133A	IDUA	iduronidase, alpha-L-	gb:NM_000203.1 /DEF=Homo sapiens iduronidase, alpha-L- (IDUA), mRNA. /FEA=mRNA /GEN=IDUA /PROD=alpha-L-iduronidase precursor /DB_XREF=gi:4557660 /UG=Hs.89560 iduronidase, alpha-L- /FL=gb:M74715.1 gb:NM_000203.1
205074_at_HG-U133A	SLC22A5	solute carrier family 22 (organic cation transporter), member 5	gb:NM_003060.1 /DEF=Homo sapiens solute carrier family 22 (organic cation transporter), member 5 (SLC22A5), mRNA. /FEA=mRNA /GEN=SLC22A5 /PROD=solute carrier family 22 (organic cationtransporter), member 5 /DB_XREF=gi:4507004 /UG=Hs.15813 solute carrier family 22 (organic cation transporter), member 5 /FL=gb:AB015050.1 gb:AF057164.1 gb:NM_003060.1
205076_s_at_HG-U133A	CRA	cisplatin resistance associated	gb:NM_006697.1 /DEF=Homo sapiens cisplatin resistance associated (CRA), mRNA. /FEA=mRNA /GEN=CRA /PROD=cisplatin resistance associated

			/DB_XREF=gi:5870890 /UG=Hs.166066 cisplatin resistance associated /FL=gb:U78557.1 gb:NM_006697.1
205101_at_HG-U133A	MHC2TA	MHC class II transactivator	gb:NM_000246.1 /DEF=Homo sapiens MHC class II transactivator (MHC2TA), mRNA. /FEA=mRNA /GEN=MHC2TA /PROD=MHC class II transactivator /DB_XREF=gi:4557748 /UG=Hs.3076 MHC class II transactivator /FL=gb:NM_000246.1 gb:U18259.1
205105_at_HG-U133A	MAN2A1	mannosidase, alpha, class 2A, member 1	gb:NM_002372.1 /DEF=Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /FEA=mRNA /GEN=MAN2A1 /PROD=mannosidase, alpha, class 2A, member 1 /DB_XREF=gi:4758697 /UG=Hs.32965 mannosidase, alpha, class 2A, member 1 /FL=gb:U31520.1 gb:NM_002372.1 gb:D63998.1
205110_s_at_HG-U133A	FGF13	fibroblast growth factor 13	gb:NM_004114.1 /DEF=Homo sapiens fibroblast growth factor 13 (FGF13), mRNA. /FEA=mRNA /GEN=FGF13 /PROD=fibroblast growth factor 13 /DB_XREF=gi:4758365 /UG=Hs.6540 fibroblast growth factor 13 /FL=gb:U66198.1 gb:AF100143.1 gb:NM_004114.1
205131_x_at_HG-U133A	SCGF	stem cell growth factor; lymphocyte secreted C-type lectin	gb:NM_002975.1 /DEF=Homo sapiens stem cell growth factor; lymphocyte secreted C-type lectin (SCGF), mRNA. /FEA=mRNA /GEN=SCGF /PROD=stem cell growth factor; lymphocyte secretedC-type lectin /DB_XREF=gi:4506802 /UG=Hs.105927 stem cell growth factor; lymphocyte secreted C-type lectin /FL=gb:AF020044.1 gb:AB009244.1 gb:NM_002975.1
205145_s_at_HG-U133A	MYL5	myosin, light polypeptide 5, regulatory	gb:NM_002477.1 /DEF=Homo sapiens myosin, light polypeptide 5, regulatory (MYL5), mRNA. /FEA=mRNA /GEN=MYL5 /PROD=myosin, light polypeptide 5, regulatory /DB_XREF=gi:4505304 /UG=Hs.170482 myosin, light polypeptide 5, regulatory /FL=gb:L03785.1 gb:NM_002477.1
205192_at_HG-U133A	MAP3K14	mitogen-activated protein kinase kinase kinase 14	gb:NM_003954.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase 14 (MAP3K14), mRNA. /FEA=mRNA /GEN=MAP3K14 /PROD=mitogen-activated protein kinase kinase kinase14 /DB_XREF=gi:4505396 /UG=Hs.47007 mitogen-activated protein kinase kinase

			kinase 14 /FL=gb:NM_003954.1
205223_at_HG-U133A	KIAA0645	KIAA0645 gene product	gb:NM_014662.1 /DEF=Homo sapiens KIAA0645 gene product (KIAA0645), mRNA. /FEA=mRNA /GEN=KIAA0645 /PROD=KIAA0645 gene product /DB_XREF=gi:7662221 /UG=Hs.155987 KIAA0645 gene product /FL=gb:AB014545.1 gb:NM_014662.1
205225_at_HG-U133A	ESR1	estrogen receptor 1	gb:NM_000125.1 /DEF=Homo sapiens estrogen receptor 1 (ESR1), mRNA. /FEA=mRNA /GEN=ESR1 /PROD=estrogen receptor 1 /DB_XREF=gi:4503602 /UG=Hs.1657 estrogen receptor 1 /FL=gb:NM_000125.1
205267_at_HG-U133A	POU2AF1	POU domain, class 2, associating factor 1	gb:NM_006235.1 /DEF=Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), mRNA. /FEA=mRNA /GEN=POU2AF1 /PROD=POU domain, class 2, associating factor 1 /DB_XREF=gi:5453933 /UG=Hs.2407 POU domain, class 2, associating factor 1 /FL=gb:NM_006235.1
205306_x_at_HG-U133A	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	Consensus includes gb:AI074145 /FEA=EST /DB_XREF=gi:3400789 /DB_XREF=est:ov13a06.x1 /CLONE=IMAGE:1637170 /UG=Hs.107318 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /FL=gb:AF056032.1 gb:NM_003679.1
205308_at_HG-U133A	LOC51101	CGI-62 protein	gb:NM_016010.1 /DEF=Homo sapiens CGI-62 protein (LOC51101), mRNA. /FEA=mRNA /GEN=LOC51101 /PROD=CGI-62 protein /DB_XREF=gi:7705774 /UG=Hs.118821 CGI-62 protein /FL=gb:AF151820.1 gb:NM_016010.1
205312_at_HG-U133A	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene spi1	gb:NM_003120.1 /DEF=Homo sapiens spleen focus forming virus (SFFV) proviral integration oncogene spi1 (SPI1), mRNA. /FEA=mRNA /GEN=SPI1 /PROD=spleen focus forming virus (SFFV) proviralintegration oncogene spi1 /DB_XREF=gi:4507174 /UG=Hs.157441 spleen focus forming virus (SFFV) proviral integration oncogene spi1 /FL=gb:NM_003120.1
205316_at_HG-U133A	SLC15A2	solute carrier family 15 (H+/peptide transporter), member 2	Consensus includes gb:BF223679 /FEA=EST /DB_XREF=gi:11130857 /DB_XREF=est:7q78g05.x1 /CLONE=IMAGE:3704625 /UG=Hs.182575 solute carrier family 15 (H+peptide transporter), member 2 /FL=gb:NM_021082.1
205349_at_HG-U133A	GNA15	guanine nucleotide binding protein (G	gb:NM_002068.1 /DEF=Homo sapiens guanine nucleotide binding protein (G

		protein), alpha 15 (Gq class)	protein), alpha 15 (Gq class) (GNA15), mRNA. /FEA=mRNA /GEN=GNA15 /PROD=guanine nucleotide binding protein (G protein),alpha 15 (Gq class) /DB_XREF=gi:4504038 /UG=Hs.73797 guanine nucleotide binding protein (G protein), alpha 15 (Gq class) /FL=gb:M63904.1 gb:NM_002068.1
205355_at_HG-U133A	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	gb:NM_001609.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, shortbranched chain (ACADSB), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACADSB /PROD=acyl-Coenzyme A dehydrogenase, shortbranchedchain precursor /DB_XREF=gi:4501858 /UG=Hs.81934 acyl-Coenzyme A dehydrogenase, shortbranched chain /FL=gb:NM_001609.1 gb:U12778.1
205366_s_at_HG-U133A	HOXB6	homeo box B6	gb:NM_018952.1 /DEF=Homo sapiens homeo box B6 (HOXB6), mRNA. /FEA=mRNA /GEN=HOXB6 /PROD=homeo box B6 /DB_XREF=gi:9506792 /UG=Hs.98428 homeo box B6 /FL=gb:NM_018952.1
205380_at_HG-U133A	PDZK1	PDZ domain containing 1	gb:NM_002614.1 /DEF=Homo sapiens PDZ domain containing 1 (PDZK1), mRNA. /FEA=mRNA /GEN=PDZK1 /PROD=PDZ domain containing 1 /DB_XREF=gi:4505702 /UG=Hs.15456 PDZ domain containing 1 /FL=gb:AF012281.1 gb:NM_002614.1
205382_s_at_HG-U133A	DF	D component of complement (adipsin)	gb:NM_001928.1 /DEF=Homo sapiens D component of complement (adipsin) (DF), mRNA. /FEA=mRNA /GEN=DF /PROD=adipsincomplement factor D precursor /DB_XREF=gi:4503308 /UG=Hs.155597 D component of complement (adipsin) /FL=gb:M84526.1 gb:NM_001928.1
205383_s_at_HG-U133A	ZNF288	zinc finger protein 288	gb:NM_015642.1 /DEF=Homo sapiens zinc finger protein 288 (ZNF288), mRNA. /FEA=mRNA /GEN=ZNF288 /PROD=zinc finger protein 288 /DB_XREF=gi:7661651 /UG=Hs.159456 zinc finger protein 288 /FL=gb:AL050276.1 gb:NM_015642.1
205414_s_at_HG-U133A	KIAA0672	KIAA0672 gene product	gb:NM_014859.1 /DEF=Homo sapiens KIAA0672 gene product (KIAA0672), mRNA. /FEA=mRNA /GEN=KIAA0672 /PROD=KIAA0672 gene product /DB_XREF=gi:7662241 /UG=Hs.6336 KIAA0672 gene product

			/FL=gb:AB014572.1 gb:NM_014859.1
205420_at_HG-U133A	PEX7	peroxisomal biogenesis factor 7	gb:NM_000288.1 /DEF=Homo sapiens peroxisomal biogenesis factor 7 (PEX7), mRNA. /FEA=mRNA /GEN=PEX7 /PROD=peroxisomal biogenesis factor 7 /DB_XREF=gi:4505730 /UG=Hs.79993 peroxisomal biogenesis factor 7 /FL=gb:U76560.1 gb:U88871.1 gb:NM_000288.1
205436_s_at_HG-U133A	H2AFX	H2A histone family, member X	gb:NM_002105.1 /DEF=Homo sapiens H2A histone family, member X (H2AFX), mRNA. /FEA=mRNA /GEN=H2AFX /PROD=H2A histone family, member X /DB_XREF=gi:4504252 /UG=Hs.147097 H2A histone family, member X /FL=gb:BC004915.1 gb:NM_002105.1
205453_at_HG-U133A	HOXB2	homeo box B2	gb:NM_002145.1 /DEF=Homo sapiens homeo box B2 (HOXB2), mRNA. /FEA=mRNA /GEN=HOXB2 /PROD=homeo box B2 /DB_XREF=gi:4504464 /UG=Hs.2733 homeo box B2 /FL=gb:NM_002145.1
205471_s_at_HG-U133A	DACH	dachshund homolog (Drosophila)	Consensus includes gb:AW772082 /FEA=EST /DB_XREF=gi:7704144 /DB_XREF=est:hn67b07.x1 /CLONE=IMAGE:3032917 /UG=Hs.63931 dachshund (Drosophila) homolog /FL=gb:NM_004392.1 gb:AF102546.1
205472_s_at_HG-U133A	DACH	dachshund homolog (Drosophila)	gb:NM_004392.1 /DEF=Homo sapiens dachshund (Drosophila) homolog (DACH), mRNA. /FEA=mRNA /GEN=DACH /PROD=dachshund (Drosophila) homolog /DB_XREF=gi:4758113 /UG=Hs.63931 dachshund (Drosophila) homolog /FL=gb:NM_004392.1 gb:AF102546.1
205504_at_HG-U133A	BTK	Bruton agammaglobulinemia tyrosine kinase	gb:NM_000061.1 /DEF=Homo sapiens Bruton agammaglobulinemia tyrosine kinase (BTK), mRNA. /FEA=mRNA /GEN=BTK /PROD=Bruton agammaglobulinemia tyrosine kinase /DB_XREF=gi:4557376 /UG=Hs.159494 Bruton agammaglobulinemia tyrosine kinase /FL=gb:NM_000061.1 gb:AF153756.1 gb:AF153757.1 gb:AF153758.1 gb:AF153759.1 gb:AF153760.1 gb:AF153761.1 gb:AF153762.1 gb:AF153364.1
205513_at_HG-U133A	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	gb:NM_001062.1 /DEF=Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1), mRNA. /FEA=mRNA /GEN=TCN1 /PROD=transcobalamin I (vitamin B12 binding protein, Rbinder family)

			/DB_XREF=gi:4507406 /UG=Hs.2012 transcobalamin I (vitamin B12 binding protein, R binder family) /FL=gb:J05068.1 gb:NM_001062.1
205528_s_at_HG-U133A	CBFA2T1	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related	Consensus includes gb:X79990.1 /DEF=H.sapiens ETO mRNA. /FEA=mRNA /GEN=ETO /DB_XREF=gi:510523 /UG=Hs.31551 core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related /FL=gb:NM_004349.1 gb:D43638.1
205529_s_at_HG-U133A	CBFA2T1	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related	gb:NM_004349.1 /DEF=Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), mRNA. /FEA=mRNA /GEN=CBFA2T1 /PROD=core-binding factor, runt domain, alpha subunit2; translocated to, 1; cyclin D-related /DB_XREF=gi:4757915 /UG=Hs.31551 core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related /FL=gb:NM_004349.1 gb:D43638.1
205541_s_at_HG-U133A	GSPT2	G1 to S phase transition 2	gb:NM_018094.1 /DEF=Homo sapiens hypothetical protein FLJ10441 (FLJ10441), mRNA. /FEA=mRNA /GEN=FLJ10441 /PROD=hypothetical protein FLJ10441 /DB_XREF=gi:8922423 /UG=Hs.59523 hypothetical protein FLJ10441 /FL=gb:NM_018094.1
205547_s_at_HG-U133A	TAGLN	transgelin	gb:NM_003186.2 /DEF=Homo sapiens transgelin (TAGLN), mRNA. /FEA=mRNA /GEN=TAGLN /PROD=transgelin /DB_XREF=gi:12621918 /UG=Hs.75777 transgelin /FL=gb:NM_003186.2 gb:M95787.1 gb:D17409.1
205557_at_HG-U133A	BPI	bactericidal/permeability-increasing protein	gb:NM_001725.1 /DEF=Homo sapiens bactericidalpermeability-increasing protein (BPI), mRNA. /FEA=mRNA /GEN=BPI /PROD=bactericidalpermeability-increasing proteinprecursor /DB_XREF=gi:4502446 /UG=Hs.89535 bactericidalpermeability-increasing protein /FL=gb:AF322588.1 gb:J04739.1 gb:NM_001725.1
205599_at_HG-U133A	TRAF1	TNF receptor-associated factor 1	gb:NM_005658.1 /DEF=Homo sapiens TNF receptor-associated factor 1 (TRAF1), mRNA. /FEA=mRNA /GEN=TRAF1 /PROD=TNF receptor-associated factor 1 /DB_XREF=gi:5032192 /UG=Hs.2134 TNF receptor-associated factor 1 /FL=gb:NM_005658.1 gb:U19261.1

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205600_x_at_HG-U133A	HOXB5	homeo box B5	Consensus includes gb:AI052747 /FEA=EST /DB_XREF=gi:3308738 /DB_XREF=est:oz27d05.x1 /CLONE=IMAGE:1676553 /UG=Hs.22554 homeo box B5 /FL=gb:M92299.1 gb:NM_002147.1
205601_s_at_HG-U133A	HOXB5	homeo box B5	gb:NM_002147.1 /DEF=Homo sapiens homeo box B5 (HOXB5), mRNA. /FEA=mRNA /GEN=HOXB5 /PROD=homeo box B5 /DB_XREF=gi:4504468 /UG=Hs.22554 homeo box B5 /FL=gb:M92299.1 gb:NM_002147.1
205607_s_at_HG-U133A	LOC57147	hypothetical protein LOC57147	gb:NM_020423.1 /DEF=Homo sapiens hypothetical protein LOC57147 (LOC57147), mRNA. /FEA=mRNA /GEN=LOC57147 /PROD=hypothetical protein LOC57147 /DB_XREF=gi:9967093 /UG=Hs.24243 hypothetical protein LOC57147 /FL=gb:NM_020423.1
205613_at_HG-U133A	LOC51760	B/K protein	gb:NM_016524.1 /DEF=Homo sapiens BK protein (LOC51760), mRNA. /FEA=mRNA /GEN=LOC51760 /PROD=BK protein /DB_XREF=gi:7706558 /UG=Hs.26971 BK protein /FL=gb:BC004518.1 gb:AF220560.1 gb:NM_016524.1
205614_x_at_HG-U133A	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	gb:NM_020998.1 /DEF=Homo sapiens macrophage stimulating 1 (hepatocyte growth factor-like) (MST1), mRNA. /FEA=mRNA /GEN=MST1 /PROD=macrophage stimulating 1 (hepatocyte growthfactor-like) /DB_XREF=gi:10337614 /UG=Hs.278657 macrophage stimulating 1 (hepatocyte growth factor-like) /FL=gb:NM_020998.1 gb:M74178.1 gb:L11924.1
205624_at_HG-U133A	CPA3	carboxypeptidase A3 (mast cell)	gb:NM_001870.1 /DEF=Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), mRNA. /FEA=mRNA /GEN=CPA3 /PROD=mast cell carboxypeptidase A3 precursor /DB_XREF=gi:4503000 /UG=Hs.646 carboxypeptidase A3 (mast cell) /FL=gb:M27717.1 gb:NM_001870.1
205627_at_HG-U133A	CDA	cytidine deaminase	gb:NM_001785.1 /DEF=Homo sapiens cytidine deaminase (CDA), mRNA. /FEA=mRNA /GEN=CDA /PROD=cytidine deaminase /DB_XREF=gi:11386156 /UG=Hs.72924 cytidine deaminase /FL=gb:NM_001785.1 gb:L27943.1
205640_at_HG-U133A	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	gb:NM_000694.1 /DEF=Homo sapiens aldehyde dehydrogenase 3 family, member B1 (ALDH3B1), mRNA. /FEA=mRNA /GEN=ALDH3B1

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			/PROD=aldehyde dehydrogenase 3B1 /DB_XREF=gi:4502042 /UG=Hs.83155 aldehyde dehydrogenase 3 family, member B1 /FL=gb:NM_000694.1 gb:U10868.1
205653_at_HG-U133A	CTSG	cathepsin G	gb:NM_001911.1 /DEF=Homo sapiens cathepsin G (CTSG), mRNA. /FEA=mRNA /GEN=CTSG /PROD=cathepsin G /DB_XREF=gi:4503148 /UG=Hs.100764 cathepsin G /FL=gb:M16117.1 gb:NM_001911.1
205663_at_HG-U133A	PCBP3	poly(rC) binding protein 3	gb:NM_020528.1 /DEF=Homo sapiens poly(rC)-binding protein 3 (PCBP3), mRNA. /FEA=mRNA /GEN=PCBP3 /PROD=poly(rC)-binding protein 3 /DB_XREF=gi:10092616 /UG=Hs.121241 poly(rC)-binding protein 3 /FL=gb:NM_020528.1 gb:AF176329.1
205668_at_HG-U133A	LY75	lymphocyte antigen 75	gb:NM_002349.1 /DEF=Homo sapiens lymphocyte antigen 75 (LY75), mRNA. /FEA=mRNA /GEN=LY75 /PROD=lymphocyte antigen 75 /DB_XREF=gi:4505052 /UG=Hs.153563 lymphocyte antigen 75 /FL=gb:AF011333.1 gb:AF064827.1 gb:NM_002349.1
205671_s_at_HG-U133A	HLA-DOB	major histocompatibility complex, class II, DO beta	gb:NM_002120.1 /DEF=Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB), mRNA. /FEA=mRNA /GEN=HLA-DOB /PROD=major histocompatibility complex, class II, DObeta /DB_XREF=gi:4504402 /UG=Hs.1802 major histocompatibility complex, class II, DO beta /FL=gb:M26040.1 gb:NM_002120.1
205674_x_at_HG-U133A	FXYD2	FXYD domain-containing ion transport regulator 2	gb:NM_001680.2 /DEF=Homo sapiens FXYD domain-containing ion transport regulator 2 (FXYD2), transcript variant a, mRNA. /FEA=mRNA /GEN=FXYD2 /PROD=FXYD domain-containing ion transport regulator2, isoform 1 /DB_XREF=gi:11125765 /UG=Hs.19520 FXYD domain-containing ion transport regulator 2 /FL=gb:NM_001680.2 gb:AF241236.1 gb:U50743.1
205690_s_at_HG-U133A	G10	maternal G10 transcript	gb:NM_003910.1 /DEF=Homo sapiens maternal G10 transcript (G10), mRNA. /FEA=mRNA /GEN=G10 /PROD=maternal G10 transcript /DB_XREF=gi:4503836 /UG=Hs.330310 maternal G10 transcript /FL=gb:NM_003910.1 gb:U11861.1

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205691_at_HG-U133A	SYNGR3	synaptogyrin 3	gb:NM_004209.2 /DEF=Homo sapiens synaptogyrin 3 (SYNGR3), mRNA. /FEA=mRNA /GEN=SYNGR3 /PROD=synaptogyrin 3 /DB_XREF=gi:6631111 /UG=Hs.6467 synaptogyrin 3 /FL=gb:NM_004209.2
205718_at_HG-U133A	ITGB7	integrin, beta 7	gb:NM_000889.1 /DEF=Homo sapiens integrin, beta 7 (ITGB7), mRNA. /FEA=mRNA /GEN=ITGB7 /PROD=integrin, beta 7 /DB_XREF=gi:4504776 /UG=Hs.1741 integrin, beta 7 /FL=gb:M68892.1 gb:M62880.1 gb:NM_000889.1
205790_at_HG-U133A	SCAP1	src family associated phosphoprotein 1	gb:NM_003726.1 /DEF=Homo sapiens src kinase-associated phosphoprotein of 55 kDa (SKAP55), mRNA. /FEA=mRNA /GEN=SKAP55 /PROD=src kinase-associated phosphoprotein of 55 kDa /DB_XREF=gi:4506964 /UG=Hs.19126 src kinase-associated phosphoprotein of 55 kDa /FL=gb:NM_003726.1
205801_s_at_HG-U133A	GRP3	guanine nucleotide exchange factor for Rap1	gb:NM_015376.1 /DEF=Homo sapiens KIAA0846 protein (KIAA0846), mRNA. /FEA=mRNA /GEN=KIAA0846 /PROD=KIAA0846 protein /DB_XREF=gi:7662333 /UG=Hs.24024 KIAA0846 protein /FL=gb:AB020653.1 gb:NM_015376.1
205805_s_at_HG-U133A	ROR1	receptor tyrosine kinase-like orphan receptor 1	gb:NM_005012.1 /DEF=Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA. /FEA=mRNA /GEN=ROR1 /PROD=receptor tyrosine kinase-like orphan receptor 1 /DB_XREF=gi:4826867 /UG=Hs.274243 receptor tyrosine kinase-like orphan receptor 1 /FL=gb:M97675.1 gb:NM_005012.1
205821_at_HG-U133A	D12S2489E	DNA segment on chromosome 12 (unique) 2489 expressed sequence	gb:NM_007360.1 /DEF=Homo sapiens DNA segment on chromosome 12 (unique) 2489 expressed sequence (D12S2489E), mRNA. /FEA=mRNA /GEN=D12S2489E /PROD=NKG2-D type II integral membrane protein /DB_XREF=gi:6679051 /UG=Hs.74085 DNA segment on chromosome 12 (unique) 2489 expressed sequence /FL=gb:NM_007360.1 gb:AF260135.1 gb:AF260136.1
205837_s_at_HG-	GYPA	glycophorin A (includes MN blood group)	gb:BC005319.1 /DEF=Homo sapiens, Similar to glycophorin A (includes MN

U133A			blood group), clone MGC:12403, mRNA, complete cds. /FEA=mRNA /PROD=Similar to glycophorin A (includes MN bloodgroup) /DB_XREF=gi:13529076 /UG=Hs.108694 glycophorin A (includes MN blood group) /FL=gb:BC005319.1 gb:U00177.1 gb:L31860.1 gb:NM_002099.2
205841_at_HG-U133A	JAK2	Janus kinase 2 (a protein tyrosine kinase)	gb:NM_004972.2 /DEF=Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA. /FEA=mRNA /GEN=JAK2 /PROD=Janus kinase 2 /DB_XREF=gi:13325062 /UG=Hs.115541 Janus kinase 2 (a protein tyrosine kinase) /FL=gb:NM_004972.2 gb:AF005216.1 gb:AF058925.1 gb:AF001362.1
205849_s_at_HG-U133A	UQCRB	ubiquinol-cytochrome c reductase binding protein	gb:NM_006294.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA. /FEA=mRNA /GEN=UQCRB /PROD=ubiquinol-cytochrome c reductase bindingprotein /DB_XREF=gi:5454151 /UG=Hs.131255 ubiquinol-cytochrome c reductase binding protein /FL=gb:M22348.1 gb:NM_006294.1
205855_at_HG-U133A	ZNF197	zinc finger protein 197	gb:NM_006991.2 /DEF=Homo sapiens zinc finger protein 197 (ZNF197), mRNA. /FEA=mRNA /GEN=ZNF197 /PROD=zinc finger protein 197 /DB_XREF=gi:12056483 /UG=Hs.170341 zinc finger protein 197 /FL=gb:NM_006991.2 gb:AF011573.1
205863_at_HG-U133A	S100A12	S100 calcium binding protein A12 (calgranulin C)	gb:NM_005621.1 /DEF=Homo sapiens S100 calcium-binding protein A12 (calgranulin C) (S100A12), mRNA. /FEA=mRNA /GEN=S100A12 /PROD=S100 calcium-binding protein A12 /DB_XREF=gi:5032058 /UG=Hs.19413 S100 calcium-binding protein A12 (calgranulin C) /FL=gb:D83664.1 gb:D49549.1 gb:NM_005621.1
205899_at_HG-U133A	CCNA1	cyclin A1	gb:NM_003914.1 /DEF=Homo sapiens cyclin A1 (CCNA1), mRNA. /FEA=mRNA /GEN=CCNA1 /PROD=cyclin A1 /DB_XREF=gi:4502610 /UG=Hs.79378 cyclin A1 /FL=gb:U66838.1 gb:NM_003914.1
205901_at_HG-U133A	PNOC	prepronociceptin	gb:NM_006228.2 /DEF=Homo sapiens prepronociceptin (PNOC), mRNA. /FEA=mRNA /GEN=PNOC /PROD=prepronociceptin /DB_XREF=gi:11079650 /UG=Hs.89040 prepronociceptin /FL=gb:NM_006228.2 gb:U48263.1

205911_at_HG-U133A	PTHR1	parathyroid hormone receptor 1	gb:NM_000316.1 /DEF=Homo sapiens parathyroid hormone receptor 1 (PTHR1), mRNA. /FEA=mRNA /GEN=PTHR1 /PROD=parathyroid hormone receptor 1 /DB_XREF=gi:4506270 /UG=Hs.1019 parathyroid hormone receptor 1 /FL=gb:L04308.1 gb:NM_000316.1 gb:U17418.1
205933_at_HG-U133A	SETBP1	SET binding protein 1	gb:NM_015559.1 /DEF=Homo sapiens KIAA0437 protein (KIAA0437), mRNA. /FEA=mRNA /GEN=KIAA0437 /PROD=KIAA0437 protein /DB_XREF=gi:7662121 /UG=Hs.151717 KIAA0437 protein /FL=gb:AB022660.1 gb:NM_015559.1
205945_at_HG-U133A	IL6R	interleukin 6 receptor	gb:NM_000565.1 /DEF=Homo sapiens interleukin 6 receptor (IL6R), mRNA. /FEA=mRNA /GEN=IL6R /PROD=interleukin 6 receptor /DB_XREF=gi:4504672 /UG=Hs.193400 interleukin 6 receptor /FL=gb:NM_000565.1
205997_at_HG-U133A	ADAM28	a disintegrin and metalloproteinase domain 28	gb:NM_021778.1 /DEF=Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 2, mRNA. /FEA=mRNA /GEN=ADAM28 /PROD=a disintegrin and metalloproteinase domain 28,isoform 2 preproprotein /DB_XREF=gi:11496995 /UG=Hs.174030 a disintegrin and metalloproteinase domain 28 /FL=gb:NM_021778.1 gb:AF137334.1 gb:NM_014265.1
206009_at_HG-U133A	ITGA9	integrin, alpha 9	gb:NM_002207.1 /DEF=Homo sapiens integin, alpha 9 (ITGA9), mRNA. /FEA=mRNA /GEN=ITGA9 /PROD=integin, alpha 9 /DB_XREF=gi:11321594 /UG=Hs.222 integrin, alpha 9 /FL=gb:NM_002207.1 gb:D25303.1
206090_s_at_HG-U133A	DISC1	disrupted in schizophrenia 1	gb:NM_018662.1 /DEF=Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /FEA=mRNA /GEN=DISC1 /PROD=disrupted in schizophrenia 1 /DB_XREF=gi:11037064 /UG=Hs.26985 disrupted in schizophrenia 1 /FL=gb:NM_018662.1 gb:AF222980.1
206111_at_HG-U133A	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	gb:NM_002934.1 /DEF=Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA. /FEA=mRNA /GEN=RNASE2 /PROD=ribonuclease, RNase A family, 2 (liver,eosinophil-derived neurotoxin) /DB_XREF=gi:4506548 /UG=Hs.728 ribonuclease, RNase

			A family, 2 (liver, eosinophil-derived neurotoxin) /FL=gb:M24157-1 gb:M30510.1 gb:NM_002934.1 gb:M28129.1
206126_at_HG-U133A	BLR1	Burkitt lymphoma receptor 1, GTP binding protein	gb:NM_001716.1 /DEF=Homo sapiens Burkitt lymphoma receptor 1, GTP-binding protein (BLR1), mRNA. /FEA=mRNA /GEN=BLR1 /PROD=Burkitt lymphoma receptor 1, GTP-bindingprotein /DB_XREF=gi:4502414 /UG=Hs.113916 Burkitt lymphoma receptor 1, GTP-binding protein /FL=gb:NM_001716.1
206135_at_HG-U133A	KIAA0535	KIAA0535 gene product	gb:NM_014682.1 /DEF=Homo sapiens KIAA0535 gene product (KIAA0535), mRNA. /FEA=mRNA /GEN=KIAA0535 /PROD=KIAA0535 gene product /DB_XREF=gi:7662167 /UG=Hs.151449 KIAA0535 gene product /FL=gb:AB011107.1 gb:NM_014682.1
206150_at_HG-U133A	TNFRSF7	tumor necrosis factor receptor superfamily, member 7	gb:NM_001242.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 7 (TNFRSF7), mRNA. /FEA=mRNA /GEN=TNFRSF7 /PROD=CD27 antigen /DB_XREF=gi:4507586 /UG=Hs.180841 tumor necrosis factor receptor superfamily, member 7 /FL=gb:M63928.1 gb:NM_001242.1
206177_s_at_HG-U133A	ARG1	arginase, liver	gb:NM_000045.2 /DEF=Homo sapiens arginase, liver (ARG1), mRNA. /FEA=mRNA /GEN=ARG1 /PROD=arginase, type I /DB_XREF=gi:10947138 /UG=Hs.289057 arginase, liver /FL=gb:NM_000045.2 gb:M14502.1
206178_at_HG-U133A	PLA2G5	phospholipase A2, group V	gb:NM_000929.1 /DEF=Homo sapiens phospholipase A2, group V (PLA2G5), mRNA. /FEA=mRNA /GEN=PLA2G5 /PROD=phospholipase A2, group V /DB_XREF=gi:4505852 /UG=Hs.290 phospholipase A2, group V /FL=gb:NM_000929.1 gb:U03090.1
206207_at_HG-U133A	CLC	Charot-Leyden crystal protein	gb:NM_001828.3 /DEF=Homo sapiens Charot-Leyden crystal protein (CLC), mRNA. /FEA=mRNA /GEN=CLC /PROD=Charot-Leyden crystal protein /DB_XREF=gi:6325464 /UG=Hs.889 Charot-Leyden crystal protein /FL=gb:L01664.1 gb:NM_001828.3
206241_at_HG-U133A	KPNA5	karyopherin alpha 5 (importin alpha 6)	gb:NM_002269.1 /DEF=Homo sapiens karyopherin alpha 5 (importin alpha 6) (KPNA5), mRNA. /FEA=mRNA /GEN=KPNA5 /PROD=karyopherin alpha 5

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			(importin alpha 6) /DB_XREF=gi:4504902 /UG=Hs.182971 karyopherin alpha 5 (importin alpha 6) /FL=gb:AF005361.1 gb:NM_002269.1
206245_s_at_HG-U133A	NS1-BP	NS1-binding protein	gb:NM_006469.1 /DEF=Homo sapiens NS1-binding protein (NS1-BP), mRNA. /FEA=mRNA /GEN=NS1-BP /PROD=NS1-binding protein /DB_XREF=gi:5453803 /UG=Hs.197298 NS1-binding protein /FL=gb:NM_006469.1
206255_at_HG-U133A	BLK	B lymphoid tyrosine kinase	gb:NM_001715.1 /DEF=Homo sapiens B lymphoid tyrosine kinase (BLK), mRNA. /FEA=mRNA /GEN=BLK /PROD=B lymphoid tyrosine kinase /DB_XREF=gi:4502412 /UG=Hs.2243 B lymphoid tyrosine kinase /FL=gb:NM_001715.1
206295_at_HG-U133A	IL18	interleukin 18 (interferon-gamma-inducing factor)	gb:NM_001562.1 /DEF=Homo sapiens interleukin-18 (interferon-gamma-inducing factor) (IL18), mRNA. /FEA=mRNA /GEN=IL18 /PROD=interleukin 18 /DB_XREF=gi:4504652 /UG=Hs.83077 interleukin 18 (interferon-gamma-inducing factor) /FL=gb:D49950.1 gb:AF077611.1 gb:NM_001562.1
206302_s_at_HG-U133A	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	gb:NM_019094.1 /DEF=Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA. /FEA=mRNA /GEN=NUDT4 /PROD=nudix (nucleoside diphosphate linked moietyX)-type motif 4 /DB_XREF=gi:10800135 /UG=Hs.92381 nudix (nucleoside diphosphate linked moiety X)-type motif 4 /FL=gb:NM_019094.1 gb:AF191649.1 gb:AF191650.1 gb:AF191653.1
206337_at_HG-U133A	CCR7	chemokine (C-C motif) receptor 7	gb:NM_001838.1 /DEF=Homo sapiens chemokine (C-C motif) receptor 7 (CCR7), mRNA. /FEA=mRNA /GEN=CCR7 /PROD=chemokine (C-C motif) receptor 7 /DB_XREF=gi:4502640 /UG=Hs.1652 chemokine (C-C motif) receptor 7 /FL=gb:L08176.1 gb:NM_001838.1 gb:L31581.1
206380_s_at_HG-U133A	PFC	properdin P factor, complement	gb:NM_002621.1 /DEF=Homo sapiens properdin P factor, complement (PFC), mRNA. /FEA=mRNA /GEN=PFC /PROD=properdin P factor, complement /DB_XREF=gi:4505736 /UG=Hs.53155 properdin P factor, complement /FL=gb:NM_002621.1 gb:M83652.1

206398_s_at_HG-U133A	CD19	CD19 antigen	gb:NM_001770.1 /DEF=Homo sapiens CD19 antigen (CD19), mRNA. /FEA=mRNA /GEN=CD19 /PROD=CD19 antigen /DB_XREF=gi:10835052 /UG=Hs.96023 CD19 antigen /FL=gb:NM_001770.1 gb:M21097.1 gb:M28170.1
206438_x_at_HG-U133A	FLJ12975	hypothetical protein FLJ12975	gb:NM_024809.1 /DEF=Homo sapiens hypothetical protein FLJ12975 (FLJ12975), mRNA. /FEA=mRNA /GEN=FLJ12975 /PROD=hypothetical protein FLJ12975 /DB_XREF=gi:13376192 /UG=Hs.167165 hypothetical protein FLJ12975 /FL=gb:NM_024809.1
206440_at_HG-U133A	VELI1	Vertebrate LIN7 homolog 1, Tax interaction protein 33	gb:NM_004664.1 /DEF=Homo sapiens Vertebrate LIN7 homolog 1, Tax interaction protein 33 (VELI1), mRNA. /FEA=mRNA /GEN=VELI1 /PROD=Vertebrate LIN7 homolog 1, Tax interactionprotein 33 /DB_XREF=gi:4759305 /UG=Hs.178215 Vertebrate LIN7 homolog 1, Tax interaction protein 33 /FL=gb:AF087693.1 gb:NM_004664.1 gb:AF173081.1
206461_x_at_HG-U133A	MT1H	metallothionein 1H	gb:NM_005951.1 /DEF=Homo sapiens metallothionein 1H (MT1H), mRNA. /FEA=mRNA /GEN=MT1H /PROD=metallothionein 1H /DB_XREF=gi:10835084 /UG=Hs.2667 metallothionein 1H /FL=gb:NM_005951.1
206488_s_at_HG-U133A	CD36	CD36 antigen (collagen type I receptor, thrombospondin receptor)	gb:NM_000072.1 /DEF=Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), mRNA. /FEA=mRNA /GEN=CD36 /PROD=CD36 antigen (collagen type I receptor,thrombospondin receptor) /DB_XREF=gi:4557418 /UG=Hs.75613 CD36 antigen (collagen type I receptor, thrombospondin receptor) /FL=gb:M24795.1 gb:M98398.1 gb:L06850.1 gb:NM_000072.1
206513_at_HG-U133A	AIM2	absent in melanoma 2	gb:NM_004833.1 /DEF=Homo sapiens absent in melanoma 2 (AIM2), mRNA. /FEA=mRNA /GEN=AIM2 /PROD=absent in melanoma 2 /DB_XREF=gi:4757733 /UG=Hs.105115 absent in melanoma 2 /FL=gb:AF024714.1 gb:NM_004833.1
206515_at_HG-U133A	CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase)	gb:NM_000896.1 /DEF=Homo sapiens cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3), mRNA. /FEA=mRNA /GEN=CYP4F3 /PROD=cytochrome P450, subfamily IVF,

			polypeptide 3 /DB_XREF=gi:4503240 /UG=Hs.106242 cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) /FL=gb:AB002454.1 gb:D12620.1 gb:NM_000896.1
206519_x_at_HG-U133A	SIGLEC6	sialic acid binding Ig-like lectin 6	gb:D86358.1 /DEF=Homo sapiens mRNA for CD33L1, complete cds. /FEA=mRNA /PROD=CD33L1 /DB_XREF=gi:2913994 /UG=Hs.117992 sialic acid binding Ig-like lectin 6 /FL=gb:U71382.1 gb:D86358.1 gb:NM_001245.1
206530_at_HG-U133A	RAB30	RAB30, member RAS oncogene family	gb:NM_014488.1 /DEF=Homo sapiens RAB30, member RAS oncogene family (RAB30), mRNA. /FEA=mRNA /GEN=RAB30 /PROD=RAB30, member RAS oncogene family /DB_XREF=gi:7657493 /UG=Hs.159505 RAB30, member RAS oncogene family /FL=gb:NM_014488.1
206550_s_at_HG-U133A	NUP155	nucleoporin 155kD	gb:NM_004298.1 /DEF=Homo sapiens nucleoporin 155kD (NUP155), mRNA. /FEA=mRNA /GEN=NUP155 /PROD=nucleoporin 155kD /DB_XREF=gi:4758843 /UG=Hs.23255 nucleoporin 155kD /FL=gb:AB018334.1 gb:NM_004298.1
206576_s_at_HG-U133A	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	gb:NM_001712.1 /DEF=Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA. /FEA=mRNA /GEN=CEACAM1 /PROD=carcinoembryonic antigen-related cell adhesionmolecule 1 (biliary glycoprotein) /DB_XREF=gi:4502404 /UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /FL=gb:NM_001712.1
206622_at_HG-U133A	TRH	thyrotropin-releasing hormone	gb:NM_007117.1 /DEF=Homo sapiens thyrotropin-releasing hormone (TRH), mRNA. /FEA=mRNA /GEN=TRH /PROD=thyrotropin-releasing hormone /DB_XREF=gi:6005919 /UG=Hs.182231 thyrotropin-releasing hormone /FL=gb:NM_007117.1
206633_at_HG-U133A	CHRNA1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	gb:NM_000079.1 /DEF=Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (CHRNA1), mRNA. /FEA=mRNA /GEN=CHRNA1 /PROD=cholinergic receptor, nicotinic, alphapolypeptide 1 (muscle) precursor /DB_XREF=gi:4557456 /UG=Hs.2266 cholinergic receptor, nicotinic, alpha

			polypeptide 1 (muscle) /FL=gb:NM_000079.1
206634_at_HG-U133A	SIX3	sine oculis homeobox homolog 3 (Drosophila)	gb:NM_005413.1 /DEF=Homo sapiens sine oculis homeobox (Drosophila) homolog 3 (SIX3), mRNA. /FEA=mRNA /GEN=SIX3 /PROD=sine oculis homeobox (Drosophila) homolog 3 /DB_XREF=gi:4885596 /UG=Hs.227277 sine oculis homeobox (Drosophila) homolog 3 /FL=gb:NM_005413.1
206676_at_HG-U133A	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	gb:M33326.1 /DEF=Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds. /FEA=mRNA /GEN=NCA /PROD=non-specific cross reacting antigen /DB_XREF=gi:189101 /UG=Hs.41 carcinoembryonic antigen-related cell adhesion molecule 8 /FL=gb:M33326.1 gb:NM_001816.1
206748_s_at_HG-U133A	SPAG9	sperm associated antigen 9	gb:NM_003971.1 /DEF=Homo sapiens sperm associated antigen 9 (SPAG9), mRNA. /FEA=mRNA /GEN=SPAG9 /PROD=sperm associated antigen 9 /DB_XREF=gi:4504524 /UG=Hs.129872 sperm associated antigen 9 /FL=gb:NM_003971.1
206759_at_HG-U133A	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23A)	gb:NM_002002.1 /DEF=Homo sapiens Fc fragment of IgE, low affinity II, receptor for (CD23A) (FCER2), mRNA. /FEA=mRNA /GEN=FCER2 /PROD=Fc fragment of IgE, low affinity II, receptorfor (CD23A) /DB_XREF=gi:4503678 /UG=Hs.1416 Fc fragment of IgE, low affinity II, receptor for (CD23A) /FL=gb:M15059.1 gb:M14766.1 gb:NM_002002.1
206760_s_at_HG-U133A	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23A)	gb:NM_002002.1 /DEF=Homo sapiens Fc fragment of IgE, low affinity II, receptor for (CD23A) (FCER2), mRNA. /FEA=mRNA /GEN=FCER2 /PROD=Fc fragment of IgE, low affinity II, receptorfor (CD23A) /DB_XREF=gi:4503678 /UG=Hs.1416 Fc fragment of IgE, low affinity II, receptor for (CD23A) /FL=gb:M15059.1 gb:M14766.1 gb:NM_002002.1
206761_at_HG-U133A	TACTILE	T cell activation, increased late expression	gb:NM_005816.1 /DEF=Homo sapiens T cell activation, increased late expression (TACTILE), mRNA. /FEA=mRNA /GEN=TACTILE /PROD=T cell activation, increased late expression /DB_XREF=gi:5032140 /UG=Hs.142023 T cell activation, increased late expression /FL=gb:M88282.1 gb:NM_005816.1
206772_at_HG-U133A	PTHR2	parathyroid hormone receptor 2	gb:NM_005048.1 /DEF=Homo sapiens parathyroid hormone receptor 2

			(PTHR2), mRNA. /FEA=mRNA /GEN=PTHR2 /PROD=parathyroid hormone receptor 2 /DB_XREF=gi:4826953 /UG=Hs.159499 parathyroid hormone receptor 2 /FL=gb:NM_005048.1 gb:U25128.1
206781_at_HG-U133A	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	gb:NM_005528.1 /DEF=Homo sapiens heat shock 40kD protein 2 (HSPF2), mRNA. /FEA=mRNA /GEN=HSPF2 /PROD=heat shock 40kD protein 2 /DB_XREF=gi:5031770 /UG=Hs.172847 DnaJ (Hsp40) homolog, subfamily C, member 4 /FL=gb:AF012106.1 gb:NM_005528.1
206804_at_HG-U133A	CD3G	CD3G antigen, gamma polypeptide (TiT3 complex)	gb:NM_000073.1 /DEF=Homo sapiens CD3G antigen, gamma polypeptide (TiT3 complex) (CD3G), mRNA. /FEA=mRNA /GEN=CD3G /PROD=CD3G gamma precursor /DB_XREF=gi:4557428 /UG=Hs.2259 CD3G antigen, gamma polypeptide (TiT3 complex) /FL=gb:NM_000073.1
206847_s_at_HG-U133A	HOXA7	homeo box A7	gb:AF026397.1 /DEF=Homo sapiens homeobox transcription factor HOXA7 (HOXA7) mRNA, complete cds. /FEA=mRNA /GEN=HOXA7 /PROD=homeobox transcription factor HOXA7 /DB_XREF=gi:2739070 /UG=Hs.70954 homeo box A7 /FL=gb:AF026397.1 gb:NM_006896.1
206850_at_HG-U133A	RRP22	RAS-related on chromosome 22	gb:NM_006477.1 /DEF=Homo sapiens RAS-related on chromsome 22 (RRP22), mRNA. /FEA=mRNA /GEN=RRP22 /PROD=RAS-related on chromsome 22 /DB_XREF=gi:5454029 /UG=Hs.73088 RAS-related on chromsome 22 /FL=gb:NM_006477.1
206871_at_HG-U133A	ELA2	elastase 2, neutrophil	gb:NM_001972.1 /DEF=Homo sapiens elastase 2, neutrophil (ELA2), mRNA. /FEA=mRNA /GEN=ELA2 /PROD=elastase 2, neutrophil /DB_XREF=gi:4503548 /UG=Hs.99863 elastase 2, neutrophil /FL=gb:M34379.1 gb:NM_001972.1
206940_s_at_HG-U133A	POU4F1	POU domain, class 4, transcription factor 1	gb:NM_006237.1 /DEF=Homo sapiens POU domain, class 4, transcription factor 1 (POU4F1), mRNA. /FEA=mRNA /GEN=POU4F1 /PROD=POU domain, class 4, transcription factor 1 /DB_XREF=gi:5453937 /UG=Hs.211588 POU domain, class 4, transcription factor 1 /FL=gb:NM_006237.1
206956_at_HG-U133A	BGLAP	bone gamma-carboxyglutamate (gla)	gb:NM_000711.1 /DEF=Homo sapiens bone gamma-carboxyglutamate (gla)

		protein (osteocalcin)	protein (osteocalcin) (BGLAP), mRNA. /FEA=mRNA /GEN=BGLAP /PROD=bone gamma-carboxyglutamate (gla) protein(osteocalcin) /DB_XREF=gi:4502400 /UG=Hs.2558 bone gamma-carboxyglutamate (gla) protein (osteocalcin) /FL=gb:NM_000711.1
206995_x_at_HG-U133A	SREC	acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells	gb:NM_003693.1 /DEF=Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA. /FEA=mRNA /GEN=SREC /PROD=acetyl LDL receptor; SREC=scavenger receptorexpressed by endothelial cells /DB_XREF=gi:4507202 /UG=Hs.57735 acetyl LDL receptor; SREC /FL=gb:D63483.1 gb:D86864.1 gb:NM_003693.1
207000_s_at_HG-U133A	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	gb:NM_005605.1 /DEF=Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), mRNA. /FEA=mRNA /GEN=PPP3CC /PROD=protein phosphatase 3 (formerly 2B), catalyticsubunit, gamma isoform (calcineurin A gamma) /DB_XREF=gi:5031988 /UG=Hs.75206 protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) /FL=gb:NM_005605.1 gb:AY007249.1
207030_s_at_HG-U133A	CSRP2	cysteine and glycine-rich protein 2	gb:NM_001321.1 /DEF=Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), mRNA. /FEA=mRNA /GEN=CSRP2 /PROD=cysteine and glycine-rich protein 2 /DB_XREF=gi:4503100 /UG=Hs.10526 cysteine and glycine-rich protein 2 /FL=gb:BC000992.2 gb:U57646.1 gb:NM_001321.1
207057_at_HG-U133A	SLC16A7	solute carrier family 16 (monocarboxylic acid transporters), member 7	gb:NM_004731.1 /DEF=Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 7 (SLC16A7), mRNA. /FEA=mRNA /GEN=SLC16A7 /PROD=solute carrier family 16 (monocarboxylic acidtransporters), member 7 /DB_XREF=gi:4759119 /UG=Hs.132183 solute carrier family 16 (monocarboxylic acid transporters), member 7 /FL=gb:AF058056.1 gb:NM_004731.1
207076_s_at_HG-U133A	ASS	argininosuccinate synthetase	gb:NM_000050.1 /DEF=Homo sapiens argininosuccinate synthetase (ASS), mRNA. /FEA=mRNA /GEN=ASS /PROD=argininosuccinate synthetase

			/DB_XREF=gi:4557336 /UG=Hs.160786 argininosuccinate synthetase /FL=gb:NM_000050.1
207168_s_at_HG-U133A	H2AFY	H2A histone family, member Y	gb:NM_004893.1 /DEF=Homo sapiens H2A histone family, member Y (H2AFY), mRNA. /FEA=mRNA /GEN=H2AFY /PROD=H2A histone family, member Y /DB_XREF=gi:4758495 /UG=Hs.75258 H2A histone family, member Y /FL=gb:AF054174.1 gb:NM_004893.1
207194_s_at_HG-U133A	ICAM4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group	gb:NM_001544.2 /DEF=Homo sapiens intercellular adhesion molecule 4, Landsteiner-Wiener blood group (ICAM4), transcript variant 1, mRNA. /FEA=mRNA /GEN=ICAM4 /PROD=intercellular adhesion molecule 4, isoform 1precursor /DB_XREF=gi:12545400 /UG=Hs.108287 intercellular adhesion molecule 4, Landsteiner-Wiener blood group /FL=gb:NM_001544.2 gb:L27671.1
207224_s_at_HG-U133A	SIGLEC7	sialic acid binding Ig-like lectin 7	gb:NM_016543.1 /DEF=Homo sapiens D-siglec precursor, (LOC51766), mRNA. /FEA=mRNA /GEN=LOC51766 /PROD=D-siglec precursor, /DB_XREF=gi:7706570 /UG=Hs.149250 D-siglec precursor, /FL=gb:AF178981.1 gb:NM_016543.1
207269_at_HG-U133A	DEFA4	defensin, alpha 4, corticostatin	gb:NM_001925.1 /DEF=Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /FEA=mRNA /GEN=DEFA4 /PROD=defensin, alpha 4, preproprotein /DB_XREF=gi:4503302 /UG=Hs.2582 defensin, alpha 4, corticostatin /FL=gb:NM_001925.1
207384_at_HG-U133A	PGLYRP	peptidoglycan recognition protein	gb:NM_005091.1 /DEF=Homo sapiens peptidoglycan recognition protein (PGLYRP), mRNA. /FEA=mRNA /GEN=PGLYRP /PROD=peptidoglycan recognition protein /DB_XREF=gi:4827035 /UG=Hs.137583 peptidoglycan recognition protein /FL=gb:AF076483.1 gb:NM_005091.1 gb:AF242517.1
207403_at_HG-U133A	IRS4	insulin receptor substrate 4	gb:NM_003604.1 /DEF=Homo sapiens insulin receptor substrate 4 (IRS4), mRNA. /FEA=mRNA /GEN=IRS4 /PROD=insulin receptor substrate 4 /DB_XREF=gi:4504732 /UG=Hs.159609 insulin receptor substrate 4 /FL=gb:AF007567.1 gb:NM_003604.1

207520_at_HG-U133A			Consensus includes gb:BG494940 /FEA=EST /DB_XREF=gi:13456455 /DB_XREF=est:602540961F1 /CLONE=IMAGE:4671854 /UG=Hs.554 Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-ARo) /FL=gb:J04137.1 gb:NM_004600.1
207543_s_at_HG-U133A	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	gb:NM_000917.1 /DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I (P4HA1), mRNA. /FEA=mRNA /GEN=P4HA1 /PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptidel /DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I /FL=gb:M24486.1 gb:NM_000917.1
207616_s_at_HG-U133A	TANK	TRAF family member-associated NFKB activator	gb:NM_004180.1 /DEF=Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA. /FEA=mRNA /GEN=TANK /PROD=TRAF family member-associated NFKB activator /DB_XREF=gi:4759249 /UG=Hs.146847 TRAF family member-associated NFKB activator /FL=gb:U63830.1 gb:NM_004180.1
207641_at_HG-U133A	TACI	transmembrane activator and CAML interactor	gb:NM_012452.1 /DEF=Homo sapiens transmembrane activator and CAML interactor (TACI), mRNA. /FEA=mRNA /GEN=TACI /PROD=transmembrane activator and CAML interactor /DB_XREF=gi:6912693 /UG=Hs.158341 transmembrane activator and CAML interactor /FL=gb:AF023614.1 gb:NM_012452.1
207654_x_at_HG-U133A	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	gb:NM_001938.1 /DEF=Homo sapiens down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1), mRNA. /FEA=mRNA /GEN=DR1 /PROD=down-regulator of transcription 1 /DB_XREF=gi:4503380 /UG=Hs.16697 down-regulator of transcription 1, TBP-binding (negative cofactor 2) /FL=gb:M97388.1 gb:NM_001938.1
207655_s_at_HG-U133A	BLNK	B-cell linker	gb:NM_013314.1 /DEF=Homo sapiens B cell linker protein (SLP65), mRNA. /FEA=mRNA /GEN=SLP65 /PROD=B cell linker protein /DB_XREF=gi:7019534 /UG=Hs.167746 B cell linker protein

			/FL=gb:AF068180.1 gb:NM_013314.1
207697_x_at_HG-U133A	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	gb:NM_005874.1 /DEF=Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 (LILRB2), mRNA. /FEA=mRNA /GEN=LILRB2 /PROD=leukocyte immunoglobulin-like receptor,subfamily B (with TM and ITIM domains), member 2 /DB_XREF=gi:5031910 /UG=Hs.22405 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /FL=gb:AF025528.1 gb:NM_005874.1
207700_s_at_HG-U133A	NCOA3	nuclear receptor coactivator 3	gb:NM_006534.1 /DEF=Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA. /FEA=mRNA /GEN=NCOA3 /PROD=nuclear receptor coactivator 3 /DB_XREF=gi:5729725 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF036892.1 gb:NM_006534.1
207734_at_HG-U133A	FLJ20340	hypothetical protein FLJ20340	gb:NM_017773.1 /DEF=Homo sapiens hypothetical protein FLJ20340 (FLJ20340), mRNA. /FEA=mRNA /GEN=FLJ20340 /PROD=hypothetical protein FLJ20340 /DB_XREF=gi:8923315 /UG=Hs.272794 hypothetical protein FLJ20340 /FL=gb:NM_017773.1
207760_s_at_HG-U133A	NCOR2	nuclear receptor co-repressor 2	gb:NM_006312.1 /DEF=Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /FEA=mRNA /GEN=NCOR2 /PROD=nuclear receptor co-repressor 2 /DB_XREF=gi:5454073 /UG=Hs.287994 nuclear receptor co-repressor 2 /FL=gb:AF113003.1 gb:NM_006312.1
207777_s_at_HG-U133A	SP140	SP140 nuclear body protein	gb:NM_007237.1 /DEF=Homo sapiens nuclear body protein Sp140 (SP140), mRNA. /FEA=mRNA /GEN=SP140 /PROD=nuclear body protein Sp140 /DB_XREF=gi:6005879 /UG=Hs.309943 nuclear body protein Sp140 /FL=gb:U63420.1 gb:NM_007237.1
207801_s_at_HG-U133A	RNF10	ring finger protein 10	gb:NM_014868.1 /DEF=Homo sapiens ring finger protein 10 (RNF10), mRNA. /FEA=mRNA /GEN=RNF10 /PROD=ring finger protein 10 /DB_XREF=gi:7662652 /UG=Hs.5094 ring finger protein 10 /FL=gb:D87451.1 gb:NM_014868.1

207802_at_HG-U133A	SGP28	specific granule protein (28 kDa)	gb:NM_006061.1 /DEF=Homo sapiens specific granule protein (28 kDa); cysteine-rich secretory protein-3 (SGP28), mRNA. /FEA=mRNA /GEN=SGP28 /PROD=specific granule protein (28 kDa); cysteine-richsecretory protein-3 /DB_XREF=gi:5174674 /UG=Hs.54431 specific granule protein (28 kDa); cysteine-rich secretory protein-3 /FL=gb:NM_006061.1
207809_s_at_HG-U133A	ATP6IP1	ATPase, H+ transporting, lysosomal interacting protein 1	gb:NM_001183.1 /DEF=Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1 (ATP6S1), mRNA. /FEA=mRNA /GEN=ATP6S1 /PROD=ATPase, H+ transporting, lysosomal subunit 1 /DB_XREF=gi:4557340 /UG=Hs.6551 ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1 /FL=gb:NM_001183.1
207819_s_at_HG-U133A	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	gb:NM_000443.2 /DEF=Homo sapiens ATP-binding cassette, sub-family B (MDRTAP), member 4 (ABCB4), transcript variant A, mRNA. /FEA=mRNA /GEN=ABCB4 /PROD=ATP-binding cassette, subfamily B, member 4;isoform A /DB_XREF=gi:9961253 /UG=Hs.73812 ATP-binding cassette, sub-family B (MDRTAP), member 4 /FL=gb:M23234.1 gb:NM_000443.2
207871_s_at_HG-U133A	ST7	suppression of tumorigenicity 7	gb:NM_018412.2 /DEF=Homo sapiens suppression of tumorigenicity 7 (ST7), transcript variant a, mRNA. /FEA=mRNA /GEN=ST7 /PROD=suppression of tumorigenicity 7, isoform a /DB_XREF=gi:11761623 /UG=Hs.5814 suppression of tumorigenicity 7 /FL=gb:NM_018412.2 gb:AF234882.1
207957_s_at_HG-U133A	PRKCB1	protein kinase C, beta 1	gb:NM_002738.1 /DEF=Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA. /FEA=mRNA /GEN=PRKCB1 /PROD=protein kinase C, beta 1 /DB_XREF=gi:4506068 /UG=Hs.77202 protein kinase C, beta 1 /FL=gb:NM_002738.1
207971_s_at_HG-U133A	KIAA0582	KIAA0582 protein	gb:NM_015147.1 /DEF=Homo sapiens KIAA0582 protein (KIAA0582), mRNA. /FEA=mRNA /GEN=KIAA0582 /PROD=KIAA0582 protein /DB_XREF=gi:13124755 /UG=Hs.79507 KIAA0582 protein /FL=gb:BC002982.1 gb:NM_015147.1 gb:BC004873.1
207983_s_at_HG-	STAG2	stromal antigen 2	gb:NM_006603.1 /DEF=Homo sapiens stromal antigen 2 (STAG2), mRNA.

U133A			/FEA=mRNA /GEN=STAG2 /PROD=stromal antigen 2 /DB_XREF=gi:5730068 /UG=Hs.8217 stromal antigen 2 /FL=gb:NM_006603.1
207996_s_at_HG-U133A	C18orf1	chromosome 18 open reading frame 1	gb:NM_004338.1 /DEF=Homo sapiens chromosome 18 open reading frame 1 (C18ORF1), mRNA. /FEA=mRNA /GEN=C18ORF1 /PROD=chromosome 18 open reading frame 1 /DB_XREF=gi:4757883 /UG=Hs.153498 chromosome 18 open reading frame 1 /FL=gb:AF009426.1 gb:NM_004338.1
208033_s_at_HG-U133A	ATBF1	AT-binding transcription factor 1	gb:NM_006885.1 /DEF=Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA. /FEA=mRNA /GEN=ATBF1 /PROD=AT-binding transcription factor 1 /DB_XREF=gi:5901893 /UG=Hs.101842 AT-binding transcription factor 1 /FL=gb:D10250.1 gb:NM_006885.1
208042_at_HG-U133A	HSU84971	fetal hypothetical protein	gb:NM_013303.1 /DEF=Homo sapiens fetal hypothetical protein (HSU84971), mRNA. /FEA=mRNA /GEN=HSU84971 /PROD=fetal hypothetical protein /DB_XREF=gi:9558744 /UG=Hs.104530 fetal hypothetical protein /FL=gb:U84971.1 gb:NM_013303.1
208091_s_at_HG-U133A	DKFZP564K0822	hypothetical protein DKFZp564K0822	gb:NM_030796.1 /DEF=Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA. /FEA=mRNA /GEN=DKFZP564K0822 /PROD=hypothetical protein DKFZp564K0822 /DB_XREF=gi:13540577 /FL=gb:NM_030796.1
208141_s_at_HG-U133A	MGC4293	hypothetical protein MGC4293	gb:NM_031304.1 /DEF=Homo sapiens hypothetical protein MGC4293 (MGC4293), mRNA. /FEA=mRNA /GEN=MGC4293 /PROD=hypothetical protein MGC4293 /DB_XREF=gi:13775227 /FL=gb:NM_031304.1
208146_s_at_HG-U133A	CPVL	carboxypeptidase, vitellogenic-like	gb:NM_031311.1 /DEF=Homo sapiens serine carboxypeptidase vitellogenic-like (LOC54504), mRNA. /FEA=mRNA /GEN=LOC54504 /PROD=serine carboxypeptidase vitellogenic-like /DB_XREF=gi:13786124 /FL=gb:NM_031311.1
208168_s_at_HG-U133A	CHIT1	chitinase 1 (chitotriosidase)	gb:NM_003465.1 /DEF=Homo sapiens chitinase 1 (chitotriosidase) (CHIT1), mRNA. /FEA=mRNA /GEN=CHIT1 /PROD=chitotriosidase /DB_XREF=gi:4502808 /UG=Hs.91093 chitinase 1 (chitotriosidase)

			/FL=gb:U29615.1 gb:NM_003465.1
208190_s_at_HG-U133A	LISCH7	liver-specific bHLH-Zip transcription factor	gb:NM_015925.1 /DEF=Homo sapiens liver-specific bHLH-Zip transcription factor (LISCH7), mRNA. /FEA=mRNA /GEN=LISCH7 /PROD=LISCH protein /DB_XREF=gi:7706247 /UG=Hs.95697 liver-specific bHLH-Zip transcription factor /FL=gb:AF130366.1 gb:NM_015925.1
208195_at_HG-U133A	TTN	titin	gb:NM_003319.1 /DEF=Homo sapiens titin (TTN), mRNA. /FEA=mRNA /GEN=TTN /PROD=titin /DB_XREF=gi:4507720 /UG=Hs.172004 titin /FL=gb:NM_003319.1
208217_at_HG-U133A	GABRR2	gamma-aminobutyric acid (GABA) receptor, rho 2	gb:NM_002043.1 /DEF=Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 2 (GABRR2), mRNA. /FEA=mRNA /GEN=GABRR2 /PROD=gamma-aminobutyric acid (GABA) receptor, rho 2precursor /DB_XREF=gi:4503870 /UG=Hs.99927 gamma-aminobutyric acid (GABA) receptor, rho 2 /FL=gb:M86868.1 gb:NM_002043.1
208229_at_HG-U133A	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	gb:NM_022975.1 /DEF=Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) (FGFR2), transcript variant 8, mRNA. /FEA=mRNA /GEN=FGFR2 /PROD=fibroblast growth factor receptor 2, isoform 8precursor /DB_XREF=gi:13186264 /UG=Hs.278581 fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) /FL=gb:NM_022975.1
208248_x_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	gb:NM_001642.1 /DEF=Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA. /FEA=mRNA /GEN=APLP2 /PROD=amyloid beta (A4) precursor-like protein 2 /DB_XREF=gi:4502146 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:L09209.1 gb:NM_001642.1 gb:L27631.1 gb:AF168956.1
208268_at_HG-U133A	ADAM28	a disintegrin and metalloproteinase	gb:NM_021777.1 /DEF=Homo sapiens a disintegrin and metalloproteinase

		domain 28	domain 28 (ADAM28), transcript variant 3, mRNA. /FEA=mRNA /GEN=ADAM28 /PROD=a disintegrin and metalloproteinase domain 28,isoform 3 preproprotein /DB_XREF=gi:11496993 /UG=Hs.174030 a disintegrin and metalloproteinase domain 28 /FL=gb:NM_021777.1 gb:AF137335.1
208302_at_HG-U133A	HB-1	minor histocompatibility antigen HB-1	gb:NM_021182.1 /DEF=Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /FEA=mRNA /GEN=HB-1 /PROD=minor histocompatibility antigen HB-1 /DB_XREF=gi:10863982 /UG=Hs.158320 minor histocompatibility antigen HB-1 /FL=gb:NM_021182.1 gb:AF103884.1
208306_x_at_HG-U133A	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	gb:NM_021983.2 /DEF=Homo sapiens major histocompatibility complex, class II, DR beta 4 (HLA-DRB4), mRNA. /FEA=mRNA /GEN=HLA-DRB4 /PROD=major histocompatibility complex, class II, DRbeta 4 /DB_XREF=gi:11875206 /UG=Hs.293934 major histocompatibility complex, class II, DR beta 4 /FL=gb:NM_021983.2
208456_s_at_HG-U133A	RRAS2	related RAS viral (r-ras) oncogene homolog 2	gb:NM_012250.1 /DEF=Homo sapiens oncogene TC21 (TC21), mRNA. /FEA=CDS /GEN=TC21 /PROD=oncogene TC21 /DB_XREF=gi:6912697 /UG=Hs.206097 oncogene TC21 /FL=gb:M31468.1 gb:NM_012250.1
208470_s_at_HG-U133A	HPR	haptoglobin-related protein	gb:NM_020995.1 /DEF=Homo sapiens haptoglobin-related protein (HPR), mRNA. /FEA=CDS /GEN=HPR /PROD=haptoglobin-related protein /DB_XREF=gi:10337588 /UG=Hs.328822 haptoglobin-related protein /FL=gb:NM_020995.1
208581_x_at_HG-U133A	MT1X	metallothionein 1X	gb:NM_005952.1 /DEF=Homo sapiens metallothionein 1X (MT1X), mRNA. /FEA=CDS /GEN=MT1X /PROD=metallothionein 1X /DB_XREF=gi:10835231 /UG=Hs.278462 metallothionein 1X /FL=gb:NM_005952.1
208611_s_at_HG-U133A	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	gb:U83867.1 /DEF=Human alpha II spectrin mRNA, complete cds. /FEA=mRNA /PROD=alpha II spectrin /DB_XREF=gi:1805279 /UG=Hs.77196 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) /FL=gb:J05243.1 gb:U83867.1 gb:NM_003127.1
208612_at_HG-U133A	GRP58	glucose regulated protein, 58kD	gb:D83485.1 /DEF=Homo sapiens mRNA for ER-60 protease, complete cds.

			/FEA=mRNA /PROD=ER-60 protease /DB_XREF=gi:1208426 /UG=Hs.289101 glucose regulated protein, 58kD /FL=gb:U42068.1 gb:D83485.1 gb:D16234.1 gb:NM_005313.1
208614_s_at_HG-U133A	FLNB	filamin B, beta (actin binding protein 278)	gb:M62994.1 /DEF=Homo sapiens thyroid autoantigen (truncated actin-binding protein) mRNA, complete cds. /FEA=mRNA /PROD=thyroid autoantigen /DB_XREF=gi:349450 /UG=Hs.81008 filamin B, beta (actin-binding protein-278) /FL=gb:AF043045.1 gb:AF042166.1 gb:M62994.1 gb:NM_001457.1
208623_s_at_HG-U133A	VIL2	villin 2 (ezrin)	gb:J05021.1 /DEF=Human cytovillin 2 (VIL2) mRNA, complete cds. /FEA=mRNA /GEN=VIL2 /DB_XREF=gi:340216 /UG=Hs.155191 villin 2 (ezrin) /FL=gb:J05021.1 gb:AL162086.1 gb:NM_003379.2
208629_s_at_HG-U133A	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Consensus includes gb:BG472176 /FEA=EST /DB_XREF=gi:13404550 /DB_XREF=est:602513910F1 /CLONE=IMAGE:4645587 /UG=Hs.75860 hydroxyacyl-Coenzyme A dehydrogenase3-ketoacyl-Coenzyme A thiolaseenoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit /FL=gb:NM_000182.1 gb:D16480.1 gb:U04627.1
208645_s_at_HG-U133A			gb:AF116710.1 /DEF=Homo sapiens PRO2640 mRNA, complete cds. /FEA=mRNA /PROD=PRO2640 /DB_XREF=gi:7959918 /UG=Hs.244621 ribosomal protein S14 /FL=gb:BC001126.1 gb:BC003401.1 gb:NM_005617.1 gb:AF116710.1
208646_at_HG-U133A			gb:AF116710.1 /DEF=Homo sapiens PRO2640 mRNA, complete cds. /FEA=mRNA /PROD=PRO2640 /DB_XREF=gi:7959918 /UG=Hs.244621 ribosomal protein S14 /FL=gb:BC001126.1 gb:BC003401.1 gb:NM_005617.1 gb:AF116710.1
208650_s_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	Consensus includes gb:BG327863 /FEA=EST /DB_XREF=gi:13134301 /DB_XREF=est:602426876F1 /CLONE=IMAGE:4564675 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:M58664.1 gb:L33930.1 gb:NM_013230.1
208651_x_at_HG-	CD24	CD24 antigen (small cell lung carcinoma	gb:M58664.1 /DEF=Homo sapiens CD24 signal transducer mRNA, complete

U133A		cluster 4 antigen)	cds. /FEA=mRNA /PROD=signal transducer CD24 /DB_XREF=gi:180167 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:M58664.1 gb:L33930.1 gb:NM_013230.1
208657_s_at_HG-U133A	MSF	MLL septin-like fusion	gb:AF142408.1 /DEF=Homo sapiens cell division control protein septin D1 mRNA, complete cds. /FEA=mRNA /PROD=cell division control protein septin D1 /DB_XREF=gi:11055010 /UG=Hs.181002 MLL septin-like fusion /FL=gb:AF142408.1 gb:AF142569.1
208664_s_at_HG-U133A	TTC3	tetratricopeptide repeat domain 3	Consensus includes gb:AU131711 /FEA=EST /DB_XREF=gi:10992065 /DB_XREF=est:AU131711 /CLONE=NT2RP3003092 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=gb:D84294.1
208674_x_at_HG-U133A	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gb:BC002594.1 /DEF=Homo sapiens, dolichyl-diphosphooligosaccharide-protein glycosyltransferase, clone MGC:2191, mRNA, complete cds. /FEA=mRNA /PROD=dolichyl-diphosphooligosaccharide-proteinglycosyltransferase /DB_XREF=gi:12803530 /UG=Hs.34789 dolichyl-diphosphooligosaccharide-protein glycosyltransferase /FL=gb:BC002594.1 gb:D29643.1 gb:NM_005216.1
208683_at_HG-U133A	CAPN2	calpain 2, (m/II) large subunit	gb:M23254.1 /DEF=Human Ca2-activated neutral protease large subunit (CANP) mRNA, complete cds. /FEA=mRNA /GEN=CANP /PROD=neutral protease large subunit /DB_XREF=gi:511636 /UG=Hs.76288 calpain 2, (mII) large subunit /FL=gb:NM_001748.3 gb:M23254.1 gb:AF261089.1
208689_s_at_HG-U133A	RPN2	ribophorin II	gb:BC003560.1 /DEF=Homo sapiens, ribophorin II, clone MGC:1817, mRNA, complete cds. /FEA=mRNA /PROD=ribophorin II /DB_XREF=gi:13097707 /UG=Hs.75722 ribophorin II /FL=gb:BC003560.1 gb:NM_002951.1
208697_s_at_HG-U133A	EIF3S6	eukaryotic translation initiation factor 3, subunit 6 (48kD)	gb:BC000734.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 3, subunit 6 (48kD), clone MGC:2060, mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic translation initiation factor 3,subunit 6 (48kD) /DB_XREF=gi:12653884 /UG=Hs.106673 eukaryotic translation initiation factor 3, subunit 6 (48kD) /FL=gb:BC000734.1 gb:U62962.1 gb:U54562.1 gb:U85947.1 gb:U94175.1 gb:NM_001568.1

208702_x_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	Consensus includes gb:AI525212 /FEA=EST /DB_XREF=gi:4439347 /DB_XREF=est:pt1.1-2.A08.r /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:BC000373.1
208703_s_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	Consensus includes gb:BG427393 /FEA=EST /DB_XREF=gi:13333995 /DB_XREF=est:602499110F1 /CLONE=IMAGE:4612562 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:BC000373.1
208710_s_at_HG-U133A	AP3D1	adaptor-related protein complex 3, delta 1 subunit	Consensus includes gb:AI424923 /FEA=EST /DB_XREF=gi:4270841 /DB_XREF=est:tg19a07.x1 /CLONE=IMAGE:2109204 /UG=Hs.75056 adaptor-related protein complex 3, delta 1 subunit /FL=gb:AF002163.1
208741_at_HG-U133A	SAP18	sin3-associated polypeptide, 18kD	Consensus includes gb:AW274856 /FEA=EST /DB_XREF=gi:6661886 /DB_XREF=est:xm61g03.x1 /CLONE=IMAGE:2688724 /UG=Hs.23964 sin3-associated polypeptide, 18kD /FL=gb:NM_005870.2 gb:U96915.1 gb:AF153608.1 gb:U78303.1
208754_s_at_HG-U133A	NAP1L1	nucleosome assembly protein 1-like 1	gb:AL162068.1 /DEF=Homo sapiens mRNA; cDNA DKFZp762G106 (from clone DKFZp762G106); complete cds. /FEA=mRNA /GEN=DKFZp762G106 /PROD=hypothetical protein /DB_XREF=gi:7328143 /UG=Hs.179662 nucleosome assembly protein 1-like 1 /FL=gb:BC002387.1 gb:AL162068.1
208819_at_HG-U133A	MEL	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog	gb:BC002977.1 /DEF=Homo sapiens, mel transforming oncogene (derived from cell line NK14)- RAB8 homolog, clone MGC:2196, mRNA, complete cds. /FEA=mRNA /PROD=mel transforming oncogene (derived from cellline NK14)- RAB8 homolog /DB_XREF=gi:12804236 /UG=Hs.5947 mel transforming oncogene (derived from cell line NK14)- RAB8 homolog /FL=gb:BC002977.1 gb:NM_005370.2
208852_s_at_HG-U133A	CANX	calnexin	Consensus includes gb:AI761759 /FEA=EST /DB_XREF=gi:5177515 /DB_XREF=est:wg67h12.x1 /CLONE=IMAGE:2370215 /UG=Hs.155560 calnexin /FL=gb:NM_001746.1 gb:BC003552.1 gb:M94859.1 gb:M98452.1 gb:L10284.1 gb:L18887.1
208858_s_at_HG-	KIAA0747	KIAA0747 protein	gb:BC004998.1 /DEF=Homo sapiens, Similar to membrane bound C2 domain

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U133A			containing protein, clone MGC:4422, mRNA, complete cds. /FEA=mRNA /PROD=Similar to membrane bound C2 domain containingprotein /DB_XREF=gi:13436457 /UG=Hs.8309 KIAA0747 protein /FL=gb:BC004998.1
208864_s_at_HG-U133A	TXN	thioredoxin	gb:AF313911.1 /DEF=Homo sapiens thioredoxin mRNA, complete cds. /FEA=mRNA /PROD=thioredoxin /DB_XREF=gi:11345419 /UG=Hs.76136 thioredoxin /FL=gb:AF313911.1 gb:BC003377.1 gb:J04026.1 gb:NM_003329.1 gb:AF276919.1 gb:AY004872.1
208890_s_at_HG-U133A	PLXNB2	plexin B2	gb:BC004542.1 /DEF=Homo sapiens, clone MGC:11315, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:11315) /DB_XREF=gi:13528689 /UG=Hs.3989 plexin B2 /FL=gb:BC004542.1
208894_at_HG-U133A	HLA-DRA	major histocompatibility complex, class II, DR alpha	gb:M60334.1 /DEF=Human MHC class II HLA-DR-alpha mRNA, complete cds. /FEA=mRNA /GEN=HLA-DRA /PROD=cell surface glycoprotein /DB_XREF=gi:188255 /UG=Hs.76807 major histocompatibility complex, class II, DR alpha /FL=gb:M60334.1 gb:NM_019111.1
208908_s_at_HG-U133A	CAST	calpastatin	gb:AF327443.1 /DEF=Homo sapiens calpastatin mRNA, complete cds. /FEA=mRNA /PROD=calpastatin /DB_XREF=gi:12056961 /UG=Hs.279607 calpastatin /FL=gb:AF327443.1 gb:U26724.2
208913_at_HG-U133A	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	Consensus includes gb:AA868560 /FEA=EST /DB_XREF=gi:2964005 /DB_XREF=est:ak43g11.s1 /CLONE=IMAGE:1408772 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 /FL=gb:AF190863.1 gb:AF233522.1 gb:AF165531.1 gb:NM_015044.1
208914_at_HG-U133A	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	Consensus includes gb:BE646414 /FEA=EST /DB_XREF=gi:9970725 /DB_XREF=est:7e86d08.x1 /CLONE=IMAGE:3292047 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 /FL=gb:AF190863.1 gb:AF233522.1 gb:AF165531.1 gb:NM_015044.1
208918_s_at_HG-	FLJ13052	NAD kinase	Consensus includes gb:AI334128 /FEA=EST /DB_XREF=gi:4070687

U133A			/DB_XREF=est:qq07e12.x1 /CLONE=IMAGE:1931854 /UG=Hs.220324 hypothetical protein FLJ13052 /FL=gb:BC001709.1
209003_at_HG-U133A	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	gb:AF070548.1 /DEF=Homo sapiens clone 24408 2-oxoglutarate carrier protein mRNA, complete cds. /FEA=mRNA /PROD=2-oxoglutarate carrier protein /DB_XREF=gi:3387910 /UG=Hs.184877 solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 /FL=gb:AF070548.1
209018_s_at_HG-U133A	PINK1	PTEN induced putative kinase 1	Consensus includes gb:BF432478 /FEA=EST /DB_XREF=gi:11444621 /DB_XREF=est:nac55d04.x1 /CLONE=IMAGE:3406494 /UG=Hs.6163 Homo sapiens protein kinase BRPK mRNA, complete cds /FL=gb:AF316873.1
209019_s_at_HG-U133A	PINK1	PTEN induced putative kinase 1	gb:AF316873.1 /DEF=Homo sapiens protein kinase BRPK mRNA, complete cds. /FEA=mRNA /PROD=protein kinase BRPK /DB_XREF=gi:13492051 /UG=Hs.6163 Homo sapiens protein kinase BRPK mRNA, complete cds /FL=gb:AF316873.1
209023_s_at_HG-U133A	STAG2	stromal antigen 2	gb:BC001765.1 /DEF=Homo sapiens, Similar to stromal antigen 2, clone MGC:1282, mRNA, complete cds. /FEA=mRNA /PROD=Similar to stromal antigen 2 /DB_XREF=gi:12804678 /UG=Hs.8217 stromal antigen 2 /FL=gb:BC001765.1
209055_s_at_HG-U133A	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	Consensus includes gb:AW268817 /FEA=EST /DB_XREF=gi:6655847 /DB_XREF=est:xv38c01.x1 /CLONE=IMAGE:2815392 /UG=Hs.155174 CDC5 (cell division cycle 5, S. pombe, homolog)-like /FL=gb:NM_001253.1 gb:U86753.1 gb:AB007892.1
209060_x_at_HG-U133A	NCOA3	nuclear receptor coactivator 3	Consensus includes gb:AI438999 /FEA=EST /DB_XREF=gi:4301251 /DB_XREF=est:tc84b12.x1 /CLONE=IMAGE:2072831 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF010227.1 gb:AF012108.1 gb:AF016031.1
209061_at_HG-U133A	NCOA3	nuclear receptor coactivator 3	Consensus includes gb:AI761748 /FEA=EST /DB_XREF=gi:5177504 /DB_XREF=est:wg67h01.x1 /CLONE=IMAGE:2370193 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF010227.1 gb:AF012108.1 gb:AF016031.1
209062_x_at_HG-	NCOA3	nuclear receptor coactivator 3	gb:AF010227.1 /DEF=Homo sapiens receptor-associated coactivator 3 (RAC3)

U133A			mRNA, complete cds. /FEA=mRNA /GEN=RAC3 /PROD=receptor-associated coactivator 3 /DB_XREF=gi:2318005 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF010227.1 gb:AF012108.1 gb:AF016031.1
209075_s_at_HG-U133A	NIFU	nitrogen fixation cluster-like	gb:AY009128.1 /DEF=Homo sapiens ISCU2 (ISCU) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=ISCU /PROD=ISCU2 /DB_XREF=gi:11545706 /UG=Hs.9908 nitrogen fixation cluster-like /FL=gb:AY009128.1
209085_x_at_HG-U133A	RFC1	replication factor C (activator 1) 1 (145kD)	gb:L14922.1 /DEF=Homo sapiens DNA-binding protein (PO-GA) mRNA, complete cds. /FEA=mRNA /PROD=DNA-binding protein /DB_XREF=gi:307337 /UG=Hs.166563 replication factor C (activator 1) 1 (145kD) /FL=gb:AF040250.1 gb:L14922.1
209101_at_HG-U133A	CTGF	connective tissue growth factor	gb:M92934.1 /DEF=Human connective tissue growth factor, complete cds. /FEA=mRNA /PROD=connective tissue growth factor /DB_XREF=gi:180923 /UG=Hs.75511 connective tissue growth factor /FL=gb:M92934.1 gb:NM_001901.1
209135_at_HG-U133A	ASPH	aspartate beta-hydroxylase	gb:AF289489.1 /DEF=Homo sapiens aspartyl beta-hydroxylase 2.8 kb transcript mRNA, complete cds; alternatively spliced. /FEA=mRNA /PROD=aspartyl beta-hydroxylase 2.8 kb transcript /DB_XREF=gi:11878115 /UG=Hs.283664 aspartate beta-hydroxylase /FL=gb:AF289489.1
209160_at_HG-U133A	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	gb:AB018580.1 /DEF=Homo sapiens mRNA for hluPGFS, complete cds. /FEA=mRNA /GEN=c-hluPGFS /PROD=hluPGFS /DB_XREF=gi:6624210 /UG=Hs.78183 aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) /FL=gb:AF149416.2 gb:NM_003739.2 gb:D17793.1 gb:AB018580.1
209167_at_HG-U133A	GPM6B	glycoprotein M6B	Consensus includes gb:AI419030 /FEA=EST /DB_XREF=gi:4264961 /DB_XREF=est:tf53b01.x1 /CLONE=IMAGE:2102953 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
209168_at_HG-U133A	GPM6B	glycoprotein M6B	Consensus includes gb:AW148844 /FEA=EST /DB_XREF=gi:6196740

			/DB_XREF=est:xf05c06.x1 /CLONE=IMAGE:2617162 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
209169_at_HG-U133A	GPM6B	glycoprotein M6B	Consensus includes gb:N63576 /FEA=EST /DB_XREF=gi:1211405 /DB_XREF=est:yy63f07.s1 /CLONE=IMAGE:278245 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
209170_s_at_HG-U133A	GPM6B	glycoprotein M6B	gb:AF016004.1 /DEF=Homo sapiens m6b1 mRNA, complete cds. /FEA=mRNA /GEN=m6b1 /DB_XREF=gi:3387766 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
209178_at_HG-U133A	DDX38	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 38	gb:AF038391.1 /DEF=Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds. /FEA=mRNA /GEN=PRP16 /PROD=pre-mRNA splicing factor /DB_XREF=gi:3123905 /UG=Hs.78054 pre-mRNA splicing factor similar to S. cerevisiae Prp16 /FL=gb:BC004235.1 gb:D86977.1 gb:AF038391.1 gb:NM_014003.1
209186_at_HG-U133A	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	gb:M23114.1 /DEF=Homo sapiens calcium-ATPase (HK1) mRNA, complete cds. /FEA=mRNA /GEN=HK1 /DB_XREF=gi:184100 /UG=Hs.1526 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 /FL=gb:M23114.1
209188_x_at_HG-U133A	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	gb:BC002809.1 /DEF=Homo sapiens, down-regulator of transcription 1, TBP-binding (negative cofactor 2), clone MGC:4292, mRNA, complete cds. /FEA=mRNA /PROD=down-regulator of transcription 1, TBP-binding(negative cofactor 2) /DB_XREF=gi:12803924 /UG=Hs.16697 down-regulator of transcription 1, TBP-binding (negative cofactor 2) /FL=gb:BC002809.1
209190_s_at_HG-U133A	DIAPH1	diaphanous homolog 1 (Drosophila)	gb:AF051782.1 /DEF=Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds. /FEA=mRNA /GEN=HDIA1 /PROD=diaphanous 1 /DB_XREF=gi:2947237 /UG=Hs.26584 diaphanous (Drosophila, homolog) 1 /FL=gb:AF051782.1 gb:NM_005219.1
209197_at_HG-U133A	KIAA0080	KIAA0080 protein	Consensus includes gb:AA626780 /FEA=EST /DB_XREF=gi:2539167 /DB_XREF=est:ad09f03.s1 /CLONE=IMAGE:877757 /UG=Hs.74554 KIAA0080 protein /FL=gb:BC004291.1

209236_at_HG-U133A			Consensus includes gb:AL389886 /DEF=Human DNA sequence from clone RP1-237C24 on chromosome 20 Contains the 3 end of the SLC23A1 gene encoding solute carrier family 23 member1 (nucleobase transporters), ESTs, STSs and GSSs /FEA=mRNA /DB_XREF=gi:10086152 /UG=Hs.82042 solute carrier family 23 (nucleobase transporters), member 1 /FL=gb:AF058319.1 gb:NM_005116.1 gb:AF164142.1
209253_at_HG-U133A	SCAM-1	vinexin beta (SH3-containing adaptor molecule-1)	gb:AF037261.1 /DEF=Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds. /FEA=mRNA /PROD=SH3-containing adaptor molecule-1 /DB_XREF=gi:3004947 /UG=Hs.33787 vinexin beta (SH3-containing adaptor molecule-1) /FL=gb:AF037261.1
209259_s_at_HG-U133A	CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	gb:AF020043.1 /DEF=Homo sapiens chromosome-associated polypeptide (HCAP) mRNA, complete cds. /FEA=mRNA /GEN=HCAP /PROD=chromosome-associated polypeptide /DB_XREF=gi:3089367 /UG=Hs.24485 chondroitin sulfate proteoglycan 6 (bamacan) /FL=gb:AF020043.1 gb:NM_005445.1 gb:AF067163.1
209267_s_at_HG-U133A	LOC64116	up-regulated by BCG-CWS	gb:AB040120.1 /DEF=Homo sapiens mRNA for BCG induced integral membrane protein BIGMo-103, complete cds. /FEA=mRNA /GEN=BIGMo-103 /PROD=BCG induced integral membrane protein BIGMo-103 /DB_XREF=gi:12657580 /UG=Hs.284205 up-regulated by BCG-CWS /FL=gb:AB040120.1
209306_s_at_HG-U133A	SWAP70	SWAP-70 protein	Consensus includes gb:AI139569 /FEA=EST /DB_XREF=gi:3645541 /DB_XREF=est:qc57a12.x1 /CLONE=IMAGE:1713694 /UG=Hs.153026 SWAP-70 protein /FL=gb:BC000616.1 gb:AF210818.1
209307_at_HG-U133A	SWAP70	SWAP-70 protein	Consensus includes gb:AB014540.1 /DEF=Homo sapiens mRNA for KIAA0640 protein, partial cds. /FEA=mRNA /GEN=KIAA0640 /PROD=KIAA0640 protein /DB_XREF=gi:3327093 /UG=Hs.153026 SWAP-70 protein /FL=gb:BC000616.1 gb:AF210818.1
209312_x_at_HG-	HLA-DRB1	major histocompatibility complex, class	gb:U65585.1 /DEF=Homo sapiens MHC class II antigen (HLA-DRB1) mRNA,

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U133A		II, DR beta 1	HLA-DRB1*PBL allele, complete cds. /FEA=mRNA /GEN=HLA-DRB1 /PROD=MHC class II antigen /DB_XREF=gi:5478215 /UG=Hs.180255 major histocompatibility complex, class II, DR beta 1 /FL=gb:M33600.1 gb:NM_002124.1 gb:M28583.1 gb:U65585.1
209321_s_at_HG-U133A	ADCY3	adenylate cyclase 3	gb:AF033861.1 /DEF=Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds. /FEA=mRNA /GEN=AC-III /PROD=type III adenylyl cyclase /DB_XREF=gi:4104225 /UG=Hs.8402 adenylate cyclase 3 /FL=gb:NM_004036.2 gb:AF033861.1
209344_at_HG-U133A	TPM4	tropomyosin 4	gb:BC002827.1 /DEF=Homo sapiens, tropomyosin 4, clone MGC:3641, mRNA, complete cds. /FEA=mRNA /PROD=tropomyosin 4 /DB_XREF=gi:12803958 /UG=Hs.250641 tropomyosin 4 /FL=gb:BC002827.1 gb:NM_003290.1
209354_at_HG-U133A	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	gb:BC002794.1 /DEF=Homo sapiens, tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator), clone MGC:3753, mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor receptor superfamily,member 14 (herpesvirus entry mediator) /DB_XREF=gi:12803894 /UG=Hs.279899 tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) /FL=gb:BC002794.1 gb:U70321.1 gb:U81232.1 gb:NM_003820.1 gb:AF153978.1
209365_s_at_HG-U133A	ECM1	extracellular matrix protein 1	gb:U65932.1 /DEF=Human extracellular matrix protein 1 (ECM1) mRNA, complete cds. /FEA=mRNA /GEN=ECM1 /PROD=extracellular matrix protein 1 /DB_XREF=gi:1488323 /UG=Hs.81071 extracellular matrix protein 1 /FL=gb:NM_004425.2 gb:U65932.1 gb:U68186.1
209369_at_HG-U133A	ANXA3	annexin A3	gb:M63310.1 /DEF=Human 1,2-cyclic-inositol-phosphate phosphodiesterase (ANX3) mRNA, complete cds. /FEA=mRNA /GEN=ANX3 /PROD=1,2-cyclic-inositol-phosphate phosphodiesterase /DB_XREF=gi:178696 /UG=Hs.1378 annexin A3 /FL=gb:BC000871.1 gb:M63310.1 gb:M20560.1 gb:NM_005139.1
209374_s_at_HG-	IGHM	immunoglobulin heavy constant mu	gb:BC001872.1 /DEF=Homo sapiens, clone MGC:1228, mRNA, complete cds.

U133A			/FEA=mRNA /PROD=Unknown (protein for MGC:1228) /DB_XREF=gi:12804852 /UG=Hs.302063 immunoglobulin heavy constant mu /FL=gb:BC002963.1 gb:BC001872.1
209380_s_at_HG-U133A	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	gb:AF146074.1 /DEF=Homo sapiens ABC protein mRNA, complete cds. /FEA=mRNA /PROD=ABC protein /DB_XREF=gi:5006890 /UG=Hs.108660 ATP-binding cassette, sub-family C (CFTRMRP), member 5 /FL=gb:AF104942.1 gb:AB019002.1 gb:AF146074.1 gb:NM_005688.1 gb:U83661.2
209399_at_HG-U133A	HLCS	holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	gb:D87328.1 /DEF=Homo sapiens mRNA for HCS, complete cds. /FEA=mRNA /PROD=HCS /DB_XREF=gi:1813423 /UG=Hs.79375 holocarboxylase synthetase (biotin-proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing) ligase) /FL=gb:D87328.1
209412_at_HG-U133A	TMEM1	transmembrane protein 1	gb:U61500.1 /DEF=Human GT334 protein (GT334) gene mRNA, complete cds. /FEA=mRNA /GEN=GT334 /PROD=GT334 protein /DB_XREF=gi:1778032 /UG=Hs.94479 transmembrane protein 1 /FL=gb:U61500.1
209428_s_at_HG-U133A	ZFPL1	zinc finger protein-like 1	Consensus includes gb:BG420865 /FEA=EST /DB_XREF=gi:13327371 /DB_XREF=est:602452067F1 /CLONE=IMAGE:4590353 /UG=Hs.155165 zinc finger protein-like 1 /FL=gb:AF001891.1 gb:AF043611.1 gb:NM_006782.1 gb:AF030291.1
209490_s_at_HG-U133A	PPT2	palmitoyl-protein thioesterase 2	gb:AF020543.1 /DEF=Homo sapiens palmitoyl-protein thioesterase-2 (PPT2) mRNA, complete cds. /FEA=mRNA /GEN=PPT2 /PROD=palmitoyl-protein thioesterase-2 /DB_XREF=gi:2501960 /UG=Hs.81737 palmitoyl-protein thioesterase 2 /FL=gb:BC001355.1 gb:AF020543.1
209499_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	Consensus includes gb:BF448647 /FEA=EST /DB_XREF=gi:11514815 /DB_XREF=est:7n90g02.x1 /CLONE=IMAGE:3572138 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF114012.1
209500_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis

			factor-related deathligand-1beta /DB_XREF=gi:7328555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF114012.1
209522_s_at_HG-U133A	CRAT	carnitine acetyltransferase	gb:BC000723.1 /DEF=Homo sapiens, Similar to carnitine acetyltransferase, clone MGC:1564, mRNA, complete cds. /FEA=mRNA /PROD=Similar to carnitine acetyltransferase /DB_XREF=gi:13111704 /UG=Hs.12068 carnitine acetyltransferase /FL=gb:BC000723.1
209523_at_HG-U133A			Consensus includes gb:AK001618.1 /DEF=Homo sapiens cDNA FLJ10756 fis, clone NT2RP3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. /FEA=mRNA /DB_XREF=gi:7022983 /UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kD /FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1
209558_s_at_HG-U133A	HIP12	huntingtin interacting protein 12	gb:AB013384.1 /DEF=Homo sapiens mRNA for HIP1R, complete cds. /FEA=mRNA /GEN=HIP1R /PROD=HIP1R /DB_XREF=gi:3721835 /UG=Hs.96731 huntingtin interacting protein-1-related /FL=gb:AB013384.1
209561_at_HG-U133A	THBS3	thrombospondin 3	gb:L38969.1 /DEF=Homo sapiens thrombospondin 3 (THBS3) mRNA, complete cds. /FEA=mRNA /GEN=THBS3 /PROD=thrombospondin 3 /DB_XREF=gi:886298 /UG=Hs.169875 thrombospondin 3 /FL=gb:NM_007112.1 gb:L38969.1
209604_s_at_HG-U133A	GATA3	GATA binding protein 3	gb:BC003070.1 /DEF=Homo sapiens, GATA-binding protein 3, clone MGC:2346, mRNA, complete cds. /FEA=mRNA /PROD=GATA-binding protein 3 /DB_XREF=gi:13111765 /UG=Hs.169946 GATA-binding protein 3 /FL=gb:BC003070.1 gb:M69106.1 gb:NM_002051.1
209616_s_at_HG-U133A	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	gb:S73751.1 /DEF=Homo sapiens acyl coenzyme A:cholesterol acyltransferase mRNA, complete cds. /FEA=mRNA /PROD=acyl coenzyme A:cholesterol acyltransferase /DB_XREF=gi:688112 /UG=Hs.76688 carboxylesterase 1 (monocytemacrophage serine esterase 1) /FL=gb:M73499.1 gb:L07764.1 gb:L07765.1 gb:AF177775.1 gb:S73751.1 gb:NM_001266.2

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209619_at_HG-U133A	CD74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	gb:K01144.1 /DEF=Human major histocompatibility class II antigen gamma chain mRNA, complete cds. /FEA=mRNA /PROD=class II antigen gamma chain /DB_XREF=gi:188469 /UG=Hs.84298 CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) /FL=gb:NM_004355.1 gb:K01144.1
209628_at_HG-U133A	P15-2	hypothetical protein P15-2	Consensus includes gb:AK023289.1 /DEF=Homo sapiens cDNA FLJ13227 fis, clone OVARC1000071, weakly similar to Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA. /FEA=mRNA /DB_XREF=gi:10435160 /UG=Hs.25010 hypothetical protein P15-2 /FL=gb:AF246127.1 gb:NM_018698.1 gb:AF201942.1
209670_at_HG-U133A	TRA	T cell receptor alpha locus	gb:M12959.1 /DEF=Human T-cell receptor active-alpha-chain mRNA from JM cell line, complete cds. /FEA=mRNA /GEN=TCRA /DB_XREF=gi:338734 /UG=Hs.74647 Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds /FL=gb:M12959.1 gb:M12423.1
209679_s_at_HG-U133A	LOC57228	hypothetical protein from clone 643	gb:BC003379.1 /DEF=Homo sapiens, hypothetical protein from clone 643, clone MGC:5115, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein from clone 643 /DB_XREF=gi:13097236 /UG=Hs.206501 hypothetical protein from clone 643 /FL=gb:BC003379.1 gb:NM_020467.1
209682_at_HG-U133A	CBLB	Cas-Br-M (murine) ectropic retroviral transforming sequence b	gb:U26710.1 /DEF=Human cbl-b mRNA, complete cds. /FEA=mRNA /PROD=cbl-b /DB_XREF=gi:862406 /UG=Hs.3144 Cas-Br-M (murine) ectropic retroviral transforming sequence b /FL=gb:U26710.1
209685_s_at_HG-U133A	PRKCB1	protein kinase C, beta 1	gb:M13975.1 /DEF=Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds. /FEA=mRNA /GEN=PRKCB1 /PROD=protein kinase C beta-II type /DB_XREF=gi:189968 /UG=Hs.77202 protein kinase C, beta 1 /FL=gb:M13975.1
209686_at_HG-U133A	S100B	S100 calcium binding protein, beta (neural)	gb:BC001766.1 /DEF=Homo sapiens, S100 calcium-binding protein, beta (neural), clone MGC:1323, mRNA, complete cds. /FEA=mRNA /PROD=S100 calcium-binding protein, beta (neural) /DB_XREF=gi:12804680 /UG=Hs.83384

			S100 calcium-binding protein, beta (neural) /FL=gb:BC001766.1 - gb:NM_006272.1
209714_s_at_HG-U133A	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	gb:AF213033.1 /DEF=Homo sapiens isolate BX-01 cyclin-dependent kinase associated protein phosphatase mRNA, complete cds. /FEA=mRNA /PROD=cyclin-dependent kinase associated proteinphosphatase /DB_XREF=gi:12734643 /UG=Hs.84113 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase) /FL=gb:AF213033.1 gb:AF213034.1 gb:AF213035.1 gb:AF213036.1 gb:AF213037.1 gb:AF213038.1 gb:AF213039.1 gb:AF213040.1 gb:AF213041.1 gb:AF213042.1 gb:AF213044.1 gb:AF213046.1 gb:AF213047.1 gb:AF213048.1 gb:AF213049.1 gb:AF213050.1 gb:AF213051.1 gb:AF213052.1 gb:AF213053.1 gb:U02681.1 gb:L25876.1 gb:NM_005192.1 gb:L27711.1
209732_at_HG-U133A	CLECSF2	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	gb:BC005254.1 /DEF=Homo sapiens, Similar to C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced), clone MGC:12289, mRNA, complete cds. /FEA=mRNA /PROD=Similar to C-type (calcium dependent,carbohydrate-recognition domain) lectin, superfamilymember 2 (activation-induced) /DB_XREF=gi:13528920 /UG=Hs.85201 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced) /FL=gb:BC005254.1 gb:AB015628.1 gb:NM_005127.1
209735_at_HG-U133A	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	gb:AF098951.2 /DEF=Homo sapiens breast cancer resistance protein (BCRP) mRNA, complete cds. /FEA=mRNA /GEN=BCRP /PROD=breast cancer resistance protein /DB_XREF=gi:12414050 /UG=Hs.194720 ATP-binding cassette, sub-family G (WHITE), member 2 /FL=gb:AF098951.2 gb:AB056867.1 gb:AF103796.1 gb:NM_004827.1
209754_s_at_HG-U133A			gb:AF113682.1 /DEF=Homo sapiens clone FLB3436 PRO0868 mRNA, complete cds. /FEA=mRNA /PROD=PRO0868 /DB_XREF=gi:6855608 /UG=Hs.11355 thymopoietin /FL=gb:U09087.1 gb:AF113682.1

209761_s_at_HG-U133A	SP110	SP110 nuclear body protein	Consensus includes gb:AA969194 /FEA=EST /DB_XREF=gi:3144374 /DB_XREF=est:op51c02.s1 /CLONE=IMAGE:1580354 /UG=Hs.38125 interferon-induced protein 75, 52kD /FL=gb:AF280094.1
209765_at_HG-U133A	ADAM19	a disintegrin and metalloproteinase domain 19 (meltrin beta)	Consensus includes gb:Y13786.2 /DEF=Homo sapiens mRNA for meltrin-betaADAM 19 homologue. /FEA=mRNA /PROD=meltrin-betaADAM 19 homologue /DB_XREF=gi:12053590 /UG=Hs.278679 a disintegrin and metalloproteinase domain 19 (meltrin beta) /FL=gb:AF311317.1
209771_x_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	Consensus includes gb:AA761181 /FEA=EST /DB_XREF=gi:2810111 /DB_XREF=est:nz09g03.s1 /CLONE=IMAGE:1287316 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:X69397.1
209772_s_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	gb:X69397.1 /DEF=H.sapiens CD24 gene, complete CDS. /FEA=mRNA /GEN=CD24 /PROD=cell surface antigen /DB_XREF=gi:396167 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:X69397.1
209780_at_HG-U133A	DKFZP564F013	hypothetical protein DKFZp564F013	gb:AL136883.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D166 (from clone DKFZp434D166); complete cds. /FEA=mRNA /GEN=DKFZp434D166 /PROD=hypothetical protein /DB_XREF=gi:12053266 /UG=Hs.128653 hypothetical protein DKFZp564F013 /FL=gb:AL136883.1
209806_at_HG-U133A	H2B/S	histone family member	gb:BC000893.1 /DEF=Homo sapiens, H2B histone family, member A, clone MGC:5132, mRNA, complete cds. /FEA=mRNA /PROD=H2B histone family, member A /DB_XREF=gi:12654150 /UG=Hs.247817 H2B histone family, member A /FL=gb:BC000893.1
209815_at_HG-U133A	PTCH	patched homolog (Drosophila)	Consensus includes gb:BG054916 /FEA=EST /DB_XREF=gi:12512119 /DB_XREF=est:nac92b02.x1 /CLONE=IMAGE:3441723 /UG=Hs.159526 patched (Drosophila) homolog /FL=gb:U43148.1
209822_s_at_HG-U133A	VLDLR	very low density lipoprotein receptor	gb:L22431.1 /DEF=Human very low density lipoprotein receptor, complete cds. /FEA=mRNA /PROD=very low density lipoprotein receptor /DB_XREF=gi:437386 /UG=Hs.73729 very low density lipoprotein receptor

			/FL=gb:D16493.1 gb:L22431.1 gb:NM_003383.1
209825_s_at_HG-U133A	UMPK	uridine monophosphate kinase	gb:BC002906.1 /DEF=Homo sapiens, Similar to uridine monophosphate kinase, clone MGC:10318, mRNA, complete cds. /FEA=mRNA /PROD=Similar to uridine monophosphate kinase /DB_XREF=gi:12804106 /UG=Hs.75939 uridine monophosphate kinase /FL=gb:BC002906.1 gb:AF236637.1
209827_s_at_HG-U133A	IL16	interleukin 16 (lymphocyte chemoattractant factor)	Consensus includes gb:NM_004513.1 /DEF=Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), mRNA. /FEA=CDS /GEN=IL16 /PROD=interleukin 16 /DB_XREF=gi:4758595 /UG=Hs.82127 interleukin 16 (lymphocyte chemoattractant factor) /FL=gb:S81601.1 gb:U82972.1 gb:AF053412.1 gb:M90391.1 gb:NM_004513.1
209831_x_at_HG-U133A	DNASE2	deoxyribonuclease II, lysosomal	gb:AB004574.1 /DEF=Homo sapiens mRNA for deoxyribonuclease II, complete cds. /FEA=mRNA /GEN=DNASE2 /PROD=deoxyribonuclease II /DB_XREF=gi:3184394 /UG=Hs.118243 deoxyribonuclease II, lysosomal /FL=gb:AF045937.1 gb:AF047016.1 gb:AB004574.1 gb:AF060222.1 gb:NM_001375.1
209876_at_HG-U133A	GIT2	G protein-coupled receptor kinase-interactor 2	gb:AF124491.1 /DEF=Homo sapiens ARF GTPase-activating protein GIT2 (KIAA0148) mRNA, complete cds. /FEA=mRNA /GEN=KIAA0148 /PROD=ARF GTPase-activating protein GIT2 /DB_XREF=gi:4691727 /UG=Hs.57734 G protein-coupled receptor kinase-interactor 2 /FL=gb:AF124491.1
209891_at_HG-U133A	AD024	AD024 protein	gb:AF225416.1 /DEF=Homo sapiens AD024 mRNA, complete cds. /FEA=mRNA /PROD=AD024 /DB_XREF=gi:9963834 /UG=Hs.21137 AD024 protein /FL=gb:NM_020675.1 gb:AF225416.1
209905_at_HG-U133A	HOXA9	homeo box A9	Consensus includes gb:AI246769 /FEA=EST /DB_XREF=gi:3842166 /DB_XREF=est:qk40f08.x1 /CLONE=IMAGE:1871463 /UG=Hs.127428 homeo box A9 /FL=gb:U82759.1
209939_x_at_HG-U133A	CFLAR	CASP8 and FADD-like apoptosis regulator	gb:AF005775.1 /DEF=Homo sapiens caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=clarp /PROD=caspase-like apoptosis regulatory protein 2 /DB_XREF=gi:2286146

			/UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:AF005775.1
209961_s_at_HG-U133A	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	gb:M60718.1 /DEF=Human hepatocyte growth factor mRNA, complete cds. /FEA=mRNA /GEN=HGF /PROD=hepatocyte growth factor /DB_XREF=gi:184031 /UG=Hs.809 hepatocyte growth factor (hepapoietin A; scatter factor) /FL=gb:M60718.1 gb:M29145.1 gb:M73239.1 gb:M73240.1
209975_at_HG-U133A	CYP2E	cytochrome P450, subfamily IIE (ethanol-inducible)	gb:AF182276.1 /DEF=Homo sapiens cytochrome P450-2E1 (CYP2E1) mRNA, complete cds. /FEA=mRNA /GEN=CYP2E1 /PROD=cytochrome P450-2E1 /DB_XREF=gi:6470140 /UG=Hs.75183 cytochrome P450, subfamily IIE (ethanol-inducible) /FL=gb:NM_000773.2 gb:J02625.1 gb:AF182276.1
209992_at_HG-U133A	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	gb:AB044805.1 /DEF=Homo sapiens mRNA for 6-phosphofructo-2-kinase heart isoform, complete cds. /FEA=mRNA /PROD=6-phosphofructo-2-kinase heart isoform /DB_XREF=gi:11933148 /UG=Hs.211585 6-phosphofructo-2-kinasefructose-2,6-biphosphatase 2 /FL=gb:AB044805.1
209994_s_at_HG-U133A	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	gb:AF016535.1 /DEF=Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds. /FEA=mRNA /GEN=mdr1 /PROD=P-glycoprotein /DB_XREF=gi:2353263 /UG=Hs.21330 ATP-binding cassette, sub-family B (MDRTAP), member 1 /FL=gb:M14758.1 gb:AF016535.1 gb:NM_000927.2
210004_at_HG-U133A	OLR1	oxidised low density lipoprotein (lectin-like) receptor 1	gb:AF035776.1 /DEF=Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds. /FEA=mRNA /PROD=oxidized low-density lipoprotein receptor /DB_XREF=gi:3941299 /UG=Hs.77729 oxidised low density lipoprotein (lectin-like) receptor 1 /FL=gb:AB010710.1 gb:AF035776.1 gb:NM_002543.1
210024_s_at_HG-U133A	UBE2E3	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	gb:AB017644.1 /DEF=Homo sapiens mRNA for ubiquitin-conjugating enzyme E2, complete cds. /FEA=mRNA /GEN=UbcH9 /PROD=ubiquitin-conjugating enzyme E2 /DB_XREF=gi:4586929 /UG=Hs.4890 ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC45) /FL=gb:BC003554.1 gb:AB017644.1 gb:AF085362.1 gb:NM_006357.1

210036_s_at_HG-U133A	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	gb:AB044806.1 /DEF=Homo sapiens HERG mRNA for HERG-USO, alternatively spliced, complete cds. /FEA=mRNA /GEN=HERG /PROD=HERG-USO /DB_XREF=gi:11933151 /UG=Hs.188021 potassium voltage-gated channel, subfamily H (eag-related), member 2 /FL=gb:AB044806.1
210038_at_HG-U133A			Consensus includes gb:AL137145 /DEF=Human DNA sequence from clone RP11-563J2 on chromosome 10 Contains ESTs, STSs, GSSs and a CpG island. Contains a novel pseudogene and the 3 part of the PRKCQ gene for protein kinase C theta /FEA=mRNA /DB_XREF=gi:9581557 /UG=Hs.211593 protein kinase C, theta /FL=gb:L07032.1 gb:NM_006257.1 gb:L01087.1
210045_at_HG-U133A	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	Consensus includes gb:AU151428 /FEA=EST /DB_XREF=gi:11012949 /DB_XREF=est:AU151428 /CLONE=NT2RP2005206 /UG=Hs.5337 isocitrate dehydrogenase 2 (NADP+), mitochondrial /FL=gb:U52144.1
210052_s_at_HG-U133A	C20orf1	chromosome 20 open reading frame 1	gb:AF098158.1 /DEF=Homo sapiens restricted expressed proliferation associated protein 100 mRNA, complete cds. /FEA=mRNA /PROD=restricted expressed proliferation associatedprotein 100 /DB_XREF=gi:6073830 /UG=Hs.9329 chromosome 20 open reading frame 1 /FL=gb:NM_012112.1 gb:BC004136.1 gb:AB024704.1 gb:AF146731.1 gb:AF098158.1 gb:AB027467.1
210053_at_HG-U133A	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100 kD	Consensus includes gb:AW138827 /FEA=EST /DB_XREF=gi:6143145 /DB_XREF=est:UI-H-BI1-aep-g-08-0-UI.s1 /CLONE=IMAGE:2720079 /UG=Hs.96103 TATA box binding protein (TBP)-associated factor, RNA polymerase II, D, 100kD /FL=gb:U80191.1 gb:NM_006951.1
210095_s_at_HG-U133A	IGFBP3	insulin-like growth factor binding protein 3	gb:M31159.1 /DEF=Human growth hormone-dependent insulin-like growth factor-binding protein mRNA, complete cds. /FEA=mRNA /GEN=IGFBP1 /DB_XREF=gi:183115 /UG=Hs.77326 insulin-like growth factor binding protein 3 /FL=gb:BC000013.1 gb:M31159.1
210116_at_HG-U133A	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	gb:AF072930.1 /DEF=Homo sapiens clone 14 T cell signal transduction molecule SAP mRNA, complete cds. /FEA=mRNA /PROD=T cell signal

			transduction molecule SAP /DB_XREF=gi:3695068 /UG=Hs.151544 SH2 domain protein 1A, Duncans disease (lymphoproliferative syndrome) /FL=gb:AF072930.1 gb:AF073019.1 gb:AF100541.1 gb:NM_002351.1
210117_at_HG-U133A	SPAG1	sperm associated antigen 1	gb:AF311312.1 /DEF=Homo sapiens infertility-related sperm protein mRNA, complete cds. /FEA=mRNA /PROD=infertility-related sperm protein /DB_XREF=gi:10863767 /UG=Hs.153057 sperm associated antigen 1 /FL=gb:AF311312.1 gb:NM_003114.1
210128_s_at_HG-U133A	LTB4R	leukotriene b4 receptor (chemokine receptor-like 1)	gb:U41070.1 /DEF=Human P2 purinergic receptor mRNA, complete cds. /FEA=mRNA /PROD=P2 purinergic receptor /DB_XREF=gi:1469913 /UG=Hs.28408 leukotriene b4 receptor (chemokine receptor-like 1) /FL=gb:U41070.1 gb:D89079.1
210140_at_HG-U133A	CST7	cystatin F (leukocystatin)	gb:AF031824.1 /DEF=Homo sapiens leukocystatin mRNA, complete cds. /FEA=mRNA /PROD=leukocystatin /DB_XREF=gi:3252857 /UG=Hs.143212 cystatin F (leukocystatin) /FL=gb:AF031824.1 gb:AF036342.1 gb:AB015225.1 gb:NM_003650.1
210145_at_HG-U133A	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	gb:M68874.1 /DEF=Homo sapiens phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds. /FEA=mRNA /GEN=cPLA2 /PROD=phosphatidylcholine 2-acylhydrolase /DB_XREF=gi:190003 /UG=Hs.211587 phospholipase A2, group IVA (cytosolic, calcium-dependent) /FL=gb:M68874.1 gb:M72393.1
210151_s_at_HG-U133A	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	gb:AF186773.1 /DEF=Homo sapiens regulatory erythroid kinase long form (RED) mRNA, alternatively spliced product, complete cds. /FEA=mRNA /GEN=RED /PROD=regulatory erythroid kinase long form /DB_XREF=gi:10441414 /UG=Hs.38018 dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 /FL=gb:AF186773.1 gb:NM_003582.1
210192_at_HG-U133A	ATP8A1	ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1	gb:AB013452.1 /DEF=Homo sapiens mRNA for ATPaseII, complete cds. /FEA=mRNA /PROD=ATPaseII /DB_XREF=gi:4704323 /UG=Hs.144931 ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1

			/FL=gb:AB013452.1
210244_at_HG-U133A	CAMP	cathelicidin antimicrobial peptide	gb:U19970.1 /DEF=Human antimicrobial LPS-binding protein CAP18 precursor mRNA, complete cds. /FEA=mRNA /PROD=CAP18 precursor /DB_XREF=gi:643476 /UG=Hs.51120 cathelicidin antimicrobial peptide /FL=gb:NM_004345.1 gb:U19970.1
210251_s_at_HG-U133A	KIAA0871	KIAA0871 protein	gb:AF112221.1 /DEF=Homo sapiens rap2 interacting protein x mRNA, complete cds. /FEA=mRNA /PROD=rap2 interacting protein x /DB_XREF=gi:6563227 /UG=Hs.7972 KIAA0871 protein /FL=gb:AF112221.1
210254_at_HG-U133A			gb:L35848.1 /DEF=Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds. /FEA=mRNA /GEN=HTm4 /PROD=IgE receptor beta subunit /DB_XREF=gi:561638 /UG=Hs.99960 membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific) /FL=gb:NM_006138.1 gb:L35848.1
210262_at_HG-U133A	TPX1	testis specific protein 1 (probe H4-1 p3-1)	gb:M25532.1 /DEF=Human testis-specific protein (Tpx-1) mRNA, complete cds. /FEA=mRNA /GEN=GAPDL5 /DB_XREF=gi:339882 /UG=Hs.2042 testis specific protein 1 (probe H4-1 p3-1) /FL=gb:M25532.1 gb:NM_003296.1
210268_at_HG-U133A	NFX1	nuclear transcription factor, X-box binding 1	gb:AF332009.1 /DEF=Homo sapiens nuclear transcription factor NFX2 (NFX2) mRNA, complete cds. /FEA=mRNA /GEN=NFX2 /PROD=nuclear transcription factor NFX2 /DB_XREF=gi:13242068 /UG=Hs.3187 nuclear transcription factor, X-box binding 1 /FL=gb:AF332009.1
210279_at_HG-U133A	GPR18	G protein-coupled receptor 18	gb:AF261135.1 /DEF=Homo sapiens GPR18-iso mRNA, complete cds. /FEA=mRNA /PROD=GPR18-iso /DB_XREF=gi:12005919 /UG=Hs.88269 Homo sapiens clone IMAGE:1837189, mRNA sequence /FL=gb:AF261135.1
210298_x_at_HG-U133A	FHL1	four and a half LIM domains 1	gb:AF098518.1 /DEF=Homo sapiens four and a half LIM domains 1 protein isoform B (FHL1). mRNA, complete cds. /FEA=mRNA /GEN=FHL1 /PROD=four and a half LIM domains 1 protein isoform B /DB_XREF=gi:3851649 /UG=Hs.239069 four and a half LIM domains 1 /FL=gb:AF098518.1 gb:AF063002.1

210299_s_at_HG-U133A	FHL1	four and a half LIM domains 1	gb:AF063002.1 /DEF=Homo sapiens LIM protein SLIMMER mRNA, complete cds. /FEA=mRNA /PROD=LIM protein SLIMMER /DB_XREF=gi:3859848 /UG=Hs.239069 four and a half LIM domains 1 /FL=gb:AF098518.1 gb:AF063002.1
210314_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	gb:AF114013.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1gamma mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor-related deathligand-1gamma /DB_XREF=gi:7328557 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF136294.1 gb:AF114013.1
210334_x_at_HG-U133A	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	gb:AB028869.1 /DEF=Homo sapiens mRNA for survivin-beta, complete cds. /FEA=mRNA /PROD=survivin-beta /DB_XREF=gi:7416052 /UG=Hs.1578 baculoviral IAP repeat-containing 5 (survivin) /FL=gb:AB028869.1
210356_x_at_HG-U133A	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	gb:BC002807.1 /DEF=Homo sapiens, membrane-spanning 4-domains, subfamily A, member 2, clone MGC:3969, mRNA, complete cds. /FEA=mRNA /PROD=membrane-spanning 4-domains, subfamily A, member2 /DB_XREF=gi:12803920 /UG=Hs.89751 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) /FL=gb:NM_021950.1 gb:BC002807.1
210358_x_at_HG-U133A	MGC2306	hypothetical protein MGC2306	gb:BC002557.1 /DEF=Homo sapiens, Similar to GATA-binding protein 2, clone MGC:2306, mRNA, complete cds. /FEA=mRNA /PROD=Similar to GATA-binding protein 2 /DB_XREF=gi:12803464 /UG=Hs.760 GATA-binding protein 2 /FL=gb:BC002557.1
210448_s_at_HG-U133A	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	gb:U49396.1 /DEF=Human ionotropic ATP receptor P2X5b mRNA, complete cds. /FEA=mRNA /PROD=P2X5b /DB_XREF=gi:1552523 /UG=Hs.77807 purinergic receptor P2X, ligand-gated ion channel, 5 /FL=gb:U49396.1 gb:AF070573.1
210487_at_HG-U133A	DNTT	deoxynucleotidyltransferase, terminal	gb:M11722.1 /DEF=Human terminal transferase mRNA, complete cds. /FEA=mRNA /GEN=LA0024A /PROD=terminal transferase

			/DB_XREF=gi:339436 /UG=Hs.272537 deoxynucleotidyltransferase, terminal /FL=gb:M11722.1 gb:NM_004088.1
210519_s_at_HG-U133A			gb:BC000906.1 /DEF=Homo sapiens, clone MGC:5333, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:5333) /DB_XREF=gi:12654176 /UG=Hs.80706 diaphorase (NADHNADPH) (cytochrome b-5 reductase) /FL=gb:BC000906.1
210563_x_at_HG-U133A	CFLAR	CASP8 and FADD-like apoptosis regulator	gb:U97075.1 /DEF=Homo sapiens FLICE-like inhibitory protein short form mRNA, complete cds. /FEA=mRNA /PROD=FLICE-like inhibitory protein short form /DB_XREF=gi:2253680 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:U97075.1
210609_s_at_HG-U133A	PIG3	quinone oxidoreductase homolog	gb:BC000474.1 /DEF=Homo sapiens, quinone oxidoreductase homolog, clone MGC:8642, mRNA, complete cds. /FEA=mRNA /PROD=quinone oxidoreductase homolog /DB_XREF=gi:12653408 /UG=Hs.50649 quinone oxidoreductase homolog /FL=gb:BC000474.1
210613_s_at_HG-U133A	SYNGR1	synaptogyrin 1	gb:BC000731.1 /DEF=Homo sapiens, synaptogyrin 1, clone MGC:1939, mRNA, complete cds. /FEA=mRNA /PROD=synaptogyrin 1 /DB_XREF=gi:12653878 /UG=Hs.6139 synaptogyrin 1 /FL=gb:BC000731.1
210616_s_at_HG-U133A	KIAA0905	yeast Sec31p homolog	gb:AB020712.1 /DEF=Homo sapiens mRNA for KIAA0905 protein, complete cds. /FEA=mRNA /GEN=KIAA0905 /PROD=KIAA0905 protein /DB_XREF=gi:4240298 /UG=Hs.70266 yeast Sec31p homolog /FL=gb:AB020712.1
210658_s_at_HG-U133A	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	gb:BC000284.1 /DEF=Homo sapiens, KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2, clone MGC:1002, mRNA, complete cds. /FEA=mRNA /PROD=KIAA1080 protein; Golgi-associated,gamma-adaptin ear containing, ARF-binding protein 2 /DB_XREF=gi:12653040 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 /FL=gb:BC000284.1
210664_s_at_HG-	TFPI	tissue factor pathway inhibitor	gb:AF021834.1 /DEF=Homo sapiens tissue factor pathway inhibitor beta

U133A		(lipoprotein-associated coagulation inhibitor)	(TFPIbeta) mRNA, complete cds. /FEA=mRNA /GEN=TFPIbeta /PROD=tissue factor pathway inhibitor beta /DB_XREF=gi:4103170 /UG=Hs.170279 tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) /FL=gb:AF021834.1
210715_s_at_HG-U133A	SPINT2	serine protease inhibitor, Kunitz type, 2	gb:AF027205.1 /DEF=Homo sapiens Kunitz-type protease inhibitor (kop) mRNA, complete cds. /FEA=mRNA /GEN=kop /PROD=Kunitz-type protease inhibitor /DB_XREF=gi:2598967 /UG=Hs.31439 serine protease inhibitor, Kunitz type, 2 /FL=gb:AF027205.1
210749_x_at_HG-U133A	DDR1	discoidin domain receptor family, member 1	gb:L11315.1 /DEF=Homo sapiens receptor tyrosine kinase mRNA, complete cds. /FEA=mRNA /PROD=receptor tyrosine kinase /DB_XREF=gi:403386 /UG=Hs.75562 discoidin domain receptor family, member 1 /FL=gb:L11315.1
210755_at_HG-U133A	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	gb:U46010.1 /DEF=Human HGF agonistantagonist mRNA, complete cds. /FEA=mRNA /PROD=HGF agonistantagonist /DB_XREF=gi:1378041 /UG=Hs.809 hepatocyte growth factor (hepapoietin A; scatter factor) /FL=gb:U46010.1
210763_x_at_HG-U133A	LY117	lymphocyte antigen 117	gb:AF031137.1 /DEF=Homo sapiens 1C7 precursor, mRNA, alternatively spliced, complete cds. /FEA=mRNA /PROD=1C7 precursor /DB_XREF=gi:2623874 /UG=Hs.88411 lymphocyte antigen 117 /FL=gb:AF031137.1
210788_s_at_HG-U133A	LOC51635	CGI-86 protein	gb:AF126782.1 /DEF=Homo sapiens retinal short-chain dehydrogenasereductase retSDR4 mRNA, complete cds. /FEA=mRNA /PROD=retinal short-chain dehydrogenasereductaseretSDR4 /DB_XREF=gi:6318547 /UG=Hs.109201 CGI-86 protein /FL=gb:AF126782.1
210789_x_at_HG-U133A	CEACAM3	carcinoembryonic antigen-related cell adhesion molecule 3	gb:L00692.1 /DEF=Human carcinoembryonic antigen (CGM1) mRNA, complete cds. /FEA=mRNA /GEN=CGM1 /PROD=carcinoembryonic antigen /DB_XREF=gi:180226 /UG=Hs.11 carcinoembryonic antigen-related cell adhesion molecule 3 /FL=gb:L00692.1
210794_s_at_HG-			Consensus includes gb:AF119863.1 /DEF=Homo sapiens PRO2160 mRNA,

U133A			complete cds. /FEA=mRNA /PROD=PRO2160 /DB_XREF=gi:7770162 /UG=Hs.112844 maternally expressed 3 /FL=gb:AF119863.1
210807_s_at_HG-U133A	SLC16A7	solute carrier family 16 (monocarboxylic acid transporters), member 7	gb:AF049608.1 /DEF=Homo sapiens monocarboxylate transporter 2 (MCT2) mRNA, complete cds. /FEA=mRNA /GEN=MCT2 /PROD=monocarboxylate transporter 2 /DB_XREF=gi:3834394 /UG=Hs.132183 solute carrier family 16 (monocarboxylic acid transporters), member 7 /FL=gb:AF049608.1
210817_s_at_HG-U133A	NDP52	nuclear domain 10 protein	gb:BC004130.1 /DEF=Homo sapiens, nuclear domain 10 protein, clone MGC:1399, mRNA, complete cds. /FEA=mRNA /PROD=nuclear domain 10 protein /DB_XREF=gi:13278698 /UG=Hs.154230 nuclear domain 10 protein /FL=gb:BC004130.1
210896_s_at_HG-U133A	ASPH	aspartate beta-hydroxylase	gb:AF306765.1 /DEF=Homo sapiens junctate mRNA, complete cds. /FEA=mRNA /PROD=junctate /DB_XREF=gi:11991236 /UG=Hs.283664 aspartate beta-hydroxylase /FL=gb:AF306765.1
210916_s_at_HG-U133A		Homo sapiens CD44 isoform RC (CD44) mRNA, complete cds	gb:AF098641.1 /DEF=Homo sapiens CD44 isoform RC (CD44) mRNA, complete cds. /FEA=mRNA /GEN=CD44 /PROD=CD44 isoform RC /DB_XREF=gi:3832517 /UG=Hs.306278 Homo sapiens CD44 isoform RC (CD44) mRNA, complete cds /FL=gb:AF098641.1
210933_s_at_HG-U133A	MGC4655	hypothetical protein MGC4655	gb:BC004908.1 /DEF=Homo sapiens, clone MGC:4655, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:4655) /DB_XREF=gi:13436196 /UG=Hs.326737 Homo sapiens, clone MGC:4655, mRNA, complete cds /FL=gb:BC004908.1
210934_at_HG-U133A	BLK	B lymphoid tyrosine kinase	gb:BC004473.1 /DEF=Homo sapiens, clone MGC:10442, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10442) /DB_XREF=gi:13325324 /UG=Hs.326772 Homo sapiens, clone MGC:10442, mRNA, complete cds /FL=gb:BC004473.1
210948_s_at_HG-U133A	LEF1	lymphoid enhancer-binding factor 1	gb:AF294627.1 /DEF=Homo sapiens lymphoid enhancer factor 1 isoform (LEF1) mRNA, complete cds. /FEA=mRNA /GEN=LEF1 /PROD=lymphoid enhancer factor 1 isoform /DB_XREF=gi:11024343 /UG=Hs.44865 lymphoid

			enhancer binding factor-1 /FL=gb:AF294627.1
210973_s_at_HG-U133A	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	gb:M63889.1 /DEF=Human heparin-binding growth factor receptor (HBGF-R-alpha-a3) mRNA, complete cds. /FEA=mRNA /GEN=HBGF-R /PROD=heparin-binding growth factor receptor /DB_XREF=gi:183882 /UG=Hs.748 fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) /FL=gb:M63889.1
210982_s_at_HG-U133A	HLA-DRA	major histocompatibility complex, class II, DR alpha	gb:M60333.1 /DEF=Human MHC class II HLA-DRA mRNA, complete cds. /FEA=mRNA /GEN=HLA-DRA /PROD=MHC cell surface glycoprotein /DB_XREF=gi:188268 /UG=Hs.76807 major histocompatibility complex, class II, DR alpha /FL=gb:M60333.1
210997_at_HG-U133A	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	gb:M77227.1 /DEF=H.sapiens competitive HGF antagonist mRNA, complete cds. /FEA=mRNA /PROD=competitive HGF antagonist /DB_XREF=gi:184029 /UG=Hs.809 hepatocyte growth factor (hepapoietin A; scatter factor) /FL=gb:M77227.1 gb:L02931.1
210998_s_at_HG-U133A	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	gb:M77227.1 /DEF=H.sapiens competitive HGF antagonist mRNA, complete cds. /FEA=mRNA /PROD=competitive HGF antagonist /DB_XREF=gi:184029 /UG=Hs.809 hepatocyte growth factor (hepapoietin A; scatter factor) /FL=gb:M77227.1 gb:L02931.1
211015_s_at_HG-U133A	HSPA4	heat shock 70kD protein 4	gb:L12723.1 /DEF=Human heat shock protein 70 (hsp70) mRNA, complete cds. /FEA=mRNA /GEN=hsp70 /PROD=heat shock protein 70 /DB_XREF=gi:292159 /UG=Hs.90093 heat shock 70kD protein 4 /FL=gb:L12723.1
211031_s_at_HG-U133A	CYLN2	cytoplasmic linker 2	gb:BC006259.1 /DEF=Homo sapiens, clone MGC:11333, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:11333) /DB_XREF=gi:13623312 /FL=gb:BC006259.1
211097_s_at_HG-U133A	PBX2	pre-B-cell leukemia transcription factor 2	gb:BC003111.1 /DEF=Homo sapiens, Similar to pre-B-cell leukemia transcription factor 2, clone MGC:2174, mRNA, complete cds. /FEA=mRNA /PROD=Similar to pre-B-cell leukemia transcriptionfactor 2

			/DB_XREF=gi:13111886 /UG=Hs.93728 pre-B-cell leukemia transcription factor 2 /FL=gb:BC003111.1
211101_x_at_HG-U133A	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	gb:U82276.1 /DEF=Human immunoglobulin-like transcript 1a mRNA, complete cds. /FEA=mRNA /PROD=immunoglobulin-like transcript 1a /DB_XREF=gi:1907318 /UG=Hs.94498 leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 /FL=gb:U82276.1
211105_s_at_HG-U133A	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	gb:U80918.1 /DEF=Homo sapiens transcription factor (NF-ATcC) mRNA, complete cds. /FEA=mRNA /GEN=NF-ATcC /PROD=transcription factor /DB_XREF=gi:4098860 /UG=Hs.96149 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 /FL=gb:U80918.1
211126_s_at_HG-U133A	CSRP2	cysteine and glycine-rich protein 2	gb:U46006.1 /DEF=Homo sapiens smooth muscle LIM protein (h-SmLIM) mRNA, complete cds. /FEA=mRNA /GEN=h-SmLIM /PROD=smooth muscle LIM protein /DB_XREF=gi:1314358 /UG=Hs.10526 cysteine and glycine-rich protein 2 /FL=gb:U46006.1
211138_s_at_HG-U133A	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	gb:BC005297.1 /DEF=Homo sapiens, Similar to kynurenine 3-monooxygenase (kynurenine 3-hydroxylase), clone MGC:12362, mRNA, complete cds. /FEA=mRNA /PROD=Similar to kynurenine 3-monooxygenase(kynurenine 3-hydroxylase) /DB_XREF=gi:13529016 /UG=Hs.107318 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) /FL=gb:BC005297.1
211275_s_at_HG-U133A	GYG	glycogenin	gb:AF087942.1 /DEF=Homo sapiens glycogenin-1L mRNA, complete cds. /FEA=mRNA /PROD=glycogenin-1L /DB_XREF=gi:5814084 /UG=Hs.174071 glycogenin /FL=gb:AF087942.1
211297_s_at_HG-U133A	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	gb:L20320.1 /DEF=Human protein serinethreonine kinase stk1 mRNA, complete cds. /FEA=mRNA /PROD=protein serinethreonine kinase /DB_XREF=gi:348242 /UG=Hs.184298 cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase) /FL=gb:L20320.1
211341_at_HG-U133A	POU4F1	POU domain, class 4, transcription factor 1	gb:L20433.1 /DEF=Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds. /FEA=mRNA /GEN=OTF1 /PROD=octamer binding

			transcription factor 1 /DB_XREF=gi:418015 /UG=Hs.211588 POU domain, class 4, transcription factor 1 /FL=gb:L20433.1
211349_at_HG-U133A	SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1	gb:AB001328.1 /DEF=Homo sapiens mRNA for pH-sensing regulatory factor of peptide transporter, complete cds. /FEA=mRNA /GEN=hPEPT1-RF /PROD=pH-sensing regulatory factor of peptidetransporter /DB_XREF=gi:2506042 /UG=Hs.2217 solute carrier family 15 (oligopeptide transporter), member 1 /FL=gb:AB001328.1
211352_s_at_HG-U133A	NCOA3	nuclear receptor coactivator 3	gb:U80737.1 /DEF=Homo sapiens CAGH16 mRNA, complete cds. /FEA=mRNA /GEN=CAGH16 /PROD=CAGH16 /DB_XREF=gi:2565049 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:U80737.1
211404_s_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	gb:BC004371.1 /DEF=Homo sapiens, clone MGC:10449, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10449) /DB_XREF=gi:13325115 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:BC004371.1
211456_x_at_HG-U133A		Homo sapiens metallothionein 1H-like protein mRNA, complete cds	gb:AF333388.1 /DEF=Homo sapiens metallothionein 1H-like protein mRNA, complete cds. /FEA=mRNA /PROD=metallothionein 1H-like protein /DB_XREF=gi:13310411 /UG=Hs.326774 Homo sapiens metallothionein 1H-like protein mRNA, complete cds /FL=gb:AF333388.1
211474_s_at_HG-U133A		Homo sapiens, clone MGC:10846 IMAGE:3616550, mRNA, complete cds	gb:BC004948.1 /DEF=Homo sapiens, clone MGC:10846, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10846) /DB_XREF=gi:13436313 /UG=Hs.41072 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 /FL=gb:BC004948.1
211495_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	gb:AF114011.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1alpha mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor-related deathligand-1alpha /DB_XREF=gi:7328553 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF046888.1 gb:NM_003808.1 gb:AF184972.1 gb:AF114011.1
211502_s_at_HG-	PFTK1	PFTAIRE protein kinase 1	gb:AF119833.1 /DEF=Homo sapiens serinethreonine protein kinase PFTAIRE-

U133A			1 mRNA, complete cds. /FEA=mRNA /PROD=serinethreonine protein kinase PFTAIRE-1 /DB_XREF=gi:12002200 /UG=Hs.57856 PFTAIRE protein kinase 1 /FL=gb:AF119833.1
211540_s_at_HG-U133A	RB1	retinoblastoma 1 (including osteosarcoma)	gb:M19701.1 /DEF=Human mutated retinoblastoma susceptibility (RB) mRNA, complete cds. /FEA=mRNA /GEN=RB1 /DB_XREF=gi:190967 /UG=Hs.75770 retinoblastoma 1 (including osteosarcoma) /FL=gb:M19701.1
211574_s_at_HG-U133A	MCP	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)	gb:D84105.1 /DEF=Human CD46 mRNA, complete cds. /FEA=mRNA /PROD=CD46 /DB_XREF=gi:1256700 /UG=Hs.83532 membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) /FL=gb:D84105.1
211584_s_at_HG-U133A	NPAT	nuclear protein, ataxia-telangiectasia locus	gb:U58852.1 /DEF=Human NPAT mRNA, complete cds. /FEA=mRNA /GEN=NPAT /DB_XREF=gi:1381666 /UG=Hs.89385 nuclear protein, ataxia-telangiectasia locus /FL=gb:U58852.1
211657_at_HG-U133A			gb:M18728.1 /DEF=Human nonspecific crossreacting antigen mRNA, complete cds. /FEA=mRNA /GEN=NCA; NCA; NCA /PROD=non-specific cross reacting antigen /DB_XREF=gi:189084 /FL=gb:M18728.1
211665_s_at_HG-U133A			gb:L20686.1 /DEF=Homo sapiens guanine nucleotide releasing factor (SOS2) mRNA, complete cds. /FEA=mRNA /GEN=SOS2 /PROD=guanine nucleotide releasing factor /DB_XREF=gi:1220367 /FL=gb:L20686.1
211668_s_at_HG-U133A	PLAU	plasminogen activator, urokinase	gb:K03226.1 /DEF=Human preprourokinase mRNA, complete cds. /FEA=mRNA /GEN=PLAU /DB_XREF=gi:340155 /FL=gb:K03226.1
211709_s_at_HG-U133A	SCGF	stem cell growth factor; lymphocyte secreted C-type lectin	gb:BC005810.1 /DEF=Homo sapiens, stem cell growth factor; lymphocyte secreted C-type lectin, clone MGC:10378, mRNA, complete cds. /FEA=mRNA /PROD=stem cell growth factor; lymphocyte secretedC-type lectin /DB_XREF=gi:13543291 /FL=gb:BC005810.1
211743_s_at_HG-U133A	PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	gb:BC005929.1 /DEF=Homo sapiens, proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein), clone MGC:14537, mRNA, complete cds. /FEA=mRNA /PROD=proteoglycan 2,

			bone marrow (natural killer cellactivator, eosinophil granule major basic protein) /DB_XREF=gi:13543541 /FL=gb:BC005929.1
211748_x_at_HG-U133A	PTGDS	prostaglandin D2 synthase (21kD, brain)	gb:BC005939.1 /DEF=Homo sapiens, prostaglandin D2 synthase (21kD, brain), clone MGC:14559, mRNA, complete cds. /FEA=mRNA /PROD=prostaglandin D2 synthase (21kD, brain) /DB_XREF=gi:13543567 /FL=gb:BC005939.1
211771_s_at_HG-U133A	POU2F2	POU domain, class 2, transcription factor 2	gb:BC006101.1 /DEF=Homo sapiens, Similar to POU domain, class 2, transcription factor 2, clone MGC:12814, mRNA, complete cds. /FEA=mRNA /PROD=Similar to POU domain, class 2, transcriptionfactor 2 /DB_XREF=gi:13543912 /FL=gb:BC006101.1
211787_s_at_HG-U133A	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	gb:BC006210.1 /DEF=Homo sapiens, Similar to eukaryotic translation initiation factor 4A, isoform 1, clone MGC:8484, mRNA, complete cds. /FEA=mRNA /PROD=Similar to eukaryotic translation initiationfactor 4A, isoform 1 /DB_XREF=gi:13623224 /FL=gb:BC006210.1
211796_s_at_HG-U133A	TRB	T cell receptor beta locus	gb:AF043179.1 /DEF=Homo sapiens T cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds. /FEA=CDS /GEN=TCRBV13S1-TCRBJ2S1 /PROD=T cell receptor beta chain /DB_XREF=gi:3002924 /UG=Hs.303157 T cell receptor beta locus /FL=gb:AF043179.1
211800_s_at_HG-U133A	USP4	ubiquitin specific protease 4 (proto-oncogene)	gb:AF017306.1 /DEF=Homo sapiens deubiquitinating enzyme UnpES (UNP) mRNA, complete cds. /FEA=CDS /GEN=UNP /PROD=UnpES /DB_XREF=gi:2656142 /UG=Hs.77500 ubiquitin specific protease 4 (proto-oncogene) /FL=gb:AF017306.1
211819_s_at_HG-U133A	SH3D5	SH3-domain protein 5 (ponsin)	gb:AF136381.1 /DEF=Homo sapiens c-Cbl-associated protein SH3P12 (SH3P12) mRNA, complete cds. /FEA=CDS /GEN=SH3P12 /PROD=c-Cbl-associated protein SH3P12 /DB_XREF=gi:6651088 /UG=Hs.108924 SH3-domain protein 5 (ponsin) /FL=gb:AF136381.1
211824_x_at_HG-U133A	DEFCAP	death effector filament-forming Ced-4-like apoptosis protein	gb:AF229062.1 /DEF=Homo sapiens NAC-delta splice variant (NAC) mRNA, complete cds, alternatively spliced. /FEA=CDS /GEN=NAC /PROD=NAC-delta

			splice variant /DB_XREF=gi:12656110 /UG=Hs.104305 death effector filament-forming Ced-4-like apoptosis protein /FL=gb:AF229062.1
211852_s_at_HG-U133A	ATRN	attractin	gb:AF106861.1 /DEF=Homo sapiens attractin-2 (ATRN) mRNA, complete cds. /FEA=CDS /GEN=ATRN /PROD=attractin-2 /DB_XREF=gi:4093195 /UG=Hs.194019 attractin /FL=gb:AF106861.1
211883_x_at_HG-U133A	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	gb:M76742.1 /DEF=Homo sapiens alternatively spliced biliary glycoprotein (BGPa) mRNA, complete cds. /FEA=CDS /GEN=BGPa /PROD=biliary glycoprotein /DB_XREF=gi:179480 /UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /FL=gb:M76742.1
211889_x_at_HG-U133A	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	gb:D12502.1 /DEF=Human mRNA for biliary glycoprotein, complete cds. /FEA=CDS /GEN=BGP /PROD=biliary glycoprotein /DB_XREF=gi:219494 /UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /FL=gb:D12502.1
211918_x_at_HG-U133A	PLAC3	placenta-specific 3	gb:AF311940.1 /DEF=Homo sapiens pregnancy-associated plasma preproprotein-A2 mRNA, complete cds. /FEA=CDS /PROD=pregnancy-associated plasma preproprotein-A2 /DB_XREF=gi:13569344 /FL=gb:AF311940.1
211934_x_at_HG-U133A	G2AN	alpha glucosidase II alpha subunit	Consensus includes gb:W87689 /FEA=EST /DB_XREF=gi:1401814 /DB_XREF=est:zh68c04.s1 /CLONE=IMAGE:417222 /UG=Hs.76847 KIAA0088 protein /FL=gb:NM_014610.1
211950_at_HG-U133A	RBAF600	retinoblastoma-associated factor 600	Consensus includes gb:AB007931.1 /DEF=Homo sapiens mRNA for KIAA0462 protein, partial cds. /FEA=mRNA /GEN=KIAA0462 /PROD=KIAA0462 protein /DB_XREF=gi:3413885 /UG=Hs.297641 KIAA0462 protein
211953_s_at_HG-U133A	KPNB3	karyopherin (importin) beta 3	Consensus includes gb:AU148466 /FEA=EST /DB_XREF=gi:11009987 /DB_XREF=est:AU148466 /CLONE=NT2RM4000332 /UG=Hs.113503 karyopherin (importin) beta 3 /FL=gb:U72761.1 gb:NM_002271.1
211984_at_HG-U133A		Human calmodulin-I (CALM1) mRNA,	Consensus includes gb:AI653730 /FEA=EST /DB_XREF=gi:4737709

		3'UTR, partial sequence	/DB_XREF=est:wb36f12.x1 /CLONE=IMAGE:2307791 /UG=Hs.279009 matrix Gla protein
211990_at_HG-U133A	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	Consensus includes gb:M27487.1 /DEF=Homo sapiens MHC class II DPw3-alpha-1 chain mRNA, complete cds. /FEA=CDS /GEN=HLA-DPA1 /PROD=MHC class II DP3-alpha /DB_XREF=gi:703088 /UG=Hs.914 Human mRNA for SB classII histocompatibility antigen alpha-chain /FL=gb:M27487.1
211991_s_at_HG-U133A	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	Consensus includes gb:M27487.1 /DEF=Homo sapiens MHC class II DPw3-alpha-1 chain mRNA, complete cds. /FEA=CDS /GEN=HLA-DPA1 /PROD=MHC class II DP3-alpha /DB_XREF=gi:703088 /UG=Hs.914 Human mRNA for SB classII histocompatibility antigen alpha-chain /FL=gb:M27487.1
212012_at_HG-U133A	D2S448	Melanoma associated gene	Consensus includes gb:BF342851 /FEA=EST /DB_XREF=gi:11289878 /DB_XREF=est:602015135F1 /CLONE=IMAGE:4150664 /UG=Hs.118893 Melanoma associated gene
212013_at_HG-U133A	D2S448	Melanoma associated gene	Consensus includes gb:D86983.1 /DEF=Human mRNA for KIAA0230 gene, partial cds. /FEA=mRNA /GEN=KIAA0230 /DB_XREF=gi:1504039 /UG=Hs.118893 Melanoma associated gene
212020_s_at_HG-U133A	MKI67	antigen identified by monoclonal antibody Ki-67	Consensus includes gb:AU152107 /FEA=EST /DB_XREF=gi:11013628 /DB_XREF=est:AU152107 /CLONE=NT2RP3000209 /UG=Hs.80976 antigen identified by monoclonal antibody Ki-67
212022_s_at_HG-U133A	MKI67	antigen identified by monoclonal antibody Ki-67	Consensus includes gb:BF001806 /FEA=EST /DB_XREF=gi:10702081 /DB_XREF=est:7g93e04.x1 /CLONE=IMAGE:3314046 /UG=Hs.80976 antigen identified by monoclonal antibody Ki-67
212032_s_at_HG-U133A	PTOV1	prostate tumor over expressed gene 1	Consensus includes gb:AL046054 /FEA=EST /DB_XREF=gi:5936153 /DB_XREF=est:DKFZp434D2072_r1 /CLONE=DKFZp434D2072 /UG=Hs.19555 prostate tumor over expressed gene 1
212058_at_HG-U133A	KIAA0332	KIAA0332 protein	Consensus includes gb:AI184562 /FEA=EST /DB_XREF=gi:3735200 /DB_XREF=est:qd60b05.x1 /CLONE=IMAGE:1733841 /UG=Hs.7976 KIAA0332 protein

212074_at_HG-U133A	KIAA0810	KIAA0810 protein	Consensus includes gb:BE972774 /FEA=EST /DB_XREF=gi:10586110 /DB_XREF=est:601652004F1 /CLONE=IMAGE:3935281 /UG=Hs.7531 KIAA0810 protein
212107_s_at_HG-U133A	DDX9	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin)	Consensus includes gb:BE561014 /FEA=EST /DB_XREF=gi:9804734 /DB_XREF=est:601344618F1 /CLONE=IMAGE:3677500 /UG=Hs.74578 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin)
212133_at_HG-U133A	MGC5466	hypothetical protein MGC5466	Consensus includes gb:AI681536 /FEA=EST /DB_XREF=gi:4891718 /DB_XREF=est:tx47e03.x1 /CLONE=IMAGE:2272732 /UG=Hs.83724 hypothetical protein MGC5466
212146_at_HG-U133A	KIAA0842	KIAA0842 protein	Consensus includes gb:AB020649.1 /DEF=Homo sapiens mRNA for KIAA0842 protein, partial cds. /FEA=mRNA /GEN=KIAA0842 /PROD=KIAA0842 protein /DB_XREF=gi:4240172 /UG=Hs.74569 KIAA0842 protein
212150_at_HG-U133A	KIAA0143	KIAA0143 protein	Consensus includes gb:AA805651 /FEA=EST /DB_XREF=gi:2874401 /DB_XREF=est:nz41a04.s1 /CLONE=IMAGE:1290318 /UG=Hs.84087 KIAA0143 protein
212171_x_at_HG-U133A	VEGF	vascular endothelial growth factor	Consensus includes gb:H95344 /FEA=EST /DB_XREF=gi:1102977 /DB_XREF=est:yu21b08.s1 /CLONE=IMAGE:234423 /UG=Hs.73793 vascular endothelial growth factor /FL=gb:AF214570.1
212185_x_at_HG-U133A	MT2A	metallothionein 2A	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS /GEN=MT2A /PROD=metallothionein 2A /DB_XREF=gi:5174763 /UG=Hs.118786 metallothionein 2A /FL=gb:NM_005953.1
212187_x_at_HG-U133A	PTGDS	prostaglandin D2 synthase (21kD, brain)	Consensus includes gb:NM_000954.1 /DEF=Homo sapiens prostaglandin D2 synthase (21kD, brain) (PTGDS), mRNA. /FEA=CDS /GEN=PTGDS /PROD=prostaglandin D2 synthase (21kD, brain) /DB_XREF=gi:4506250 /UG=Hs.8272 prostaglandin D2 synthase (21kD, brain) /FL=gb:AY026356.1

			gb:NM_000954.1
212188_at_HG-U133A	LOC115207	hypothetical protein BC013764	Consensus includes gb:AA551075 /FEA=EST /DB_XREF=gi:2321327 /DB_XREF=est:nk74h06.s1 /CLONE=IMAGE:1019291 /UG=Hs.109438 Homo sapiens clone 24775 mRNA sequence
212207_at_HG-U133A	KIAA1025	KIAA1025 protein	Consensus includes gb:BG426689 /FEA=EST /DB_XREF=gi:13333195 /DB_XREF=est:602493234F1 /CLONE=IMAGE:4607168 /UG=Hs.4084 KIAA1025 protein
212222_at_HG-U133A	KIAA0077	KIAA0077 protein	Consensus includes gb:AU143855 /FEA=EST /DB_XREF=gi:11005376 /DB_XREF=est:AU143855 /CLONE=HEMBA1000210 /UG=Hs.112396 KIAA0077 protein
212229_s_at_HG-U133A			Consensus includes gb:AK001699.1 /DEF=Homo sapiens cDNA FLJ10837 fis, clone NT2RP4001260, highly similar to Homo sapiens mRNA for KIAA0875 protein. /FEA=mRNA /DB_XREF=gi:7023121 /UG=Hs.184227 F-box only protein 21 /FL=gb:AF174601.1
212231_at_HG-U133A	FBXO21	F-box only protein 21	Consensus includes gb:AB020682.1 /DEF=Homo sapiens mRNA for KIAA0875 protein, partial cds. /FEA=mRNA /GEN=KIAA0875 /PROD=KIAA0875 protein /DB_XREF=gi:4240238 /UG=Hs.184227 F-box only protein 21 /FL=gb:AF174601.1
212232_at_HG-U133A	KIAA1014	KIAA1014 protein	Consensus includes gb:AB023231.1 /DEF=Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA=mRNA /GEN=KIAA1014 /PROD=KIAA1014 protein /DB_XREF=gi:4589677 /UG=Hs.6834 KIAA1014 protein
212236_x_at_HG-U133A			Consensus includes gb:Z19574 /DEF=H.sapiens gene for cytokeratin 17 /FEA=mRNA /DB_XREF=gi:30378 /UG=Hs.2785 keratin 17
212250_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp564C1563 (from clone DKFZp564C1563)	Consensus includes gb:AV700332 /FEA=EST /DB_XREF=gi:10302303 /DB_XREF=est:AV700332 /CLONE=GKCDIF11 /UG=Hs.243901 Homo sapiens cDNA FLJ20738 fis, clone HEP08257
212251_at_HG-U133A		Homo sapiens mRNA; cDNA	Consensus includes gb:AI972475 /FEA=EST /DB_XREF=gi:5769391

		DKFZp564C1563 (from clone DKFZp564C1563)	/DB_XREF=est:wr40b09.x1 /CLONE=IMAGE:2490137 /UG=Hs.243901 Homo sapiens cDNA FLJ20738 fis, clone HEP08257
212259_s_at_HG-U133A	HPIP	hematopoietic PBX-interacting protein	Consensus includes gb:BF344265 /FEA=EST /DB_XREF=gi:11291478 /DB_XREF=est:602017327F1 /CLONE=IMAGE:4152943 /UG=Hs.8068 hematopoietic PBX-interacting protein
212268_at_HG-U133A	SERPINB1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	Consensus includes gb:NM_030666.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 (SERPINB1), mRNA. /FEA=CDS /GEN=SERPINB1 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 1 /DB_XREF=gi:13489086 /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 /FL=gb:NM_030666.1
212271_at_HG-U133A	MAPK1	mitogen-activated protein kinase 1	Consensus includes gb:AA195999 /FEA=EST /DB_XREF=gi:1791623 /DB_XREF=est:zp99f06.s1 /CLONE=IMAGE:628355 /UG=Hs.324473 mitogen-activated protein kinase 1
212281_s_at_HG-U133A	MAC30	hypothetical protein	Consensus includes gb:BF038366 /FEA=EST /DB_XREF=gi:10744142 /DB_XREF=est:601459338F1 /CLONE=IMAGE:3862808 /UG=Hs.199695 hypothetical protein
212285_s_at_HG-U133A	AGRN	agrin	Consensus includes gb:AW008051 /FEA=EST /DB_XREF=gi:5856829 /DB_XREF=est:wv48h10.x1 /CLONE=IMAGE:2532835 /UG=Hs.273330 Homo sapiens, clone IMAGE:3506210, mRNA, partial cds
212287_at_HG-U133A	JJAZ1	joined to JAZF1	Consensus includes gb:BF382924 /FEA=EST /DB_XREF=gi:11364313 /DB_XREF=est:601816985F1 /CLONE=IMAGE:4050909 /UG=Hs.197803 KIAA0160 protein
212293_at_HG-U133A	KIAA0630	KIAA0630 protein	Consensus includes gb:BG111260 /FEA=EST /DB_XREF=gi:12604766 /DB_XREF=est:602281701F1 /CLONE=IMAGE:4369057 /UG=Hs.12259 KIAA0630 protein
212309_at_HG-U133A	CLASP2	CLIP-associating protein 2	Consensus includes gb:AV725315 /FEA=EST /DB_XREF=gi:10830580 /DB_XREF=est:AV725315 /CLONE=HTCCAG11 /UG=Hs.108614 KIAA0627

			protein; Drosophila multiple asters (Mast)-like homolog 2
212311_at_HG-U133A	KIAA0746	KIAA0746 protein	Consensus includes gb:AA522514 /FEA=EST /DB_XREF=gi:2263226 /DB_XREF=est:ni38c01.s1 /CLONE=IMAGE:979104 /UG=Hs.49500 KIAA0746 protein
212313_at_HG-U133A		Homo sapiens cDNA FLJ11714 fis, clone HEMBA1005219, weakly similar to NUCLEAR PROTEIN SNF7	Consensus includes gb:BC004344.1 /DEF=Homo sapiens, clone IMAGE:3633354, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3633354) /DB_XREF=gi:13279286 /UG=Hs.5019 Homo sapiens, clone IMAGE:3633354, mRNA, partial cds
212314_at_HG-U133A	KIAA0746	KIAA0746 protein	Consensus includes gb:AB018289.1 /DEF=Homo sapiens mRNA for KIAA0746 protein, partial cds. /FEA=mRNA /GEN=KIAA0746 /PROD=KIAA0746 protein /DB_XREF=gi:3882212 /UG=Hs.49500 KIAA0746 protein
212345_s_at_HG-U133A	DKFZP586F2423	hypothetical protein DKFZp586F2423	Consensus includes gb:BE675139 /FEA=EST /DB_XREF=gi:10035680 /DB_XREF=est:7f03b12.x1 /CLONE=IMAGE:3293567 /UG=Hs.13659 hypothetical protein DKFZp586F2423
212346_s_at_HG-U133A			Consensus includes gb:AK026392.1 /DEF=Homo sapiens cDNA: FLJ22739 fis, clone HUV00686. /FEA=mRNA /DB_XREF=gi:10439242 /UG=Hs.102402 Mad4 homolog
212349_at_HG-U133A	POFUT1	protein O-fucosyltransferase 1	Consensus includes gb:AL045513 /FEA=EST /DB_XREF=gi:5433649 /DB_XREF=est:DKFZp434J015_r1 /CLONE=DKFZp434J015 /UG=Hs.178292 KIAA0180 protein
212357_at_HG-U133A	KIAA0280	KIAA0280 protein	Consensus includes gb:AI096888 /FEA=EST /DB_XREF=gi:3446470 /DB_XREF=est:qb58f08.x1 /CLONE=IMAGE:1704327 /UG=Hs.75400 KIAA0280 protein
212365_at_HG-U133A	MYO1B	myosin IB	Consensus includes gb:BF215996 /FEA=EST /DB_XREF=gi:11109582 /DB_XREF=est:601881549F1 /CLONE=IMAGE:4093740 /UG=Hs.121576 Homo sapiens cDNA FLJ20153 fis, clone COL08656, highly similar to AJ001381 Homo sapiens incomplete cDNA for a mutated allele

212382_at_HG-U133A		Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:BF433429 /FEA=EST /DB_XREF=gi:11445592 /DB_XREF=est:7q53a12.x1 /CLONE=IMAGE:3702046 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212385_at_HG-U133A		Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:AU118026 /FEA=EST /DB_XREF=gi:10933043 /DB_XREF=est:AU118026 /CLONE=HEMBA1002729 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212386_at_HG-U133A		Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:BF592782 /FEA=EST /DB_XREF=gi:11685106 /DB_XREF=est:7j94d06.x1 /CLONE=IMAGE:3442594 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212387_at_HG-U133A		Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:BG495771 /FEA=EST /DB_XREF=gi:13457287 /DB_XREF=est:602540396F1 /CLONE=IMAGE:4671599 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212397_at_HG-U133A	RDX	radixin	Consensus includes gb:AL137751.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434I0812 (from clone DKFZp434I0812); partial cds. /FEA=mRNA /GEN=DKFZp434I0812 /PROD=hypothetical protein /DB_XREF=gi:6808387 /UG=Hs.263671 Homo sapiens mRNA; cDNA DKFZp434I0812 (from clone DKFZp434I0812); partial cds
212400_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp586A0618 (from clone DKFZp586A0618)	Consensus includes gb:AL043266 /FEA=EST /DB_XREF=gi:5935844 /DB_XREF=est:DKFZp434L1423_s1 /CLONE=DKFZp434L1423 /UG=Hs.111334 ferritin, light polypeptide
212417_at_HG-U133A	SCAMP1	secretory carrier membrane protein 1	Consensus includes gb:BF058944 /FEA=EST /DB_XREF=gi:10812840 /DB_XREF=est:7k36c05.x1 /CLONE=IMAGE:3477489 /UG=Hs.31218 secretory carrier membrane protein 1
212449_s_at_HG-U133A	LYPLA1	lysophospholipase I	Consensus includes gb:BG288007 /FEA=EST /DB_XREF=gi:13042412 /DB_XREF=est:602387785F1 /CLONE=IMAGE:4516701 /UG=Hs.12540 lysophospholipase I
212463_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone	Consensus includes gb:BE379006 /FEA=EST /DB_XREF=gi:9324371 /DB_XREF=est:601236272F1 /CLONE=IMAGE:3608680 /UG=Hs.99766 Homo

		DKFZp564J0323)	sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
212469_at_HG-U133A	IDN3	IDN3 protein	Consensus includes gb:AB019494.1 /DEF=Homo sapiens IDN3 mRNA, partial cds. /FEA=mRNA /GEN=IDN3 /DB_XREF=gi:4760548 /UG=Hs.225767 IDN3 protein
212479_s_at_HG-U133A	FLJ13910	hypothetical protein FLJ13910	Consensus includes gb:AK022815.1 /DEF=Homo sapiens cDNA FLJ12753 fis, clone NT2RP2001226. /FEA=mRNA /DB_XREF=gi:10434432 /UG=Hs.75277 hypothetical protein FLJ13910
212480_at_HG-U133A	KIAA0376	KIAA0376 protein	Consensus includes gb:AB002374.1 /DEF=Human mRNA for KIAA0376 gene, partial cds. /FEA=mRNA /GEN=KIAA0376 /DB_XREF=gi:2280484 /UG=Hs.4791 KIAA0376 protein
212481_s_at_HG-U133A	TPM4	tropomyosin 4	Consensus includes gb:AI214061 /FEA=EST /DB_XREF=gi:3777662 /DB_XREF=est:ap29d10.x1 /CLONE=IMAGE:1956787 /UG=Hs.250641 tropomyosin 4
212484_at_HG-U133A	MTVR	Mouse Mammary Turmor Virus Receptor homolog	Consensus includes gb:BF974389 /FEA=EST /DB_XREF=gi:12341604 /DB_XREF=est:602244063F1 /CLONE=IMAGE:4335182 /UG=Hs.18686 Mouse Mammary Turmor Virus Receptor homolog
212509_s_at_HG-U133A		ESTs, Weakly similar to N-WASP [H.sapiens]	Consensus includes gb:BF968134 /FEA=EST /DB_XREF=gi:12335349 /DB_XREF=est:602269121F1 /CLONE=IMAGE:4357349 /UG=Hs.250723 FK506 binding protein 12-rapamycin associated protein 1
212531_at_HG-U133A	LCN2	lipocalin 2 (oncogene 24p3)	Consensus includes gb:NM_005564.1 /DEF=Homo sapiens lipocalin 2 (oncogene 24p3) (LCN2), mRNA. /FEA=CDS /GEN=LCN2 /PROD=lipocalin 2 (oncogene 24p3) /DB_XREF=gi:5031852 /UG=Hs.204238 lipocalin 2 (oncogene 24p3) /FL=gb:NM_005564.1
212535_at_HG-U133A		Homo sapiens cDNA FLJ32156 fis, clone PLACE6000137	Consensus includes gb:AA142929 /FEA=EST /DB_XREF=gi:1712307 /DB_XREF=est:zl40g07.s1 /CLONE=IMAGE:504444 /UG=Hs.288993 ESTs
212538_at_HG-U133A	KIAA1058	KIAA1058 protein	Consensus includes gb:AL576253 /FEA=EST /DB_XREF=gi:12938214 /DB_XREF=est:AL576253 /CLONE=CS0DI073YM22 (3 prime) /UG=Hs.8021 KIAA1058 protein

212549_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)	Consensus includes gb:BE645861 /FEA=EST /DB_XREF=gi:9970172 /DB_XREF=est:7e77d05.x1 /CLONE=IMAGE:3288489 /UG=Hs.24064 Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
212569_at_HG-U133A	KIAA0650	KIAA0650 protein	Consensus includes gb:AV699744 /FEA=EST /DB_XREF=gi:10301715 /DB_XREF=est:AV699744 /CLONE=GKCEDF05 /UG=Hs.8118 KIAA0650 protein
212577_at_HG-U133A	KIAA0650	KIAA0650 protein	Consensus includes gb:AA868754 /FEA=EST /DB_XREF=gi:2964199 /DB_XREF=est:ak52e09.s1 /CLONE=IMAGE:1409608 /UG=Hs.8118 KIAA0650 protein
212579_at_HG-U133A	KIAA0650	KIAA0650 protein	Consensus includes gb:AB014550.1 /DEF=Homo sapiens mRNA for KIAA0650 protein, partial cds. /FEA=mRNA /GEN=KIAA0650 /PROD=KIAA0650 protein /DB_XREF=gi:3327113 /UG=Hs.8118 KIAA0650 protein
212586_at_HG-U133A	ARTS-1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	Consensus includes gb:AA195244 /FEA=EST /DB_XREF=gi:1784944 /DB_XREF=est:zr36b02.s1 /CLONE=IMAGE:665451 /UG=Hs.247043 type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
212587_s_at_HG-U133A	PTPRC	protein tyrosine phosphatase, receptor type, C	Consensus includes gb:AI809341 /FEA=EST /DB_XREF=gi:5395907 /DB_XREF=est:we96c09.x1 /CLONE=IMAGE:2348944 /UG=Hs.170121 protein tyrosine phosphatase, receptor type, C
212589_at_HG-U133A	RRAS2	related RAS viral (r-ras) oncogene homolog 2	Consensus includes gb:AI753792 /FEA=EST /DB_XREF=gi:5132144 /DB_XREF=est:cr16f06.x2 /CLONE=HBMSC_cr16f06 /UG=Hs.206097 oncogene TC21
212590_at_HG-U133A			Consensus includes gb:AI431643 /FEA=EST /DB_XREF=gi:4304619 /DB_XREF=est:tg74f12.x1 /CLONE=IMAGE:2114543 /UG=Hs.206097 oncogene TC21
212592_at_HG-U133A		Homo sapiens, clone MGC:24130 IMAGE:4692359, mRNA, complete cds	Consensus includes gb:AV733266 /FEA=EST /DB_XREF=gi:10850811 /DB_XREF=est:AV733266 /CLONE=cdAAJG04 /UG=Hs.76325 step II splicing factor SLU7

212601_at_HG-U133A	KIAA0399	KIAA0399 protein	Consensus includes gb:AB007859.2 /DEF=Homo sapiens mRNA for KIAA0399 protein, partial cds. /FEA=mRNA /GEN=KIAA0399 /PROD=KIAA0399 protein /DB_XREF=gi:6634028 /UG=Hs.100955 KIAA0399 protein
212614_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)	Consensus includes gb:BG285011 /FEA=EST /DB_XREF=gi:13036541 /DB_XREF=est:602409278F1 /CLONE=IMAGE:4538275 /UG=Hs.12702 Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)
212629_s_at_HG-U133A	PRKCL2	protein kinase C-like 2	Consensus includes gb:AI633689 /FEA=EST /DB_XREF=gi:4685019 /DB_XREF=est:th71d03.x1 /CLONE=IMAGE:2124101 /UG=Hs.69171 protein kinase C-like 2
212658_at_HG-U133A	LHFPL2	lipoma HMGIC fusion partner-like 2	Consensus includes gb:N66633 /FEA=EST /DB_XREF=gi:1218758 /DB_XREF=est:yy70f02.s1 /CLONE=IMAGE:278907 /UG=Hs.79299 lipoma HMGIC fusion partner-like 2
212660_at_HG-U133A	KIAA0239	KIAA0239 protein	Consensus includes gb:AI735639 /FEA=EST /DB_XREF=gi:5057163 /DB_XREF=est:at18h12.x1 /CLONE=IMAGE:2355527 /UG=Hs.9729 KIAA0239 protein
212667_at_HG-U133A	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	Consensus includes gb:AL575922 /FEA=EST /DB_XREF=gi:12937561 /DB_XREF=est:AL575922 /CLONE=CS0DI067YN03 (3 prime) /UG=Hs.111779 secreted protein, acidic, cysteine-rich (osteonectin)
212686_at_HG-U133A	KIAA1157	KIAA1157 protein	Consensus includes gb:AB032983.1 /DEF=Homo sapiens mRNA for KIAA1157 protein, partial cds. /FEA=mRNA /GEN=KIAA1157 /PROD=KIAA1157 protein /DB_XREF=gi:6330128 /UG=Hs.21894 KIAA1157 protein
212719_at_HG-U133A	SCOP	SCN Circadian Oscillatory Protein (SCOP)	Consensus includes gb:AB011178.1 /DEF=Homo sapiens mRNA for KIAA0606 protein, partial cds. /FEA=mRNA /GEN=KIAA0606 /PROD=KIAA0606 protein /DB_XREF=gi:3043735 /UG=Hs.38176 KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP)
212733_at_HG-U133A	KIAA0226	KIAA0226 gene product	Consensus includes gb:AI798908 /FEA=EST /DB_XREF=gi:5364380

			/DB_XREF=est:we94b11.x1 /CLONE=IMAGE:2348733 /UG=Hs.141296 KIAA0226 gene product
212735_at_HG-U133A	KIAA0226	KIAA0226 gene product	Consensus includes gb:BF448041 /FEA=EST /DB_XREF=gi:11513102 /DB_XREF=est:7q97f09.x1 /CLONE=IMAGE:3706504 /UG=Hs.141296 KIAA0226 gene product
212750_at_HG-U133A	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	Consensus includes gb:AB020630.1 /DEF=Homo sapiens mRNA for KIAA0823 protein, partial cds. /FEA=mRNA /GEN=KIAA0823 /PROD=KIAA0823 protein /DB_XREF=gi:4240131 /UG=Hs.45719 KIAA0823 protein
212778_at_HG-U133A	KIAA0602	KIAA0602 protein	Consensus includes gb:AL583340 /FEA=EST /DB_XREF=gi:12952206 /DB_XREF=est:AL583340 /CLONE=CS0DL012YA08 (3 prime) /UG=Hs.37656 KIAA0602 protein
212783_at_HG-U133A	DKFZp761B2423	hypothetical protein DKFZp761B2423	Consensus includes gb:AI538172 /FEA=EST /DB_XREF=gi:4452307 /DB_XREF=est:ti75f08.x1 /CLONE=IMAGE:2137863 /UG=Hs.91065 hypothetical protein DKFZp761B2423
212812_at_HG-U133A		Homo sapiens cDNA: FLJ22642 fis, clone HSI06970	Consensus includes gb:AI700633 /FEA=EST /DB_XREF=gi:4988533 /DB_XREF=est:we38g03.x1 /CLONE=IMAGE:2343412 /UG=Hs.288232 Homo sapiens cDNA: FLJ22642 fis, clone HSI06970
212813_at_HG-U133A	FLJ14529	hypothetical protein FLJ14529	Consensus includes gb:AA149644 /FEA=EST /DB_XREF=gi:1720445 /DB_XREF=est:zl39d08.s1 /CLONE=IMAGE:504303 /UG=Hs.55016 hypothetical protein FLJ21935
212827_at_HG-U133A	IGHM	immunoglobulin heavy constant mu	Consensus includes gb:X17115.1 /DEF=Human mRNA for IgM heavy chain complete sequence. /FEA=mRNA /DB_XREF=gi:33450 /UG=Hs.302063 immunoglobulin heavy constant mu
212828_at_HG-U133A	SYNJ2	synaptojanin 2	Consensus includes gb:AA191573 /FEA=EST /DB_XREF=gi:1780272 /DB_XREF=est:zp81b09.s1 /CLONE=IMAGE:626585 /UG=Hs.61289 synaptojanin 2
212838_at_HG-U133A	KIAA1010	KIAA1010 protein	Consensus includes gb:AB023227.1 /DEF=Homo sapiens mRNA for

			KIAA1010 protein, partial cds. /FEA=mRNA /GEN=KIAA1010 /PROD=KIAA1010 protein /DB_XREF=gi:4589669 /UG=Hs.23860 KIAA1010 protein
212886_at_HG-U133A	DKFZP434C171	DKFZP434C171 protein	Consensus includes gb:AL080169.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171); partial cds. /FEA=mRNA /GEN=DKFZp434C171 /PROD=hypothetical protein /DB_XREF=gi:5262637 /UG=Hs.209100 DKFZP434C171 protein
212895_s_at_HG-U133A	ABR	active BCR-related gene	Consensus includes gb:AL527773 /FEA=EST /DB_XREF=gi:12791266 /DB_XREF=est:AL527773 /CLONE=CS0DC026YF10 (3 prime) /UG=Hs.118021 active BCR-related gene
212914_at_HG-U133A	PKP4	plakophilin 4	Consensus includes gb:AV648364 /FEA=EST /DB_XREF=gi:9869378 /DB_XREF=est:AV648364 /CLONE=GLCBIF04 /UG=Hs.152151 plakophilin 4
212953_x_at_HG-U133A	CALR	calreticulin	Consensus includes gb:BE251303 /FEA=EST /DB_XREF=gi:9121413 /DB_XREF=est:601107814F1 /CLONE=IMAGE:3344018 /UG=Hs.16488 calreticulin
212956_at_HG-U133A	KIAA0882	KIAA0882 protein	Consensus includes gb:AI348094 /FEA=EST /DB_XREF=gi:4085300 /DB_XREF=est:qp61g12.x1 /CLONE=IMAGE:1927558 /UG=Hs.90419 KIAA0882 protein
212960_at_HG-U133A	KIAA0882	KIAA0882 protein	Consensus includes gb:BE646554 /FEA=EST /DB_XREF=gi:9970865 /DB_XREF=est:7e89a04.x1 /CLONE=IMAGE:3292302 /UG=Hs.90419 KIAA0882 protein
212967_x_at_HG-U133A	NAP1L1	nucleosome assembly protein 1-like 1	Consensus includes gb:AW148801 /FEA=EST /DB_XREF=gi:6196697 /DB_XREF=est:xf04e10.x1 /CLONE=IMAGE:2617098 /UG=Hs.179662 nucleosome assembly protein 1-like 1
212970_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKFZp434E033)	Consensus includes gb:AI694303 /FEA=EST /DB_XREF=gi:4971643 /DB_XREF=est:wd45c03.x1 /CLONE=IMAGE:2331076 /UG=Hs.15740 Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKFZp434E033)
212973_at_HG-U133A	RPIA	ribose 5-phosphate isomerase A (ribose	Consensus includes gb:AI692341 /FEA=EST /DB_XREF=gi:4969681

		5-phosphate epimerase)	/DB_XREF=est:wd85g04.x1 /CLONE=IMAGE:2338422 /UG=Hs.79886 ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)
212975_at_HG-U133A	KIAA0870	KIAA0870 protein	Consensus includes gb:AB020677.2 /DEF=Homo sapiens mRNA for KIAA0870 protein, partial cds. /FEA=mRNA /GEN=KIAA0870 /PROD=KIAA0870 protein /DB_XREF=gi:6635136 /UG=Hs.18166 KIAA0870 protein
212985_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKFZp434E033)	Consensus includes gb:BF115739 /FEA=EST /DB_XREF=gi:10985215 /DB_XREF=est:7n64b08.x1 /CLONE=IMAGE:3569246 /UG=Hs.15740 Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKFZp434E033)
212989_at_HG-U133A		Homo sapiens mRNA for Hmob33 protein, 3' untranslated region	Consensus includes gb:AI377497 /FEA=EST /DB_XREF=gi:4187350 /DB_XREF=est:tc37c06.x1 /CLONE=IMAGE:2066794 /UG=Hs.153716 Homo sapiens mRNA for Hmob33 protein, 3 untranslated region
212998_x_at_HG-U133A	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	Consensus includes gb:AI583173 /FEA=EST /DB_XREF=gi:4569070 /DB_XREF=est:tq64e04.x1 /CLONE=IMAGE:2213598 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1
213048_s_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	Consensus includes gb:W26593 /FEA=EST /DB_XREF=gi:1307454 /DB_XREF=est:33g5 /UG=Hs.145279 SET translocation (myeloid leukemia-associated)
213049_at_HG-U133A	DKFZp566D133	DKFZp566D133 protein	Consensus includes gb:BG436400 /FEA=EST /DB_XREF=gi:13342906 /DB_XREF=est:602509062F1 /CLONE=IMAGE:4619679 /UG=Hs.167031 DKFZP566D133 protein
213073_at_HG-U133A	KIAA0321	KIAA0321 protein	Consensus includes gb:AB002319.1 /DEF=Human mRNA for KIAA0321 gene, partial cds. /FEA=mRNA /GEN=KIAA0321 /DB_XREF=gi:2224582 /UG=Hs.8663 KIAA0321 protein
213081_at_HG-U133A	ZNF297	zinc finger protein 297	Consensus includes gb:AL523144 /FEA=EST /DB_XREF=gi:12786637 /DB_XREF=est:AL523144 /CLONE=CS0DC001YO14 (3 prime) /UG=Hs.206770 zinc finger protein 297 /FL=gb:NM_005453.2
213101_s_at_HG-	IL27	interleukin 27	Consensus includes gb:Z78330 /FEA=EST /DB_XREF=gi:1495103

U133A			/DB_XREF=est:HSZ78330 /CLONE=2.49 (CEPH) /UG=Hs.10927 hypothetical protein EUROIMAGE1875335
213142_x_at_HG-U133A	LOC54103	hypothetical protein	Consensus includes gb:AV700415 /FEA=EST /DB_XREF=gi:10302386 /DB_XREF=est:AV700415 /CLONE=GKCDGA04 /UG=Hs.12969 hypothetical protein
213147_at_HG-U133A	HOXA10	homeo box A10	Consensus includes gb:AI375919 /FEA=EST /DB_XREF=gi:4175909 /DB_XREF=est:tc14d04.x1 /CLONE=IMAGE:2063815 /UG=Hs.110637 homeo box A10 /FL=gb:NM_018951.1
213150_at_HG-U133A	HOXA10	homeo box A10	Consensus includes gb:BF792917 /FEA=EST /DB_XREF=gi:12097902 /DB_XREF=est:602253224F1 /CLONE=IMAGE:4345588 /UG=Hs.110637 homeo box A10 /FL=gb:NM_018951.1
213159_at_HG-U133A	KIAA0805	KIAA0805 protein	Consensus includes gb:AB018348.1 /DEF=Homo sapiens mRNA for KIAA0805 protein, partial cds. /FEA=mRNA /GEN=KIAA0805 /PROD=KIAA0805 protein /DB_XREF=gi:3882330 /UG=Hs.55947 KIAA0805 protein
213238_at_HG-U133A	ATP10D	ATPase, Class V, type 10D	Consensus includes gb:AI478147 /FEA=EST /DB_XREF=gi:4371373 /DB_XREF=est:tm34f06.x1 /CLONE=IMAGE:2160035 /UG=Hs.173540 ATPase, Class V, type 10D
213249_at_HG-U133A	FBXL7	F-box and leucine-rich repeat protein 7	Consensus includes gb:AU145127 /FEA=EST /DB_XREF=gi:11006648 /DB_XREF=est:AU145127 /CLONE=HEMBA1003978 /UG=Hs.76798 f-box and leucine-rich repeat protein 7 /FL=gb:AF199356.1 gb:NM_012304.1
213288_at_HG-U133A		Homo sapiens clone 23620 mRNA sequence	Consensus includes gb:AI761250 /FEA=EST /DB_XREF=gi:5176917 /DB_XREF=est:wi68f01.x1 /CLONE=IMAGE:2398489 /UG=Hs.90797 Homo sapiens clone 23620 mRNA sequence
213295_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122)	Consensus includes gb:AA555096 /FEA=EST /DB_XREF=gi:2325635 /DB_XREF=est:nj40e01.s1 /CLONE=IMAGE:994968 /UG=Hs.26295 Homo sapiens mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122)
213309_at_HG-U133A	PLCL2	phospholipase C-like 2	Consensus includes gb:AL117515.1 /DEF=Homo sapiens mRNA; cDNA

			DKFZp434L0735 (from clone DKFZp434L0735); partial cds. /FEA=mRNA /GEN=DKFZp434L0735 /PROD=hypothetical protein /DB_XREF=gi:5912029 /UG=Hs.54886 phospholipase C, epsilon 2
213313_at_HG-U133A	GAPCENA	rab6 GTPase activating protein (GAP and centrosome-associated)	Consensus includes gb:AI922519 /FEA=EST /DB_XREF=gi:5658483 /DB_XREF=est:wm89a07.x1 /CLONE=IMAGE:2443092 /UG=Hs.55099 rab6 GTPase activating protein (GAP and centrosome-associated)
213353_at_HG-U133A	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	Consensus includes gb:BF693921 /FEA=EST /DB_XREF=gi:11979329 /DB_XREF=est:602082488F1 /CLONE=IMAGE:4246917 /UG=Hs.180513 ATP-binding cassette, sub-family A (ABC1), member 5
213370_s_at_HG-U133A	DKFZP434L243	DKFZP434L243 protein	Consensus includes gb:BF057298 /FEA=EST /DB_XREF=gi:10811194 /DB_XREF=est:7k18g10.x1 /CLONE=IMAGE:3444691 /UG=Hs.21695. DKFZP434L243 protein
213447_at_HG-U133A	IPW	imprinted in Prader-Willi syndrome	Consensus includes gb:AI672541 /FEA=EST /DB_XREF=gi:4852272 /DB_XREF=est:wb32d12.x1 /CLONE=IMAGE:2307383 /UG=Hs.5022 imprinted in Prader-Willi syndrome
213452_at_HG-U133A	ZNF184	zinc finger protein 184 (Kruppel-like)	Consensus includes gb:AI811577 /FEA=EST /DB_XREF=gi:5398143 /DB_XREF=est:tw74g05.x1 /CLONE=IMAGE:2265464 /UG=Hs.158174 zinc finger protein 184 (Kruppel-like)
213453_x_at_HG-U133A	GAPD	glyceraldehyde-3-phosphate dehydrogenase	Consensus includes gb:BF689355 /FEA=EST /DB_XREF=gi:11974763 /DB_XREF=est:602184994T1 /CLONE=IMAGE:4299431 /UG=Hs.169476 glyceraldehyde-3-phosphate dehydrogenase
213474_at_HG-U133A		ESTs	Consensus includes gb:AI890903 /FEA=EST /DB_XREF=gi:5596067 /DB_XREF=est:wm91f10.x1 /CLONE=IMAGE:2443339 /UG=Hs.119683 ESTs
213504_at_HG-U133A	MOV34-34KD	COP9 subunit 6 (MOV34 homolog, 34 kD)	Consensus includes gb:W63732 /FEA=EST /DB_XREF=gi:1371312 /DB_XREF=est:zd30b06.s1 /CLONE=IMAGE:342131 /UG=Hs.15591 COP9 subunit 6 (MOV34 homolog, 34 kD)
213511_s_at_HG-U133A		Homo sapiens, clone MGC:17492 IMAGE:3453013, mRNA, complete cds	Consensus includes gb:AI167164 /FEA=EST /DB_XREF=gi:3700334 /DB_XREF=est:oo08c10.x1 /CLONE=IMAGE:1565586 /UG=Hs.23200

			myotubularin related protein 1
213514_s_at_HG-U133A	DIAPH1	diaphanous homolog 1 (Drosophila)	Consensus includes gb:AU158818 /FEA=EST /DB_XREF=gi:11020339 /DB_XREF=est:AU158818 /CLONE=THYRO1000147 /UG=Hs.26584 diaphanous (Drosophila, homolog) 1
213539_at_HG-U133A	CD3D	CD3D antigen, delta polypeptide (TiT3 complex)	Consensus includes gb:NM_000732.1 /DEF=Homo sapiens CD3D antigen, delta polypeptide (TiT3 complex) (CD3D), mRNA. /FEA=CDS /GEN=CD3D /PROD=CD3D antigen, delta polypeptide (TiT3 complex) /DB_XREF=gi:4502668 /UG=Hs.95327 CD3D antigen, delta polypeptide (TiT3 complex) /FL=gb:NM_000732.1
213572_s_at_HG-U133A	SERPINB1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	Consensus includes gb:AI554300 /FEA=EST /DB_XREF=gi:4486663 /DB_XREF=est:tq05e07.x1 /CLONE=IMAGE:2207940 /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1
213582_at_HG-U133A	ATP11A	ATPase, Class VI, type 11A	Consensus includes gb:BF439472 /FEA=EST /DB_XREF=gi:11451989 /DB_XREF=est:nab65a05.x1 /CLONE=IMAGE:3272361 /UG=Hs.29189 ATPase, Class VI, type 11A
213600_at_HG-U133A	KIAA0545	KIAA0545 protein	Consensus includes gb:AA425633 /FEA=EST /DB_XREF=gi:2107236 /DB_XREF=est:zv47a01.s1 /CLONE=IMAGE:756744 /UG=Hs.129943 KIAA0545 protein
213622_at_HG-U133A	COL9A2	collagen, type IX, alpha 2	Consensus includes gb:AI733465 /FEA=EST /DB_XREF=gi:5054578 /DB_XREF=est:oq93g07.x5 /CLONE=IMAGE:1593948 /UG=Hs.37165 collagen, type IX, alpha 2 /FL=gb:NM_001852.1
213624_at_HG-U133A	ASM3A	acid sphingomyelinase-like phosphodiesterase	Consensus includes gb:AA873600 /FEA=EST /DB_XREF=gi:2969722 /DB_XREF=est:ob12a02.s1 /CLONE=IMAGE:1323434 /UG=Hs.42945 acid sphingomyelinase-like phosphodiesterase
213639_s_at_HG-U133A	KIAA0557	KIAA0557 protein	Consensus includes gb:AI871396 /FEA=EST /DB_XREF=gi:5545445 /DB_XREF=est:wl81f07.x1 /CLONE=IMAGE:2431333 /UG=Hs.101414 KIAA0557 protein
213674_x_at_HG-	IGHG3	immunoglobulin heavy constant gamma	Consensus includes gb:AI858004 /FEA=EST /DB_XREF=gi:5511620

U133A		3 (G3m marker)	/DB_XREF=est:wj69b09.x1 /CLONE=IMAGE:2408057 /UG=Hs.284277 Homo sapiens immunoglobulin mu chain antibody MO30 (IgM) mRNA, complete cds
213689_x_at_HG-U133A	RPL5	ribosomal protein L5	Consensus includes gb:AL137958 /FEA=EST /DB_XREF=gi:6854638 /DB_XREF=est:DKFZp761C1715_r1 /CLONE=DKFZp761C1715 /UG=Hs.180946 ribosomal protein L5
213716_s_at_HG-U133A	SECTM1	secreted and transmembrane 1	Consensus includes gb:BF939675 /FEA=EST /DB_XREF=gi:12357086 /DB_XREF=est:nac79g07.x1 /CLONE=IMAGE:3440820 /UG=Hs.326612 Homo sapiens secreted and transmembrane 1 (SECTM1), mRNA
213725_x_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071)	Consensus includes gb:AI693140 /FEA=EST /DB_XREF=gi:4970480 /DB_XREF=est:wd68a05.x1 /CLONE=IMAGE:2336720 /UG=Hs.22907 Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071)
213737_x_at_HG-U133A		ESTs	Consensus includes gb:AI620911 /FEA=EST /DB_XREF=gi:4630037 /DB_XREF=est:tu05d12.x1 /CLONE=IMAGE:2250167 /UG=Hs.205125 ESTs
213772_s_at_HG-U133A	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	Consensus includes gb:BF196572 /FEA=EST /DB_XREF=gi:11084646 /DB_XREF=est:7m98a04.x1 /CLONE=IMAGE:3563023 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2
213779_at_HG-U133A			Consensus includes gb:AL031186 /DEF=Human DNA sequence from clone CTA-984G1 on chromosome 22q12.1-12.2 Contains the 5 part of the EWSR1 gene for Ewing sarcoma breakpoint region 1 protein, a novel gene and the 3 part of a novel gene with Collagen triple helix repeats. Contains ESTs... /FEA=mRNA_1 /DB_XREF=gi:4581429 /UG=Hs.289106 Human DNA sequence from clone CTA-984G1 on chromosome 22q12.1-12.2 Contains the 5 part of the EWSR1 gene for Ewing sarcoma breakpoint region 1 protein, a novel gene and the 3 part of a novel gene with Collagen triple helix repeats. Contains ESTs, GSSs a
213798_s_at_HG-	CAP	adenylyl cyclase-associated protein	Consensus includes gb:AA806142 /FEA=EST /DB_XREF=gi:2874892

U133A			/DB_XREF=est:oe29d06.s1 /CLONE=IMAGE:1409963 /UG=Hs.104125 adenylyl cyclase-associated protein
213810_s_at_HG-U133A	FLJ10342	hypothetical protein FLJ10342	Consensus includes gb:AW007137 /FEA=EST /DB_XREF=gi:5855915 /DB_XREF=est:wt09f08.x1 /CLONE=IMAGE:2506983 /UG=Hs.101514 hypothetical protein FLJ10342
213844_at_HG-U133A	HOXA5	homeo box A5	Consensus includes gb:NM_019102.1 /DEF=Homo sapiens homeo box A5 (HOXA5), mRNA. /FEA=CDS /GEN=HOXA5 /PROD=homeobox protein (HOX-1.3) /DB_XREF=gi:9506790 /UG=Hs.37034 homeo box A5 /FL=gb:NM_019102.1
213846_at_HG-U133A	COX7C	cytochrome c oxidase subunit VIIc	Consensus includes gb:AA382702 /FEA=EST /DB_XREF=gi:2035020 /DB_XREF=est:EST95939 /UG=Hs.3462 cytochrome c oxidase subunit VIIc
213850_s_at_HG-U133A	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	Consensus includes gb:AI984932 /FEA=EST /DB_XREF=gi:5812209 /DB_XREF=est:wr86e12.x1 /CLONE=IMAGE:2494606 /UG=Hs.51957 splicing factor, argininеserine-rich 2, interacting protein
213854_at_HG-U133A	SYNGR1	synaptogyrin 1	Consensus includes gb:BF511590 /FEA=EST /DB_XREF=gi:11594888 /DB_XREF=est:UI-H-BI4-aol-b-08-0-UI.s1 /CLONE=IMAGE:3085023 /UG=Hs.6139 synaptogyrin 1
213857_s_at_HG-U133A	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Consensus includes gb:BG230614 /FEA=EST /DB_XREF=gi:12725656 /DB_XREF=est:naf41b12.x1 /CLONE=IMAGE:4143335 /UG=Hs.82685 CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
213891_s_at_HG-U133A		Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:AI927067 /FEA=EST /DB_XREF=gi:5663031 /DB_XREF=est:wo87f01.x1 /CLONE=IMAGE:2462329 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
213894_at_HG-U133A	KIAA0960	KIAA0960 protein	Consensus includes gb:BF447246 /FEA=EST /DB_XREF=gi:11512384 /DB_XREF=est:7p46g06.x1 /CLONE=IMAGE:3648970 /UG=Hs.29900 KIAA0960 protein
213895_at_HG-U133A	EMP1	epithelial membrane protein 1	Consensus includes gb:BF445047 /FEA=EST /DB_XREF=gi:11510185 /DB_XREF=est:nad20g10.x1 /CLONE=IMAGE:3366330 /UG=Hs.79368 epithelial

			membrane protein 1
213902_at_HG-U133A	ASAH	N-acylsphingosine amidohydrolase (acid ceramidase)	Consensus includes gb:AI379338 /FEA=EST /DB_XREF=gi:4189191 /DB_XREF=est:tc73g05.x1 /CLONE=IMAGE:2070296 /UG=Hs.75811 N-acylsphingosine amidohydrolase (acid ceramidase)
213922_at_HG-U133A	KIAA0847	KIAA0847 protein	Consensus includes gb:AW294686 /FEA=EST /DB_XREF=gi:6701322 /DB_XREF=est:UI-H-BW0-ail-h-04-0-UI.s1 /CLONE=IMAGE:2729719 /UG=Hs.125836 KIAA0847 protein
213927_at_HG-U133A		ESTs	Consensus includes gb:AV753204 /FEA=EST /DB_XREF=gi:10911052 /DB_XREF=est:AV753204 /CLONE=NPDBDB08 /UG=Hs.170267 ESTs
213942_at_HG-U133A	EGFL3	EGF-like-domain, multiple 3	Consensus includes gb:AL134303 /FEA=EST /DB_XREF=gi:6602490 /DB_XREF=est:DKFZp547K034_r1 /CLONE=DKFZp547K034 /UG=Hs.56186 EGF-like-domain, multiple 3
213944_x_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp434J194 (from clone DKFZp434J194)	Consensus includes gb:BG236220 /FEA=EST /DB_XREF=gi:12750151 /DB_XREF=est:naf25h11.x1 /CLONE=IMAGE:4142085 /UG=Hs.323067 Homo sapiens mRNA; cDNA DKFZp434J194 (from clone DKFZp434J194)
213963_s_at_HG-U133A	SAP30	sin3-associated polypeptide, 30kD	Consensus includes gb:AW589975 /FEA=EST /DB_XREF=gi:7277100 /DB_XREF=est:hg28b08.x1 /CLONE=IMAGE:2946903 /UG=Hs.20985 sin3-associated polypeptide, 30kD
213979_s_at_HG-U133A	CTBP1	C-terminal binding protein 1	Consensus includes gb:BF984434 /FEA=EST /DB_XREF=gi:12387246 /DB_XREF=est:602307971F1 /CLONE=IMAGE:4399313 /UG=Hs.239737 C-terminal binding protein 1
214000_s_at_HG-U133A	RGS10	regulator of G-protein signalling 10	Consensus includes gb:AI744627 /FEA=EST /DB_XREF=gi:5113004 /DB_XREF=est:wg04g05.x1 /CLONE=IMAGE:2364152 /UG=Hs.82280 regulator of G-protein signalling 10
214017_s_at_HG-U133A	DDX34	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 34	Consensus includes gb:AA039439 /FEA=EST /DB_XREF=gi:1515780 /DB_XREF=est:zk39a11.s1 /CLONE=IMAGE:485180 /UG=Hs.151706 KIAA0134 gene product
214030_at_HG-U133A	FLJ14393	hypothetical protein FLJ14393	Consensus includes gb:BE501352 /FEA=EST /DB_XREF=gi:9703760

			/DB_XREF=est:7a41e05.x1 /CLONE=IMAGE:3221312 /UG=Hs.23294 ESTs, Weakly similar to T15138 hypothetical protein T28F2.4 - Caenorhabditis elegans C.elegans
214051_at_HG-U133A	TMSNB	thymosin, beta, identified in neuroblastoma cells	Consensus includes gb:BF677486 /FEA=EST /DB_XREF=gi:11951381 /DB_XREF=est:602085745F1 /CLONE=IMAGE:4249834 /UG=Hs.56145 thymosin, beta, identified in neuroblastoma cells
214109_at_HG-U133A	LRBA	vesicle trafficking, beach and anchor containing	Consensus includes gb:AI659561 /FEA=EST /DB_XREF=gi:4763131 /DB_XREF=est:tu12d08.x1 /CLONE=IMAGE:2250831 /UG=Hs.62354 cell division cycle 4-like
214116_at_HG-U133A	BTD	biotinidase	Consensus includes gb:AI767414 /FEA=EST /DB_XREF=gi:5233843 /DB_XREF=est:wi95g11.x1 /CLONE=IMAGE:2401124 /UG=Hs.78885 biotinidase
214144_at_HG-U133A	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	Consensus includes gb:BF432147 /FEA=EST /DB_XREF=gi:11444261 /DB_XREF=est:nab80a07.x1 /CLONE=IMAGE:3273900 /UG=Hs.194638 polymerase (RNA) II (DNA directed) polypeptide D
214152_at_HG-U133A	PIGB	phosphatidylinositol glycan, class B	Consensus includes gb:AU144243 /FEA=EST /DB_XREF=gi:11005764 /DB_XREF=est:AU144243 /CLONE=HEMBA1001328 /UG=Hs.247118 phosphatidylinositol glycan, class B
214203_s_at_HG-U133A	PRODH	proline dehydrogenase (oxidase) 1	Consensus includes gb:AA074145 /FEA=EST /DB_XREF=gi:1614015 /DB_XREF=est:zf78g06.s1 /CLONE=IMAGE:383098 /UG=Hs.274550 proline oxidase homolog
214228_x_at_HG-U133A			Consensus includes gb:AJ277151 /DEF=Homo sapiens ox40 gene for CD134 antigen, exons 1-7 /FEA=mRNA /DB_XREF=gi:8926701 /UG=Hs.129780 tumor necrosis factor receptor superfamily, member 4
214238_at_HG-U133A		Homo sapiens clone DT1P1B6 mRNA, CAG repeat region	Consensus includes gb:AI093572 /FEA=EST /DB_XREF=gi:3432548 /DB_XREF=est:qb15f11.x1 /CLONE=IMAGE:1696365 /UG=Hs.18081 Homo sapiens clone DT1P1B6 mRNA, CAG repeat region
214310_s_at_HG-	ZFPL1	zinc finger protein-like 1	Consensus includes gb:AI767884 /FEA=EST /DB_XREF=gi:5234393

U133A			/DB_XREF=est:wi98g11.x1 /CLONE=IMAGE:2401412 /UG=Hs.155165 zinc finger protein-like 1
214315_x_at_HG-U133A	CALR	calreticulin	Consensus includes gb:AI348935 /FEA=EST /DB_XREF=gi:4086141 /DB_XREF=est:tb60a01.x1 /CLONE=IMAGE:2058696 /UG=Hs.16488 calreticulin
214316_x_at_HG-U133A	CALR	calreticulin	Consensus includes gb:AI378706 /FEA=EST /DB_XREF=gi:4188559 /DB_XREF=est:tb91f09.x1 /CLONE=IMAGE:2061737 /UG=Hs.16488 calreticulin
214317_x_at_HG-U133A	RPS9	ribosomal protein S9	Consensus includes gb:BE348997 /FEA=EST /DB_XREF=gi:9260850 /DB_XREF=est:ht47e11.x1 /CLONE=IMAGE:3149900 /UG=Hs.180920 ribosomal protein S9
214321_at_HG-U133A	NOV	nephroblastoma overexpressed gene	Consensus includes gb:BF440025 /FEA=EST /DB_XREF=gi:11452542 /DB_XREF=est:nac52c12.x1 /CLONE=IMAGE:3406079 /UG=Hs.235935 nephroblastoma overexpressed gene
214394_x_at_HG-U133A	FLJ20897	hypothetical protein FLJ20897	Consensus includes gb:AI613383 /FEA=EST /DB_XREF=gi:4622550 /DB_XREF=est:tt80e08.x1 /CLONE=IMAGE:2247110 /UG=Hs.223241 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
214395_x_at_HG-U133A	FLJ20897	hypothetical protein FLJ20897	Consensus includes gb:AI335509 /FEA=EST /DB_XREF=gi:4072436 /DB_XREF=est:tb66h02.x1 /CLONE=IMAGE:2059347 /UG=Hs.223241 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
214430_at_HG-U133A	GLA	galactosidase, alpha	Consensus includes gb:NM_000169.1 /DEF=Homo sapiens galactosidase, alpha (GLA), mRNA. /FEA=CDS /GEN=GLA /PROD=galactosidase, alpha /DB_XREF=gi:4504008 /UG=Hs.69089 galactosidase, alpha /FL=gb:BC002689.1 gb:NM_000169.1
214439_x_at_HG-U133A	BIN1	bridging integrator 1	Consensus includes gb:AF043899.1 /DEF=Homo sapiens amphiphysin IIc1 mRNA, complete cds. /FEA=CDS /PROD=amphiphysin IIc1 /DB_XREF=gi:3064256 /UG=Hs.193163 bridging integrator 1 /FL=gb:AF043899.1

214450_at_HG-U133A	CTSW	cathepsin W (lymphopain)	Consensus includes gb:NM_001335.1 /DEF=Homo sapiens cathepsin W (lymphopain) (CTSW), mRNA. /FEA=CDS /GEN=CTSW /PROD=cathepsin W (lymphopain) /DB_XREF=gi:4503156 /UG=Hs.87450 cathepsin W (lymphopain) /FL=gb:AF013611.1 gb:NM_001335.1
214452_at_HG-U133A	BCAT1	branched chain aminotransferase 1, cytosolic	Consensus includes gb:NM_005504.1 /DEF=Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /FEA=CDS /GEN=BCAT1 /PROD=branched chain aminotransferase 1, cytosolic /DB_XREF=gi:5031606 /UG=Hs.157205 branched chain aminotransferase 1, cytosolic /FL=gb:U21551.1 gb:NM_005504.1
214475_x_at_HG-U133A	CAPN3	calpain 3, (p94)	Consensus includes gb:AF127764.1 /DEF=Homo sapiens calpain 3 (CAPN3) mRNA, alternatively spliced, complete cds. /FEA=CDS /GEN=CAPN3 /PROD=calpain 3 /DB_XREF=gi:4704751 /UG=Hs.40300 calpain 3, (p94) /FL=gb:AF127764.1
214500_at_HG-U133A	H2AFY	H2A histone family, member Y	Consensus includes gb:AF044286.1 /DEF=Homo sapiens histone macroH2A1.1 mRNA, complete cds. /FEA=CDS /PROD=histone macroH2A1.1 /DB_XREF=gi:3493530 /UG=Hs.75258 H2A histone family, member Y /FL=gb:AF044286.1
214501_s_at_HG-U133A	H2AFY	H2A histone family, member Y	Consensus includes gb:AF044286.1 /DEF=Homo sapiens histone macroH2A1.1 mRNA, complete cds. /FEA=CDS /PROD=histone macroH2A1.1 /DB_XREF=gi:3493530 /UG=Hs.75258 H2A histone family, member Y /FL=gb:AF044286.1
214505_s_at_HG-U133A	FHL1	four and a half LIM domains 1	Consensus includes gb:AF220153.1 /DEF=Homo sapiens four and a half LIM domains 1 protein isoform C (FHL1) mRNA, complete cds, alternatively spliced. /FEA=CDS /GEN=FHL1 /PROD=four and a half LIM domains 1 protein isoform C /DB_XREF=gi:6942192 /UG=Hs.239069 four and a half LIM domains 1 /FL=gb:AF220153.1
214523_at_HG-U133A	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	Consensus includes gb:NM_001805.1 /DEF=Homo sapiens CCAATenhancer binding protein (CEBP), epsilon (CEBPE), mRNA. /FEA=CDS /GEN=CEBPE

			/PROD=CCAATenhancer binding protein (CEBP), epsilon /DB_XREF=gi:4502766 /UG=Hs.158323 CCAATenhancer binding protein (CEBP), epsilon /FL=gb:NM_001805.1
214558_at_HG-U133A	GPR12	G protein-coupled receptor 12	Consensus includes gb:NM_005288.1 /DEF=Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /FEA=CDS /GEN=GPR12 /PROD=G protein-coupled receptor 12 /DB_XREF=gi:4885294 /UG=Hs.123034 G protein-coupled receptor 12 /FL=gb:NM_005288.1
214575_s_at_HG-U133A	AZU1	azurocidin 1 (cationic antimicrobial protein 37)	Consensus includes gb:NM_001700.1 /DEF=Homo sapiens azurocidin 1 (cationic antimicrobial protein 37) (AZU1), mRNA. /FEA=CDS /GEN=AZU1 /PROD=azurocidin 1 (cationic antimicrobial protein37) /DB_XREF=gi:11342669 /UG=Hs.72885 azurocidin 1 (cationic antimicrobial protein 37) /FL=gb:NM_001700.1
214615_at_HG-U133A	P2Y10	putative purinergic receptor	Consensus includes gb:NM_014499.1 /DEF=Homo sapiens putative purinergic receptor (P2Y10), mRNA. /FEA=CDS /GEN=P2Y10 /PROD=putative purinergic receptor /DB_XREF=gi:10092632 /UG=Hs.296433 putative purinergic receptor /FL=gb:NM_014499.1
214651_s_at_HG-U133A	HOXA9	homeo box A9	Consensus includes gb:U41813.1 /DEF=Human class I homeoprotein (HOXA9) mRNA, partial cds. /FEA=mRNA /GEN=HOXA9 /PROD=HOXA9 /DB_XREF=gi:1184168 /UG=Hs.127428 homeo box A9 /FL=gb:NM_002142.1
214686_at_HG-U133A	ZNF266	zinc finger protein 266	Consensus includes gb:AA868898 /FEA=EST /DB_XREF=gi:2964343 /DB_XREF=est:ak55b08.s1 /CLONE=IMAGE:1409847 /UG=Hs.118281 zinc finger protein 266
214693_x_at_HG-U133A	DJ328E19.C1.1	hypothetical protein DJ328E19.C1.1	Consensus includes gb:BE732345 /FEA=EST /DB_XREF=gi:10146337 /DB_XREF=est:601566954F1 /CLONE=IMAGE:3841692 /UG=Hs.41569 phosphatidic acid phosphatase type 2A
214700_x_at_HG-U133A			Consensus includes gb:AK000323.1 /DEF=Homo sapiens cDNA FLJ20316 fis, clone HEP07903, highly similar to U79263 Human clone 23760 mRNA. /FEA=mRNA /DB_XREF=gi:7020332 /UG=Hs.225841 DKFZP434D193 protein

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214761_at_HG-U133A	OAZ	OLF-1/EBF associated zinc finger gene	Consensus includes gb:AW149417 /FEA=EST /DB_XREF=gi:6197313 /DB_XREF=est:xf36h07.x1 /CLONE=IMAGE:2620189 /UG=Hs.137168 OLF-1EBF associated zinc finger gene
214786_at_HG-U133A	MAP3K1	mitogen-activated protein kinase kinase kinase 1	Consensus includes gb:AA361361 /FEA=EST /DB_XREF=gi:2013679 /DB_XREF=est:EST70631 /UG=Hs.298727 mitogen-activated protein kinase kinase kinase 1
214789_x_at_HG-U133A	SRP46	Splicing factor, arginine/serine-rich, 46kD	Consensus includes gb:AA524274 /FEA=EST /DB_XREF=gi:2265202 /DB_XREF=est:ng34d08.s1 /CLONE=IMAGE:936687 /UG=Hs.155160 Splicing factor, argininеserine-rich, 46kD
214849_at_HG-U133A		Homo sapiens, clone MGC:5564, mRNA, complete cds	Consensus includes gb:AW500220 /FEA=EST /DB_XREF=gi:7112628 /DB_XREF=est:UI-HF-BN0-akd-c-02-0-UI.r1 /CLONE=IMAGE:3076610 /UG=Hs.332496 Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS
214875_x_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	Consensus includes gb:AW001847 /FEA=EST /DB_XREF=gi:5848763 /DB_XREF=est:wt81a04.x1 /CLONE=IMAGE:2513838 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2
214894_x_at_HG-U133A	MACF1	microtubule-actin crosslinking factor 1	Consensus includes gb:AK023285.1 /DEF=Homo sapiens cDNA FLJ13223 fis, clone OVARC1000001, highly similar to Homo sapiens mRNA for actin binding protein ABP620. /FEA=mRNA /DB_XREF=gi:10435154 /UG=Hs.108258 actin binding protein; macrophin (microfilament and actin filament cross-linker protein)
214911_s_at_HG-U133A			Consensus includes gb:S78771.1 /DEF=NAT=CpG island-associated gene human, mRNA, 1741 nt. /FEA=mRNA /DB_XREF=gi:244232 /UG=Hs.75243 bromodomain-containing 2
214924_s_at_HG-U133A			Consensus includes gb:AK000754.1 /DEF=Homo sapiens cDNA FLJ20747 fis, clone HEP05884, highly similar to J03068 Human DNF1552. /FEA=mRNA /DB_XREF=gi:7021038 /UG=Hs.6705 KIAA1042 protein

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214949_at_HG-U133A			Consensus includes gb:AL050136.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141). /FEA=mRNA /DB_XREF=gi:4884346 /UG=Hs.140945 Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141)
214950_at_HG-U133A			Consensus includes gb:L39064 /DEF=Homo sapiens interleukin 9 receptor precursor (IL9R) gene, complete cds /FEA=mRNA /DB_XREF=gi:632992 /UG=Hs.1702 interleukin 9 receptor
215001_s_at_HG-U133A	GLUL	glutamate-ammonia ligase (glutamine synthase)	Consensus includes gb:AL161952.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M0813 (from clone DKFZp434M0813); partial cds. /FEA=mRNA /GEN=DKFZp434M0813 /PROD=hypothetical protein /DB_XREF=gi:7328002 /UG=Hs.170171 glutamate-ammonia ligase (glutamine synthase)
215049_x_at_HG-U133A	CD163	CD163 antigen	Consensus includes gb:Z22969.1 /DEF=H.sapiens mRNA for M130 antigen cytoplasmic variant 1. /FEA=mRNA /PROD=M130 antigen cytoplasmic variant 1 /DB_XREF=gi:312143 /UG=Hs.74076 CD163 antigen
215087_at_HG-U133A			Consensus includes gb:AL109730.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 68600. /FEA=mRNA /DB_XREF=gi:5689835 /UG=Hs.306331 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 68600
215100_at_HG-U133A			Consensus includes gb:AL022724 /DEF=Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs /FEA=mRNA /DB_XREF=gi:4468306 /UG=Hs.97411 Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs
215115_x_at_HG-U133A	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	Consensus includes gb:AI613045 /FEA=EST /DB_XREF=gi:4622212 /DB_XREF=est:ty68g03.x1 /CLONE=IMAGE:2284276 /UG=Hs.169081 ets variant gene 6 (TEL oncogene)
215215_s_at_HG-			Consensus includes gb:AC004381 /DEF=Homo sapiens Chromosome 16 BAC

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U133A			clone CIT987SK-44M2 /FEA=CDS_1 /DB_XREF=gi:2982169 /UG=Hs.307353 Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2
215227_x_at_HG-U133A	ACP1	acid phosphatase 1, soluble	Consensus includes gb:BG035989 /FEA=EST /DB_XREF=gi:12430674 /DB_XREF=est:602326204F1 /CLONE=IMAGE:4414128 /UG=Hs.75393 acid phosphatase 1, soluble
215346_at_HG-U133A	TNFRSF5	tumor necrosis factor receptor superfamily, member 5	Consensus includes gb:BF664114 /FEA=EST /DB_XREF=gi:11938009 /DB_XREF=est:602145911F1 /CLONE=IMAGE:4309610 /UG=Hs.25648 tumor necrosis factor receptor superfamily, member 5
215379_x_at_HG-U133A	IGLJ3	immunoglobulin lambda joining 3	Consensus includes gb:AV698647 /FEA=EST /DB_XREF=gi:10300618 /DB_XREF=est:AV698647 /CLONE=GKCBJC12 /UG=Hs.289110 immunoglobulin lambda joining 3
215450_at_HG-U133A	SNRPE	small nuclear ribonucleoprotein polypeptide E	Consensus includes gb:W87901 /FEA=EST /DB_XREF=gi:1401985 /DB_XREF=est:zh66f04.r1 /CLONE=IMAGE:417055 /UG=Hs.1066 small nuclear ribonucleoprotein polypeptide E
215537_x_at_HG-U133A			Consensus includes gb:AJ012008 /DEF=Homo sapiens genes encoding RNCC protein, DDAH protein, Ly6-C protein, Ly6-D protein and immunoglobulin receptor /FEA=mRNA_4 /DB_XREF=gi:5304874 /UG=Hs.247362 dimethylarginine dimethylaminohydrolase 2
215622_x_at_HG-U133A	HSPC226	hypothetical protein HSPC226	Consensus includes gb:AL137671.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434L1850 (from clone DKFZp434L1850); partial cds. /FEA=mRNA /GEN=DKFZp434L1850 /PROD=hypothetical protein /DB_XREF=gi:6807837 /UG=Hs.30127 hypothetical protein
215785_s_at_HG-U133A	CYFIP2	cytoplasmic FMR1 interacting protein 2	Consensus includes gb:AL161999.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761H087 (from clone DKFZp761H087); partial cds. /FEA=mRNA /GEN=DKFZp761H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG=Hs.258503 p53 inducible protein
215855_s_at_HG-U133A			Consensus includes gb:AK021741.1 /DEF=Homo sapiens cDNA FLJ11679 fis, clone HEMBA1004807. /FEA=mRNA /DB_XREF=gi:10432986 /UG=Hs.287439

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			Homo sapiens cDNA FLJ11679 fis, clone HEMBA1004807
215925_s_at_HG-U133A			Consensus includes gb:AF283777.2 /DEF=Homo sapiens clone TCBAP0702 mRNA sequence. /FEA=mRNA /DB_XREF=gi:10281735 /UG=Hs.116481 CD72 antigen
216015_s_at_HG-U133A			Consensus includes gb:AK027194.1 /DEF=Homo sapiens cDNA: FLJ23541 fis, clone LNG08276, highly similar to AF054176 Homo sapiens angiotensinvasopressin receptor AIIAVP mRNA. /FEA=mRNA /DB_XREF=gi:10440263 /UG=Hs.159483 chromosome 1 open reading frame 7
216032_s_at_HG-U133A	SDBCAG84	serologically defined breast cancer antigen 84	Consensus includes gb:AF091085.1 /DEF=Homo sapiens clone 638 unknown mRNA, complete sequence. /FEA=mRNA /PROD=unknown /DB_XREF=gi:3860007 /UG=Hs.169992 hypothetical 43.2 Kd protein
216044_x_at_HG-U133A			Consensus includes gb:AK027146.1 /DEF=Homo sapiens cDNA: FLJ23493 fis, clone LNG01831, highly similar to HSU66589 Human ribosomal protein L5 pseudogene mRNA. /FEA=mRNA /DB_XREF=gi:10440199 /UG=Hs.180946 ribosomal protein L5
216095_x_at_HG-U133A	MTMR1	myotubularin related protein 1	Consensus includes gb:AF057354.1 /DEF=Homo sapiens myotubularin-related protein 1a mRNA, partial cds. /FEA=mRNA /PROD=myotubularin-related protein 1a /DB_XREF=gi:5138901 /UG=Hs.23200 myotubularin related protein 1
216218_s_at_HG-U133A	PLCL2	phospholipase C-like 2	Consensus includes gb:AK023546.1 /DEF=Homo sapiens cDNA FLJ13484 fis, clone PLACE1003888, weakly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11). /FEA=mRNA /DB_XREF=gi:10435512 /UG=Hs.54886 phospholipase C, epsilon 2
216304_x_at_HG-U133A			Consensus includes gb:AJ295618 /DEF=Homo sapiens FTSH gene for putative ATPases, exons 1 and 2 and join CDS /FEA=mRNA /DB_XREF=gi:9506352 /UG=Hs.206521 YME1 (S.cerevisiae)-like 1

216320_x_at_HG-U133A			Consensus includes gb:U37055 /DEF=Human hepatocyte growth_factor-like protein gene, complete cds /FEA=mRNA /DB_XREF=gi:1311660 /UG=Hs.278657 macrophage stimulating 1 (hepatocyte growth factor-like)
216356_x_at_HG-U133A	BAIAP3	BAI1-associated protein 3	Consensus includes gb:AB018277.1 /DEF=Homo sapiens mRNA for KIAA0734 protein, partial cds. /FEA=mRNA /GEN=KIAA0734 /PROD=KIAA0734 protein /DB_XREF=gi:3882188 /UG=Hs.101516 BAI1-associated protein 3
216363_at_HG-U133A			Consensus includes gb:S73614.1 /DEF=Homo sapiens transgenic-JHD mouse 2357 immunoglobulin heavy chain variable region (IgG VH251) mRNA, partial cds. /FEA=mRNA /GEN=IgG VH251 /DB_XREF=gi:688334 /UG=Hs.283878 Homo sapiens transgenic-JHD mouse 2357 immunoglobulin heavy chain variable region (IgG VH251) mRNA, partial cds
216379_x_at_HG-U133A			Consensus includes gb:AK000168.1 /DEF=Homo sapiens cDNA FLJ20161 fis, clone COL09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA. /FEA=mRNA /DB_XREF=gi:7020079 /UG=Hs.332045 Homo sapiens cDNA FLJ20161 fis, clone COL09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA
216399_s_at_HG-U133A			Consensus includes gb:AK025663.1 /DEF=Homo sapiens cDNA: FLJ22010 fis, clone HEP07134. /FEA=mRNA /DB_XREF=gi:10438253 /UG=Hs.285848 KIAA1454 protein
216449_x_at_HG-U133A			Consensus includes gb:AK025862.1 /DEF=Homo sapiens cDNA: FLJ22209 fis, clone HRC01496. /FEA=mRNA /DB_XREF=gi:10438505 /UG=Hs.288528 Homo sapiens cDNA: FLJ22209 fis, clone HRC01496
216450_x_at_HG-U133A			Consensus includes gb:AK025862.1 /DEF=Homo sapiens cDNA: FLJ22209 fis, clone HRC01496. /FEA=mRNA /DB_XREF=gi:10438505 /UG=Hs.288528 Homo sapiens cDNA: FLJ22209 fis, clone HRC01496
216609_at_HG-U133A		Homo sapiens thioredoxin delta 3 (TXN delta 3) mRNA, partial cds	Consensus includes gb:AF065241.1 /DEF=Homo sapiens thioredoxin delta 3 (TXN delta 3) mRNA, partial cds. /FEA=mRNA /GEN=TXN delta 3

			/PROD=thioredoxin delta 3 /DB_XREF=gi:3153858 /UG=Hs.306243 Homo sapiens thioredoxin delta 3 (TXN delta 3) mRNA, partial cds
216640_s_at_HG-U133A			Consensus includes gb:AK026926.1 /DEF=Homo sapiens cDNA: FLJ23273 fis, clone HEP02611, highly similar to HSU79278 Human protein disulfide isomerase-related protein P5 mRNA. /FEA=mRNA /DB_XREF=gi:10439898 /UG=Hs.182429 protein disulfide isomerase-related protein
216652_s_at_HG-U133A			Consensus includes gb:AL137673.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone DKFZp434H0872). /FEA=mRNA /DB_XREF=gi:6807841 /UG=Hs.306454 Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone DKFZp434H0872)
216680_s_at_HG-U133A	EPHB4	EphB4	Consensus includes gb:BC004264.1 /DEF=Homo sapiens, Similar to EphB4, clone IMAGE:3611312, mRNA, partial cds. /FEA=mRNA /PROD=Similar to EphB4 /DB_XREF=gi:13279061 /UG=Hs.155227 EphB4
216698_x_at_HG-U133A			Consensus includes gb:AF065854 /DEF=Homo sapiens OR7E12P pseudogene, complete sequence /FEA=CDS /DB_XREF=gi:3831591 /UG=Hs.120017 olfactory receptor, family 7, subfamily E, member 12 pseudogene
216833_x_at_HG-U133A		Human glycophorin HeP2 mRNA, partial cds	Consensus includes gb:U05255.1 /DEF=Human glycophorin HeP2 mRNA, partial cds. /FEA=mRNA /PROD=glycophorin HeP2 /DB_XREF=gi:454085 /UG=Hs.307185 Human glycophorin HeP2 mRNA, partial cds
216860_s_at_HG-U133A	GDF11	growth differentiation factor 11	Consensus includes gb:AF028333.1 /DEF=Homo sapiens growthdifferentiation factor-11 (GDF11) mRNA, partial cds. /FEA=mRNA /GEN=GDF11 /PROD=growthdifferentiation factor-11 /DB_XREF=gi:6649913 /UG=Hs.34941 growth differentiation factor 11
217047_s_at_HG-U133A			Consensus includes gb:AK027138.1 /DEF=Homo sapiens cDNA: FLJ23485 fis, clone KAIA05211. /FEA=mRNA /DB_XREF=gi:10440190 /UG=Hs.177664 KIAA0914 gene product
217080_s_at_HG-	HOMER-2B	Homer, neuronal immediate early gene,	Consensus includes gb:Y19026.1 /DEF=Homo sapiens mRNA for Homer-2

U133A		2	protein, Homer-2B splicing form. /FEA=mRNA /GEN=Homer-2 /PROD=Homer-2 protein, Homer-2B splicing form /DB_XREF=gi:6996435 /UG=Hs.93564 Homer, neuronal immediate early gene, 2
217156_at_HG-U133A			Consensus includes gb:U04628 /DEF=Human 78 kDa gastrin binding protein GBP gene, complete cds /FEA=CDS /DB_XREF=gi:606608 /UG=Hs.247943 Human 78 kDa gastrin binding protein GBP gene, complete cds
217179_x_at_HG-U133A			Consensus includes gb:X79782.1 /DEF=H.sapiens (T1.1) mRNA for IG lambda light chain. /FEA=mRNA /PROD=immunoglobulin lambda light chain /DB_XREF=gi:506428 /UG=Hs.247949 H.sapiens (T1.1) mRNA for IG lambda light chain
217185_s_at_HG-U133A			Consensus includes gb:Z95118 /DEF=Human DNA sequence from clone 354J5 on chromosome 6q21-22. Contains pseudogene similar to zinc finger protein (ZPR1), EST, STS, GSS /FEA=CDS /DB_XREF=gi:3821018 /UG=Hs.211509 zinc finger protein 259, pseudogene
217223_s_at_HG-U133A			Consensus includes gb:U07000 /DEF=Human breakpoint cluster region (BCR) gene, complete cds /FEA=CDS_4 /DB_XREF=gi:487344 /UG=Hs.234799 breakpoint cluster region
217225_x_at_HG-U133A	PM5	pM5 protein	Consensus includes gb:AL512687.1 /DEF=Homo sapiens mRNA; cDNA DKFZp547A1913 (from clone DKFZp547A1913). /FEA=mRNA /GEN=DKFZp547A1913 /PROD=hypothetical protein /DB_XREF=gi:12224839 /UG=Hs.227823 pM5 protein
217375_at_HG-U133A			Consensus includes gb:Z93929 /DEF=Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism /FEA=CDS /DB_XREF=gi:3425887 /UG=Hs.247809 Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism

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217383_at_HG-U133A			Consensus includes gb:S81916.1 /DEF=phosphoglycerate kinase {alternatively spliced} human, phosphoglycerate kinase deficient patient with episodes of muscl, mRNA Partial Mutant, 307 nt. /FEA=mRNA /PROD=phosphoglycerate kinase /DB_XREF=gi:1470308 /UG=Hs.169313 Phosphoglycerate kinase {alternatively spliced} human, phosphoglycerate kinase deficient patient with episodes of muscl, mRNA Partial Mutant, 307 nt
217398_x_at_HG-U133A			Consensus includes gb:AK026525.1 /DEF=Homo sapiens cDNA: FLJ22872 fis, clone KAT02551, highly similar to HUMGAPDH Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA. /FEA=mRNA /DB_XREF=gi:10439402 /UG=Hs.169476 glyceraldehyde-3-phosphate dehydrogenase
217418_x_at_HG-U133A	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	Consensus includes gb:X12530.1 /DEF=Human mRNA for B lymphocyte antigen CD20 (B1, Bp35). /FEA=mRNA /DB_XREF=gi:29773 /UG=Hs.89751 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)
217419_x_at_HG-U133A			Consensus includes gb:AK021586.1 /DEF=Homo sapiens cDNA FLJ11524 fis, clone HEMBA1002547, highly similar to Homo sapiens agrin precursor mRNA. /FEA=mRNA /DB_XREF=gi:10432794 /UG=Hs.273330 Homo sapiens, clone IMAGE:3506210, mRNA, partial cds
217478_s_at_HG-U133A			Consensus includes gb:X76775 /DEF=H.sapiens HLA-DMA gene /FEA=mRNA_1 /DB_XREF=gi:512468 /UG=Hs.77522 major histocompatibility complex, class II, DM alpha
217504_at_HG-U133A	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	Consensus includes gb:AA099357 /FEA=EST /DB_XREF=gi:1645257 /DB_XREF=est:zk85c01.s1 /CLONE=IMAGE:489600 /UG=Hs.15780 ATP-binding cassette, sub-family A (ABC1), member 6
217520_x_at_HG-U133A		ESTs, Moderately similar to HERC2 [H.sapiens]	Consensus includes gb:BG396614 /FEA=EST /DB_XREF=gi:13290062 /DB_XREF=est:602459468F1 /CLONE=IMAGE:4581928 /UG=Hs.154999 ESTs, Moderately similar to HERC2 H.sapiens

217521_at_HG-U133A		ESTs	Consensus includes gb:N54942 /FEA=EST /DB_XREF=gi:1196262 /DB_XREF=est:yv38b08.s1 /CLONE=IMAGE:244983 /UG=Hs.276590 ESTs
217559_at_HG-U133A	RPL10L	ribosomal protein L10-like	Consensus includes gb:AI001784 /FEA=EST /DB_XREF=gi:3202255 /DB_XREF=est:ot41g06.s1 /CLONE=IMAGE:1619386 /UG=Hs.308332 ESTs, Highly similar to A42735 ribosomal protein L10, cytosolic H.sapiens
217716_s_at_HG-U133A	SEC61A1	protein transport protein SEC61 alpha subunit isoform 1	gb:NM_013336.1 /DEF=Homo sapiens sec61 homolog (HSEC61), mRNA. /FEA=mRNA /GEN=HSEC61 /PROD=sec61 homolog /DB_XREF=gi:7019414 /UG=Hs.306079 sec61 homolog /FL=gb:BC002951.1 gb:AF346602.1 gb:AF084458.1 gb:NM_013336.1
217768_at_HG-U133A	LOC51637	CGI-99 protein	gb:NM_016039.1 /DEF=Homo sapiens CGI-99 protein (LOC51637), mRNA. /FEA=mRNA /GEN=LOC51637 /PROD=CGI-99 protein /DB_XREF=gi:7706321 /UG=Hs.110803 CGI-99 protein /FL=gb:BC001722.1 gb:AF151857.1 gb:AF100755.1 gb:NM_016039.1
217816_s_at_HG-U133A	pcnp	PEST-containing nuclear protein	gb:NM_020357.1 /DEF=Homo sapiens PEST-containing nuclear protein (pcnp), mRNA. /FEA=mRNA /GEN=pcnp /PROD=PEST-containing nuclear protein /DB_XREF=gi:9966826 /UG=Hs.283728 PEST-containing nuclear protein /FL=gb:AB037675.1 gb:NM_020357.1
217838_s_at_HG-U133A	RNB6	RNB6	gb:NM_016337.1 /DEF=Homo sapiens RNB6 (RNB6), mRNA. /FEA=mRNA /GEN=RNB6 /PROD=RNB6 /DB_XREF=gi:7706686 /UG=Hs.241471 RNB6 /FL=gb:AF052504.1 gb:NM_016337.1
217916_s_at_HG-U133A	BM-009	hypothetical protein BM-009	gb:NM_016623.1 /DEF=Homo sapiens hypothetical protein (BM-009), mRNA. /FEA=mRNA /GEN=BM-009 /PROD=hypothetical protein /DB_XREF=gi:7705303 /UG=Hs.92918 hypothetical protein /FL=gb:BC003599.1 gb:AF208851.1 gb:NM_016623.1
217920_at_HG-U133A		Homo sapiens, clone MGC:27474 IMAGE:4714032, mRNA, complete cds	Consensus includes gb:H97940 /FEA=EST /DB_XREF=gi:1118825 /DB_XREF=est:yx04d03.s1 /CLONE=IMAGE:260741 /UG=Hs.239114 mannosidase, alpha, class 1A, member 2 /FL=gb:AF027156.1 gb:NM_006699.1

217950_at_HG-U133A	NOSIP	eNOS interacting protein	gb:NM_015953.1 /DEF=Homo sapiens CGI-25 protein (LOC51070), mRNA. /FEA=mRNA /GEN=LOC51070 /PROD=CGI-25 protein /DB_XREF=gi:7705715 /UG=Hs.7236 CGI-25 protein /FL=gb:AF132959.1 gb:NM_015953.1
217963_s_at_HG-U133A	HCS	cytochrome c	gb:NM_014380.1 /DEF=Homo sapiens p75NTR-associated cell death executor; ovarian granulosa cell protein (13kD) (DXS6984E), mRNA. /FEA=mRNA /GEN=DXS6984E /PROD=p75NTR-associated cell death executor; ovariangranulosa cell protein (13kD) /DB_XREF=gi:7657043 /UG=Hs.17775 p75NTR-associated cell death executor; ovarian granulosa cell protein (13kD) /FL=gb:NM_014380.1 gb:AF187064.1
217966_s_at_HG-U133A	C1orf24	chromosome 1 open reading frame 24	gb:NM_022083.1 /DEF=Homo sapiens niban protein (NIBAN), mRNA. /FEA=mRNA /GEN=NIBAN /PROD=niban protein /DB_XREF=gi:11545796 /UG=Hs.48778 niban protein /FL=gb:AB050477.1 gb:NM_022083.1 gb:AF288391.1
217979_at_HG-U133A	NET-6	tetraspan NET-6 protein	gb:NM_014399.1 /DEF=Homo sapiens tetraspan NET-6 protein (NET-6), mRNA. /FEA=mRNA /GEN=NET-6 /PROD=tetraspan NET-6 protein /DB_XREF=gi:7657372 /UG=Hs.284243 tetraspan NET-6 protein /FL=gb:AF120265.1 gb:AF100759.1 gb:NM_014399.1
217988_at_HG-U133A	HEI10	enhancer of invasion 10	gb:NM_021178.1 /DEF=Homo sapiens enhancer of invasion 10 (HEI10), mRNA. /FEA=mRNA /GEN=HEI10 /PROD=enhancer of invasion 10 /DB_XREF=gi:10863978 /UG=Hs.107003 enhancer of invasion 10 /FL=gb:NM_021178.1 gb:BC000369.1 gb:BC001218.1 gb:BC004435.1 gb:AF216381.1
217989_at_HG-U133A	LOC51170	retinal short-chain dehydrogenase/reductase retSDR2	gb:NM_016245.1 /DEF=Homo sapiens retinal short-chain dehydrogenasereductase retSDR2 (LOC51170), mRNA. /FEA=mRNA /GEN=LOC51170 /PROD=retinal short-chain dehydrogenasereductaseretSDR2 /DB_XREF=gi:7705904 /UG=Hs.12150 retinal short-chain dehydrogenasereductase retSDR2 /FL=gb:AF126780.1 gb:NM_016245.1
217994_x_at_HG-			gb:NM_017871.1 /DEF=Homo sapiens hypothetical protein FLJ20542

U133A			(FLJ20542), mRNA. /FEA=mRNA /GEN=FLJ20542 /PROD=hypothetical protein FLJ20542 /DB_XREF=gi:8923511 /UG=Hs.6449 hypothetical protein FLJ20542 /FL=gb:AL136813.1 gb:NM_017871.1
218039_at_HG-U133A	ANKT	nucleolar protein ANKT	gb:NM_016359.1 /DEF=Homo sapiens clone HQ0310 PRO0310p1 (LOC51203), mRNA. /FEA=mRNA /GEN=LOC51203 /PROD=clone HQ0310 PRO0310p1 /DB_XREF=gi:7705950 /UG=Hs.279905 clone HQ0310 PRO0310p1 /FL=gb:AF305711.1 gb:BC001308.1 gb:AF290612.1 gb:AF090915.1 gb:NM_016359.1
218041_x_at_HG-U133A	PRO1068	hypothetical protein PRO1068	gb:NM_018573.1 /DEF=Homo sapiens hypothetical protein PRO1068 (PRO1068), mRNA. /FEA=mRNA /GEN=PRO1068 /PROD=hypothetical protein PRO1068 /DB_XREF=gi:8924006 /UG=Hs.321158 hypothetical protein PRO1068 /FL=gb:AF116620.1 gb:NM_018573.1
218051_s_at_HG-U133A	FLJ12442	hypothetical protein FLJ12442	gb:NM_022908.1 /DEF=Homo sapiens hypothetical protein FLJ12442 (FLJ12442), mRNA. /FEA=mRNA /GEN=FLJ12442 /PROD=hypothetical protein FLJ12442 /DB_XREF=gi:12597652 /UG=Hs.84753 hypothetical protein FLJ12442 /FL=gb:NM_022908.1
218089_at_HG-U133A	C20orf4	chromosome 20 open reading frame 4	gb:NM_015511.1 /DEF=Homo sapiens DKFZP564N1363 protein (DKFZP564N1363), mRNA. /FEA=mRNA /GEN=DKFZP564N1363 /PROD=DKFZP564N1363 protein /DB_XREF=gi:7661627 /UG=Hs.11314 DKFZP564N1363 protein /FL=gb:BC001751.1 gb:AF132957.1 gb:AL117419.1 gb:AF113672.1 gb:NM_015511.1
218090_s_at_HG-U133A			gb:NM_018117.8 /DEF=Homo sapiens WD40 repeat domain 11 protein (WDR11), mRNA. /FEA=mRNA /GEN=WDR11 /PROD=WD40 repeat domain 11 protein /DB_XREF=gi:13324687 /UG=Hs.16677 WD repeat domain 15 /FL=gb:AF320223.1 gb:NM_018117.8
218094_s_at_HG-U133A	C20orf35	chromosome 20 open reading frame 35	gb:NM_018478.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HSMNP1 (HSMNP1), mRNA. /FEA=mRNA /GEN=HSMNP1 /PROD=uncharacterized hypothalamus protein HSMNP1

			/DB_XREF=gi:8923782 /UG=Hs.179666 uncharacterized hypothalamus protein HSMNP1 /FL=gb:BC001105.1 gb:AF220191.1 gb:NM_018478.1
218100_s_at_HG-U133A	ESRRBL1	estrogen-related receptor beta like 1	gb:NM_018010.1 /DEF=Homo sapiens hypothetical protein FLJ10147 (FLJ10147), mRNA. /FEA=mRNA /GEN=FLJ10147 /PROD=hypothetical protein FLJ10147 /DB_XREF=gi:8922255 /UG=Hs.170318 hypothetical protein FLJ10147 /FL=gb:AF139576.1 gb:AF245220.1 gb:NM_018010.1
218109_s_at_HG-U133A	FLJ14153	hypothetical protein FLJ14153	gb:NM_022736.1 /DEF=Homo sapiens hypothetical protein FLJ14153 (FLJ14153), mRNA. /FEA=mRNA /GEN=FLJ14153 /PROD=hypothetical protein FLJ14153 /DB_XREF=gi:12232392 /UG=Hs.7503 hypothetical protein FLJ14153 /FL=gb:NM_022736.1 gb:AB014732.1
218122_s_at_HG-U133A	SENP2	sentrin-specific protease	gb:NM_021627.1 /DEF=Homo sapiens sentrin-specific protease (SENP2), mRNA. /FEA=mRNA /GEN=SENP2 /PROD=sentrin-specific protease /DB_XREF=gi:11055993 /UG=Hs.3355 sentrin-specific protease /FL=gb:AF151697.2 gb:NM_021627.1
218144_s_at_HG-U133A	FLJ22056	hypothetical protein FLJ22056	gb:NM_022489.1 /DEF=Homo sapiens hypothetical protein FLJ22056 (FLJ22056), mRNA. /FEA=mRNA /GEN=FLJ22056 /PROD=hypothetical protein FLJ22056 /DB_XREF=gi:11968044 /UG=Hs.24956 hypothetical protein FLJ22056 /FL=gb:NM_022489.1
218151_x_at_HG-U133A	FLJ11856	hypothetical protein FLJ11856	gb:NM_024531.1 /DEF=Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA. /FEA=mRNA /GEN=FLJ11856 /PROD=hypothetical protein FLJ11856 /DB_XREF=gi:13375681 /UG=Hs.6459 hypothetical protein FLJ11856 /FL=gb:BC002917.1 gb:NM_024531.1
218168_s_at_HG-U133A	CABC1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	gb:NM_020247.1 /DEF=Homo sapiens hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142 (LOC56997), mRNA. /FEA=mRNA /GEN=LOC56997 /PROD=hypothetical protein, cloneTelethon(Italy_B41)_Strait02270_FL142 /DB_XREF=gi:9910387 /UG=Hs.273186 hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142 /FL=gb:BC005171.1 gb:NM_020247.1

218172_s_at_HG-U133A	PRO2577	hypothetical protein PRO2577	gb:NM_018630.1 /DEF=Homo sapiens hypothetical protein PRO2577 (PRO2577), mRNA. /FEA=mRNA /GEN=PRO2577 /PROD=hypothetical protein PRO2577 /DB_XREF=gi:8924181 /UG=Hs.241576 hypothetical protein PRO2577 /FL=gb:AF116708.1 gb:NM_018630.1
218191_s_at_HG-U133A	FLJ11240	hypothetical protein FLJ11240	gb:NM_018368.1 /DEF=Homo sapiens hypothetical protein FLJ11240 (FLJ11240), mRNA. /FEA=mRNA /GEN=FLJ11240 /PROD=hypothetical protein FLJ11240 /DB_XREF=gi:8922955 /UG=Hs.301308 hypothetical protein FLJ11240 /FL=gb:AF113224.1 gb:AF211480.1 gb:NM_018368.1
218223_s_at_HG-U133A	LOC51177	CK2 interacting protein 1; HQ0024c protein	gb:NM_016274.1 /DEF=Homo sapiens CK2 interacting protein 1; HQ0024c protein (LOC51177), mRNA. /FEA=mRNA /GEN=LOC51177 /PROD=CK2 interacting protein 1; HQ0024c protein /DB_XREF=gi:7705918 /UG=Hs.173380 CK2 interacting protein 1; HQ0024c protein /FL=gb:AF291105.1 gb:AF073836.1 gb:NM_016274.1 gb:AF168676.1
218224_at_HG-U133A	PNMA1	paraneoplastic antigen MA1	gb:NM_006029.2 /DEF=Homo sapiens paraneoplastic antigen MA1 (PNMA1), mRNA. /FEA=mRNA /GEN=PNMA1 /PROD=paraneoplastic antigen MA1 /DB_XREF=gi:11141858 /UG=Hs.194709 paraneoplastic antigen MA1 /FL=gb:AF037364.2 gb:NM_006029.2
218237_s_at_HG-U133A	SLC38A1	solute carrier family 38, member 1	gb:NM_030674.1 /DEF=Homo sapiens amino acid transporter system A1 (ATA1), mRNA. /FEA=mRNA /GEN=ATA1 /PROD=amino acid transporter system A1 /DB_XREF=gi:13492978 /UG=Hs.18272 amino acid transporter system A1 /FL=gb:AF271070.1 gb:NM_030674.1
218259_at_HG-U133A	KIAA1243	KIAA1243 protein	gb:NM_014048.1 /DEF=Homo sapiens KIAA1243 protein (KIAA1243), mRNA. /FEA=mRNA /GEN=KIAA1243 /PROD=NPD001 protein /DB_XREF=gi:7662513 /UG=Hs.151076 KIAA1243 protein /FL=gb:AF078853.1 gb:NM_014048.1
218319_at_HG-U133A	PELI1	pellino homolog 1 (Drosophila)	gb:NM_020651.2 /DEF=Homo sapiens pellino (Drosophila) homolog 1 (PELI1), mRNA. /FEA=mRNA /GEN=PELI1 /PROD=pellino protein /DB_XREF=gi:11037062 /UG=Hs.7886 pellino (Drosophila) homolog 1 /FL=gb:AF302505.1 gb:AF300987.1 gb:NM_020651.2

218329_at_HG-U133A	PRDM4	PR domain containing 4	gb:NM_012406.2 /DEF=Homo sapiens PR domain containing 4 (PRDM4), mRNA. /FEA=mRNA /GEN=PRDM4 /PROD=PR domain containing 4 /DB_XREF=gi:9055315 /UG=Hs.21807 PR domain containing 4 /FL=gb:AF144757.2 gb:NM_012406.2
218331_s_at_HG-U133A	FLJ20360	hypothetical protein FLJ20360	gb:NM_017782.1 /DEF=Homo sapiens hypothetical protein FLJ20360 (FLJ20360), mRNA. /FEA=mRNA /GEN=FLJ20360 /PROD=hypothetical protein FLJ20360 /DB_XREF=gi:8923334 /UG=Hs.26434 hypothetical protein FLJ20360 /FL=gb:BC001759.1 gb:NM_017782.1
218338_at_HG-U133A	EDR1	early development regulator 1 (polyhomeotic 1 homolog)	gb:NM_004426.1 /DEF=Homo sapiens early development regulator 1 (homolog of polyhomeotic 1) (EDR1), mRNA. /FEA=mRNA /GEN=EDR1 /PROD=early development regulator 1 /DB_XREF=gi:11038623 /UG=Hs.305985 early development regulator 1 (homolog of polyhomeotic 1) /FL=gb:NM_004426.1
218341_at_HG-U133A	FLJ11838	hypothetical protein FLJ11838	gb:NM_024664.1 /DEF=Homo sapiens hypothetical protein FLJ11838 (FLJ11838), mRNA. /FEA=mRNA /GEN=FLJ11838 /PROD=hypothetical protein FLJ11838 /DB_XREF=gi:13375918 /UG=Hs.72531 hypothetical protein FLJ11838 /FL=gb:NM_024664.1
218351_at_HG-U133A	FLJ20502	hypothetical protein FLJ20502	gb:NM_017845.1 /DEF=Homo sapiens hypothetical protein FLJ20502 (FLJ20502), mRNA. /FEA=mRNA /GEN=FLJ20502 /PROD=hypothetical protein FLJ20502 /DB_XREF=gi:8923457 /UG=Hs.23956 hypothetical protein FLJ20502 /FL=gb:AF182421.1 gb:NM_017845.1
218354_at_HG-U133A	LOC51693	unknown	gb:NM_016209.1 /DEF=Homo sapiens unknown (LOC51693), mRNA. /FEA=mRNA /GEN=LOC51693 /PROD=unknown /DB_XREF=gi:7706428 /UG=Hs.27445 unknown /FL=gb:AF089106.1 gb:AF161524.1 gb:NM_016209.1
218355_at_HG-U133A	KIF4A	kinesin family member 4A	gb:NM_012310.2 /DEF=Homo sapiens kinesin family member 4A (KIF4A), mRNA. /FEA=mRNA /GEN=KIF4A /PROD=kinesin family member 4 /DB_XREF=gi:7305204 /UG=Hs.279766 kinesin family member 4A /FL=gb:AF179308.1 gb:AF071592.2 gb:NM_012310.2

218379_at_HG-U133A	RBM7	RNA binding motif protein 7	gb:NM_016090.1 /DEF=Homo sapiens RNA binding motif protein 7 (RBM7), mRNA. /FEA=mRNA /GEN=RBM7 /PROD=RNA binding motif protein 7 /DB_XREF=gi:9994184 /UG=Hs.5887 RNA binding motif protein 7 /FL=gb:AF156098.1 gb:NM_016090.1
218384_at_HG-U133A	CRHSP-24	calcium-regulated heat-stable protein (24kD)	gb:NM_014316.1 /DEF=Homo sapiens calcium-regulated heat-stable protein (24kD) (CRHSP-24), mRNA. /FEA=mRNA /GEN=CRHSP-24 /PROD=calcium-regulated heat-stable protein (24kD) /DB_XREF=gi:7656994 /UG=Hs.92198 calcium-regulated heat-stable protein (24kD) /FL=gb:BC001333.1 gb:BC003366.1 gb:AF115345.1 gb:NM_014316.1
218424_s_at_HG-U133A	FLJ10829	dudulin 2	gb:NM_018234.1 /DEF=Homo sapiens hypothetical protein FLJ10829 (FLJ10829), mRNA. /FEA=mRNA /GEN=FLJ10829 /PROD=hypothetical protein FLJ10829 /DB_XREF=gi:8922696 /UG=Hs.57655 hypothetical protein FLJ10829 /FL=gb:NM_018234.1
218464_s_at_HG-U133A	FLJ10700	hypothetical protein FLJ10700	gb:NM_018182.1 /DEF=Homo sapiens hypothetical protein FLJ10700 (FLJ10700), mRNA. /FEA=mRNA /GEN=FLJ10700 /PROD=hypothetical protein FLJ10700 /DB_XREF=gi:8922595 /UG=Hs.295909 hypothetical protein FLJ10700 /FL=gb:NM_018182.1
218468_s_at_HG-U133A	CKTSF1B1	cysteine knot superfamily 1, BMP antagonist 1	gb:AF154054.1 /DEF=Homo sapiens DRM (DRM) mRNA, complete cds. /FEA=mRNA /GEN=DRM /PROD=DRM /DB_XREF=gi:10863087 /UG=Hs.40098 cysteine knot superfamily 1, BMP antagonist 1 /FL=gb:AF154054.1 gb:AF045800.1 gb:AF110137.2 gb:NM_013372.1
218469_at_HG-U133A	CKTSF1B1	cysteine knot superfamily 1, BMP antagonist 1	gb:NM_013372.1 /DEF=Homo sapiens cysteine knot superfamily 1, BMP antagonist 1 (CKTSF1B1), mRNA. /FEA=mRNA /GEN=CKTSF1B1 /PROD=cysteine knot superfamily 1, BMP antagonist 1 /DB_XREF=gi:7019348 /UG=Hs.40098 cysteine knot superfamily 1, BMP antagonist 1 /FL=gb:AF154054.1 gb:AF045800.1 gb:AF110137.2 gb:NM_013372.1
218482_at_HG-U133A	DC6	DC6 protein	gb:NM_020189.1 /DEF=Homo sapiens DC6 protein (DC6), mRNA.

			/FEA=mRNA /GEN=DC6 /PROD=DC6 protein /DB_XREF=gi:9910185 /UG=Hs.283740 DC6 protein /FL=gb:AF201940.1 gb:AF173296.1 gb:NM_020189.1
218499_at_HG-U133A	MST4	Mst3 and SOK1-related kinase	gb:NM_016542.1 /DEF=Homo sapiens serinethreonine protein kinase MASK (LOC51765), mRNA. /FEA=mRNA /GEN=LOC51765 /PROD=serinethreonine protein kinase MASK /DB_XREF=gi:7706568 /UG=Hs.23643 serinethreonine protein kinase MASK /FL=gb:AB040057.1 gb:NM_016542.1
218516_s_at_HG-U133A	FLJ20421	hypothetical protein FLJ20421	gb:NM_017813.1 /DEF=Homo sapiens hypothetical protein FLJ20421 (FLJ20421), mRNA. /FEA=mRNA /GEN=FLJ20421 /PROD=hypothetical protein FLJ20421 /DB_XREF=gi:8923391 /UG=Hs.263727 hypothetical protein FLJ20421 /FL=gb:NM_017813.1
218517_at_HG-U133A	FLJ22479	hypothetical protein FLJ22479	gb:NM_024900.1 /DEF=Homo sapiens hypothetical protein FLJ22479 (FLJ22479), mRNA. /FEA=mRNA /GEN=FLJ22479 /PROD=hypothetical protein FLJ22479 /DB_XREF=gi:13376356 /UG=Hs.238246 hypothetical protein FLJ22479 /FL=gb:NM_024900.1
218531_at_HG-U133A	FLJ21749	hypothetical protein FLJ21749	gb:NM_025124.1 /DEF=Homo sapiens hypothetical protein FLJ21749 (FLJ21749), mRNA. /FEA=mRNA /GEN=FLJ21749 /PROD=hypothetical protein FLJ21749 /DB_XREF=gi:13376700 /UG=Hs.288761 hypothetical protein FLJ21749 /FL=gb:NM_025124.1
218543_s_at_HG-U133A	FLJ22693	hypothetical protein FLJ22693	gb:NM_022750.1 /DEF=Homo sapiens hypothetical protein FLJ22693 (FLJ22693), mRNA. /FEA=mRNA /GEN=FLJ22693 /PROD=hypothetical protein FLJ22693 /DB_XREF=gi:12232412 /UG=Hs.12646 hypothetical protein FLJ22693 /FL=gb:AL136766.1 gb:NM_022750.1
218549_s_at_HG-U133A	LOC51115	CGI-90 protein	gb:NM_016033.1 /DEF=Homo sapiens CGI-90 protein (LOC51115), mRNA. /FEA=mRNA /GEN=LOC51115 /PROD=CGI-90 protein /DB_XREF=gi:7705802 /UG=Hs.44222 CGI-90 protein /FL=gb:AF151848.1 gb:NM_016033.1
218577_at_HG-U133A	FLJ20331	hypothetical protein FLJ20331	gb:NM_017768.1 /DEF=Homo sapiens hypothetical protein FLJ20331 (FLJ20331), mRNA. /FEA=mRNA /GEN=FLJ20331 /PROD=hypothetical protein

			FLJ20331 /DB_XREF=gi:8923306 /UG=Hs.50848 hypothetical protein FLJ20331 /FL=gb:BC003407.1 gb:NM_017768.1
218582_at_HG-U133A	FLJ20445	hypothetical protein FLJ20445	gb:NM_017824.1 /DEF=Homo sapiens hypothetical protein FLJ20445 (FLJ20445), mRNA. /FEA=mRNA /GEN=FLJ20445 /PROD=hypothetical protein FLJ20445 /DB_XREF=gi:8923414 /UG=Hs.10340 hypothetical protein FLJ20445 /FL=gb:NM_017824.1
218589_at_HG-U133A	P2Y5	purinergic receptor (family A group 5)	gb:NM_005767.1 /DEF=Homo sapiens purinergic receptor (family A group 5) (P2Y5), mRNA. /FEA=mRNA /GEN=P2Y5 /PROD=purinergic receptor (family A group 5) /DB_XREF=gi:5031968 /UG=Hs.189999 purinergic receptor (family A group 5) /FL=gb:AF000546.1 gb:NM_005767.1
218614_at_HG-U133A	FLJ10652	hypothetical protein FLJ10652	gb:NM_018169.1 /DEF=Homo sapiens hypothetical protein FLJ10652 (FLJ10652), mRNA. /FEA=mRNA /GEN=FLJ10652 /PROD=hypothetical protein FLJ10652 /DB_XREF=gi:8922572 /UG=Hs.236844 hypothetical protein FLJ10652 /FL=gb:NM_018169.1
218642_s_at_HG-U133A	MGC2217	hypothetical protein MGC2217	gb:NM_024300.1 /DEF=Homo sapiens hypothetical protein MGC2217 (MGC2217), mRNA. /FEA=mRNA /GEN=MGC2217 /PROD=hypothetical protein MGC2217 /DB_XREF=gi:13236525 /UG=Hs.323164 hypothetical protein MGC2217 /FL=gb:BC002546.1 gb:NM_024300.1
218645_at_HG-U133A	ZNF277	zinc finger protein 277	gb:NM_021994.1 /DEF=Homo sapiens zinc finger protein 277 (ZNF277), mRNA. /FEA=mRNA /GEN=ZNF277 /PROD=zinc finger protein 277 /DB_XREF=gi:11496268 /UG=Hs.42636 zinc finger protein 277 /FL=gb:NM_021994.1 gb:AF209198.1
218662_s_at_HG-U133A	HCAP-G	chromosome condensation protein G	gb:NM_022346.1 /DEF=Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /FEA=mRNA /GEN=HCAP-G /PROD=chromosome condensation protein G /DB_XREF=gi:11641252 /UG=Hs.193602 chromosome condensation protein G /FL=gb:AF235023.1 gb:NM_022346.1 gb:AF331796.1 gb:BC000827.1 gb:AB013299.1
218663_at_HG-U133A	HCAP-G	chromosome condensation protein G	gb:NM_022346.1 /DEF=Homo sapiens chromosome condensation protein G

			(HCAP-G), mRNA. /FEA=mRNA /GEN=HCAP-G /PROD=chromosome condensation protein G /DB_XREF=gi:11641252 /UG=Hs.193602 chromosome condensation protein G /FL=gb:AF235023.1 gb:NM_022346.1 gb:AF331796.1 gb:BC000827.1 gb:AB013299.1
218692_at_HG-U133A	FLJ20366	hypothetical protein FLJ20366	gb:NM_017786.1 /DEF=Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA. /FEA=mRNA /GEN=FLJ20366 /PROD=hypothetical protein FLJ20366 /DB_XREF=gi:8923340 /UG=Hs.8358 hypothetical protein FLJ20366 /FL=gb:NM_017786.1
218718_at_HG-U133A	PDGFC	platelet derived growth factor C	gb:NM_016205.1 /DEF=Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /FEA=mRNA /GEN=PDGFC /PROD=secretory growth factor-like protein fallotein /DB_XREF=gi:9994186 /UG=Hs.43080 platelet derived growth factor C /FL=gb:AF091434.1 gb:AF244813.1 gb:AB033831.1 gb:NM_016205.1
218764_at_HG-U133A	MGC5363	hypothetical protein MGC5363	gb:NM_024064.1 /DEF=Homo sapiens hypothetical protein MGC5363 (MGC5363), mRNA. /FEA=mRNA /GEN=MGC5363 /PROD=hypothetical protein MGC5363 /DB_XREF=gi:13129041 /UG=Hs.1880 hypothetical protein MGC5363 /FL=gb:BC001000.2 gb:NM_024064.1
218836_at_HG-U133A	FLJ22638	hypothetical protein FLJ22638	gb:NM_024839.1 /DEF=Homo sapiens hypothetical protein FLJ22638 (FLJ22638), mRNA. /FEA=mRNA /GEN=FLJ22638 /PROD=hypothetical protein FLJ22638 /DB_XREF=gi:13376252 /UG=Hs.183232 hypothetical protein FLJ22638 /FL=gb:NM_024839.1
218913_s_at_HG-U133A	LOC51291	Gem-interacting protein	gb:NM_016573.1 /DEF=Homo sapiens Gem-interacting protein (LOC51291), mRNA. /FEA=mRNA /GEN=LOC51291 /PROD=Gem-interacting protein /DB_XREF=gi:7706106 /UG=Hs.49427 Gem-interacting protein /FL=gb:AF132541.1 gb:NM_016573.1
218916_at_HG-U133A	FLJ23436	hypothetical protein FLJ23436	gb:NM_024671.1 /DEF=Homo sapiens hypothetical protein FLJ23436 (FLJ23436), mRNA. /FEA=mRNA /GEN=FLJ23436 /PROD=hypothetical protein FLJ23436 /DB_XREF=gi:13375931 /UG=Hs.85658 hypothetical protein

			FLJ23436 /FL=gb:NM_024671.1
218933_at_HG-U133A	MGC5347	hypothetical protein MGC5347	gb:NM_024063.1 /DEF=Homo sapiens hypothetical protein MGC5347 (MGC5347), mRNA. /FEA=mRNA /GEN=MGC5347 /PROD=hypothetical protein MGC5347 /DB_XREF=gi:13129039 /UG=Hs.5555 hypothetical protein MGC5347 /FL=gb:BC000981.2 gb:NM_024063.1
218938_at_HG-U133A	MGC11279	hypothetical protein MGC11279	gb:NM_024326.1 /DEF=Homo sapiens hypothetical protein MGC11279 (MGC11279), mRNA. /FEA=mRNA /GEN=MGC11279 /PROD=hypothetical protein MGC11279 /DB_XREF=gi:13236572 /UG=Hs.10915 hypothetical protein MGC11279 /FL=gb:BC002912.1 gb:NM_024326.1
218942_at_HG-U133A	FLJ22055	hypothetical protein FLJ22055	gb:NM_024779.1 /DEF=Homo sapiens hypothetical protein FLJ22055 (FLJ22055), mRNA. /FEA=mRNA /GEN=FLJ22055 /PROD=hypothetical protein FLJ22055 /DB_XREF=gi:13376135 /UG=Hs.144502 hypothetical protein FLJ22055 /FL=gb:NM_024779.1
218974_at_HG-U133A	FLJ10159	hypothetical protein FLJ10159	gb:NM_018013.1 /DEF=Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /FEA=mRNA /GEN=FLJ10159 /PROD=hypothetical protein FLJ10159 /DB_XREF=gi:8922262 /UG=Hs.22505 hypothetical protein FLJ10159 /FL=gb:NM_018013.1
219013_at_HG-U133A	FLJ21634	hypothetical protein FLJ21634	gb:NM_022087.1 /DEF=Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA. /FEA=mRNA /GEN=FLJ21634 /PROD=hypothetical protein FLJ21634 /DB_XREF=gi:11545800 /UG=Hs.97056 hypothetical protein FLJ21634 /FL=gb:NM_022087.1
219027_s_at_HG-U133A	MYO9A	myosin IXA	gb:NM_006901.1 /DEF=Homo sapiens myosin IXA (MYO9A), mRNA. /FEA=mRNA /GEN=MYO9A /PROD=myosin IXA /DB_XREF=gi:5902011 /UG=Hs.23395 myosin IXA /FL=gb:AF117888.1 gb:NM_006901.1
219029_at_HG-U133A	FLJ21657	hypothetical protein FLJ21657	gb:NM_022483.1 /DEF=Homo sapiens hypothetical protein FLJ21657 (FLJ21657), mRNA. /FEA=mRNA /GEN=FLJ21657 /PROD=hypothetical protein FLJ21657 /DB_XREF=gi:11968034 /UG=Hs.26498 hypothetical protein FLJ21657 /FL=gb:NM_022483.1

219033_at_HG-U133A	FLJ21308	hypothetical protein FLJ21308	gb:NM_024615.1 /DEF=Homo sapiens hypothetical protein FLJ21308 (FLJ21308), mRNA. /FEA=mRNA /GEN=FLJ21308 /PROD=hypothetical protein FLJ21308 /DB_XREF=gi:13375831 /UG=Hs.29977 hypothetical protein FLJ21308 /FL=gb:NM_024615.1
219036_at_HG-U133A	BITE	p10-binding protein	gb:NM_024491.1 /DEF=Homo sapiens p10-binding protein (BITE), mRNA. /FEA=mRNA /GEN=BITE /PROD=p10-binding protein /DB_XREF=gi:13346499 /UG=Hs.42315 p10-binding protein /FL=gb:AF202146.1 gb:NM_024491.1
219073_s_at_HG-U133A	OSBPL10	oxysterol binding protein-like 10	gb:NM_017784.1 /DEF=Homo sapiens hypothetical protein FLJ20363 (FLJ20363), mRNA. /FEA=mRNA /GEN=FLJ20363 /PROD=hypothetical protein FLJ20363 /DB_XREF=gi:8923336 /UG=Hs.321622 hypothetical protein FLJ20363 /FL=gb:BC003168.1 gb:NM_017784.1
219076_s_at_HG-U133A	PXMP2	peroxisomal membrane protein 2 (22kD)	gb:NM_018663.1 /DEF=Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA. /FEA=mRNA /GEN=LOC55895 /PROD=22kDa peroxisomal membrane protein-like /DB_XREF=gi:8923891 /UG=Hs.49912 22kDa peroxisomal membrane protein-like /FL=gb:AF250136.1 gb:NM_018663.1
219079_at_HG-U133A	b5&b5R	flavohemoprotein b5+b5R	gb:NM_016230.1 /DEF=Homo sapiens flavohemoprotein b5+b5R (LOC51167), mRNA. /FEA=mRNA /GEN=LOC51167 /PROD=flavohemoprotein b5+b5R /DB_XREF=gi:7705898 /UG=Hs.5741 flavohemoprotein b5+b5R /FL=gb:AF169803.1 gb:NM_016230.1
219084_at_HG-U133A	NSD1	nuclear receptor binding SET domain protein 1	gb:NM_022455.1 /DEF=Homo sapiens hypothetical protein FLJ22263 similar to nuclear receptor-binding SET-domain protein 1 (FLJ22263), mRNA. /FEA=mRNA /GEN=FLJ22263 /PROD=hypothetical protein FLJ22263 similar to nuclearreceptor-binding SET-domain protein 1 /DB_XREF=gi:11967992 /UG=Hs.99010 hypothetical protein FLJ22263 similar to nuclear receptor-binding SET-domain protein 1 /FL=gb:NM_022455.1
219090_at_HG-U133A	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger),	gb:NM_020689.2 /DEF=Homo sapiens sodium calcium exchanger (NCKX3), mRNA. /FEA=mRNA /GEN=NCKX3 /PROD=sodium calcium exchanger

		member 3	/DB_XREF=gi:10518346 /UG=Hs.12321 sodium calcium exchanger /FL=gb:AF169257.2 gb:NM_020689.2
219099_at_HG-U133A	C12orf5	chromosome 12 open reading frame 5	gb:NM_020375.1 /DEF=Homo sapiens chromosome 12 open reading frame 5 (C12ORF5), mRNA. /FEA=mRNA /GEN=C12ORF5 /PROD=chromosome 12 open reading frame 5 /DB_XREF=gi:9966848 /UG=Hs.24792 chromosome 12 open reading frame 5 /FL=gb:NM_020375.1
219111_s_at_HG-U133A	MGC2835	ATP-dependent RNA helicase	gb:NM_024072.1 /DEF=Homo sapiens hypothetical protein MGC2835 (MGC2835), mRNA. /FEA=mRNA /GEN=MGC2835 /PROD=hypothetical protein MGC2835 /DB_XREF=gi:13129055 /UG=Hs.70582 hypothetical protein MGC2835 /FL=gb:BC001132.1 gb:BC001848.1 gb:NM_024072.1
219138_at_HG-U133A	RPL14	ribosomal protein L14	Consensus includes gb:BC000606.1 /DEF=Homo sapiens, Similar to ribosomal protein L14, clone MGC:1644, mRNA, complete cds. /FEA=mRNA /PROD=Similar to ribosomal protein L14 /DB_XREF=gi:12653648 /UG=Hs.738 ribosomal protein L14 /FL=gb:BC000606.1 gb:D87735.1 gb:NM_003973.1
219156_at_HG-U133A	FLJ11271	hypothetical protein FLJ11271	gb:NM_018373.1 /DEF=Homo sapiens hypothetical protein FLJ11271 (FLJ11271), mRNA. /FEA=mRNA /GEN=FLJ11271 /PROD=hypothetical protein FLJ11271 /DB_XREF=gi:8922963 /UG=Hs.109654 hypothetical protein FLJ11271 /FL=gb:NM_018373.1
219202_at_HG-U133A	FLJ22341	hypothetical protein FLJ22341	gb:NM_024599.1 /DEF=Homo sapiens hypothetical protein FLJ22341 (FLJ22341), mRNA. /FEA=mRNA /GEN=FLJ22341 /PROD=hypothetical protein FLJ22341 /DB_XREF=gi:13375798 /UG=Hs.25485 hypothetical protein FLJ22341 /FL=gb:NM_024599.1
219221_at_HG-U133A	FLJ22332	hypothetical protein FLJ22332	gb:NM_024724.1 /DEF=Homo sapiens hypothetical protein FLJ22332 (FLJ22332), mRNA. /FEA=mRNA /GEN=FLJ22332 /PROD=hypothetical protein FLJ22332 /DB_XREF=gi:13376033 /UG=Hs.111092 hypothetical protein FLJ22332 /FL=gb:NM_024724.1
219229_at_HG-U133A	SLC21A11	solute carrier family 21 (organic anion transporter), member 11	gb:NM_013272.2 /DEF=Homo sapiens solute carrier family 21 (organic anion transporter), member 11 (SLC21A11), mRNA. /FEA=mRNA /GEN=SLC21A11

			/PROD=solute carrier family 21 (organic aniontransporter), member 11 /DB_XREF=gi:7706713 /UG=Hs.14805 solute carrier family 21 (organic anion transporter), member 11 /FL=gb:AF205074.1 gb:AF187816.1 gb:AB031050.2 gb:NM_013272.2
219234_x_at_HG-U133A	FLJ23142	hypothetical protein FLJ23142	gb:NM_024583.1 /DEF=Homo sapiens hypothetical protein FLJ23142 (FLJ23142), mRNA. /FEA=mRNA /GEN=FLJ23142 /PROD=hypothetical protein FLJ23142 /DB_XREF=gi:13375765 /UG=Hs.20999 hypothetical protein FLJ23142 /FL=gb:NM_024583.1
219271_at_HG-U133A	FLJ12691	hypothetical protein FLJ12691	gb:NM_024572.1 /DEF=Homo sapiens hypothetical protein FLJ12691 (FLJ12691), mRNA. /FEA=mRNA /GEN=FLJ12691 /PROD=hypothetical protein FLJ12691 /DB_XREF=gi:13375743 /UG=Hs.15830 hypothetical protein FLJ12691 /FL=gb:NM_024572.1
219280_at_HG-U133A	WDR9	WD repeat domain 9	gb:NM_018963.1 /DEF=Homo sapiens WD repeat domain 9 (WDR9), mRNA. /FEA=mRNA /GEN=WDR9 /PROD=WD repeat domain 9 /DB_XREF=gi:11321643 /UG=Hs.225674 WD repeat domain 9 /FL=gb:NM_018963.1
219291_at_HG-U133A	MDS009	x 009 protein	gb:NM_020234.1 /DEF=Homo sapiens x 009 protein (MDS009), mRNA. /FEA=mRNA /GEN=MDS009 /PROD=x 009 protein /DB_XREF=gi:9910425 /UG=Hs.64641 x 009 protein /FL=gb:AF168717.1 gb:NM_020234.1
219312_s_at_HG-U133A	RINZF	zinc finger protein RINZF	gb:NM_023929.1 /DEF=Homo sapiens hypothetical protein FLJ12752 (FLJ12752), mRNA. /FEA=mRNA /GEN=FLJ12752 /PROD=hypothetical protein FLJ12752 /DB_XREF=gi:12965200 /UG=Hs.237146 hypothetical protein FLJ12752 /FL=gb:NM_023929.1
219329_s_at_HG-U133A	3-Apr	apoptosis related protein APR-3	gb:NM_016085.1 /DEF=Homo sapiens apoptosis related protein APR-3 (APR-3), mRNA. /FEA=mRNA /GEN=APR-3 /PROD=apoptosis related protein APR-3 /DB_XREF=gi:7706360 /UG=Hs.9527 apoptosis related protein APR-3 /FL=gb:AF144055.2 gb:NM_016085.1
219337_at_HG-U133A	FLJ20584	hypothetical protein FLJ20584	gb:NM_017891.1 /DEF=Homo sapiens hypothetical protein FLJ20584

			(FLJ20584), mRNA. /FEA=mRNA /GEN=FLJ20584 /PROD=hypothetical protein FLJ20584 /DB_XREF=gi:8923546 /UG=Hs.126704 hypothetical protein FLJ20584 /FL=gb:NM_017891.1
219358_s_at_HG-U133A	CENTA2	centaurin, alpha 2	gb:NM_018404.1 /DEF=Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA. /FEA=mRNA /GEN=HSA272195 /PROD=centaurin-alpha 2 protein /DB_XREF=gi:8923762 /UG=Hs.28802 centaurin-alpha 2 protein /FL=gb:NM_018404.1
219360_s_at_HG-U133A	TRPM4	transient receptor potential cation channel, subfamily M, member 4	gb:NM_017636.1 /DEF=Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA. /FEA=mRNA /GEN=FLJ20041 /PROD=hypothetical protein FLJ20041 /DB_XREF=gi:8923048 /UG=Hs.31608 hypothetical protein FLJ20041 /FL=gb:NM_017636.1
219362_at_HG-U133A	FLJ22643	hypothetical protein FLJ22643	gb:NM_024635.1 /DEF=Homo sapiens hypothetical protein FLJ22643 (FLJ22643), mRNA. /FEA=mRNA /GEN=FLJ22643 /PROD=hypothetical protein FLJ22643 /DB_XREF=gi:13375865 /UG=Hs.43579 hypothetical protein FLJ22643 /FL=gb:NM_024635.1
219452_at_HG-U133A	LOC64174	putative dipeptidase	gb:NM_022355.1 /DEF=Homo sapiens putative dipeptidase (LOC64174), mRNA. /FEA=mRNA /GEN=LOC64174 /PROD=putative dipeptidase /DB_XREF=gi:11641268 /UG=Hs.115537 putative dipeptidase /FL=gb:NM_022355.1
219457_s_at_HG-U133A	RIN3	RAB5 interacting protein 3	gb:NM_024832.1 /DEF=Homo sapiens hypothetical protein FLJ22439 (FLJ22439), mRNA. /FEA=mRNA /GEN=FLJ22439 /PROD=hypothetical protein FLJ22439 /DB_XREF=gi:13376237 /UG=Hs.180040 hypothetical protein FLJ22439 /FL=gb:NM_024832.1
219463_at_HG-U133A	C20orf103	chromosome 20 open reading frame 103	gb:NM_012261.1 /DEF=Homo sapiens similar to S68401 (cattle) glucose induced gene (HS1119D91), mRNA. /FEA=mRNA /GEN=HS1119D91 /PROD=similar to S68401 (cattle) glucose induced gene /DB_XREF=gi:7110632 /UG=Hs.22920 similar to S68401 (cattle) glucose induced gene /FL=gb:NM_012261.1

219471_at_HG-U133A	FLJ21562	hypothetical protein FLJ21562	gb:NM_025113.1 /DEF=Homo sapiens hypothetical protein FLJ21562 (FLJ21562), mRNA. /FEA=mRNA /GEN=FLJ21562 /PROD=hypothetical protein FLJ21562 /DB_XREF=gi:13376686 /UG=Hs.288708 hypothetical protein FLJ21562 /FL=gb:NM_025113.1
219477_s_at_HG-U133A	LOC55901	TMTSP for transmembrane molecule with thrombospondin module	gb:NM_018676.1 /DEF=Homo sapiens TMTSP for transmembrane molecule with thrombospondin module (LOC55901), mRNA. /FEA=mRNA /GEN=LOC55901 /PROD=TMTSP for transmembrane molecule withthrombospondin module /DB_XREF=gi:8923893 /UG=Hs.325667 TMTSP for transmembrane molecule with thrombospondin module /FL=gb:AB044385.1 gb:NM_018676.1
219478_at_HG-U133A	WFDC1	WAP four-disulfide core domain 1	gb:NM_021197.1 /DEF=Homo sapiens WAP four-disulfide core domain 1 (WFDC1), mRNA. /FEA=mRNA /GEN=WFDC1 /PROD=WAP four-disulfide core domain 1 /DB_XREF=gi:10864006 /UG=Hs.36688 WAP four-disulfide core domain 1 /FL=gb:AF302109.1 gb:AF169631.1 gb:NM_021197.1
219518_s_at_HG-U133A	FLJ22637	hypothetical protein FLJ22637	gb:NM_025165.1 /DEF=Homo sapiens hypothetical protein FLJ22637 (FLJ22637), mRNA. /FEA=mRNA /GEN=FLJ22637 /PROD=hypothetical protein FLJ22637 /DB_XREF=gi:13376767 /UG=Hs.296178 hypothetical protein FLJ22637 /FL=gb:NM_025165.1
219574_at_HG-U133A	FLJ20668	hypothetical protein FLJ20668	gb:NM_017923.1 /DEF=Homo sapiens hypothetical protein FLJ20668 (FLJ20668), mRNA. /FEA=mRNA /GEN=FLJ20668 /PROD=hypothetical protein FLJ20668 /DB_XREF=gi:8923612 /UG=Hs.12920 hypothetical protein FLJ20668 /FL=gb:NM_017923.1
219598_s_at_HG-U133A			gb:NM_016104.1 /DEF=Homo sapiens PTD013 protein (PTD013), mRNA. /FEA=mRNA /GEN=PTD013 /PROD=PTD013 protein /DB_XREF=gi:7706668 /UG=Hs.279857 PTD013 protein /FL=gb:AF092134.1 gb:NM_016104.1
219615_s_at_HG-U133A	KCNK5	potassium channel, subfamily K, member 5 (TASK-2)	gb:NM_003740.1 /DEF=Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5), mRNA. /FEA=mRNA /GEN=KCNK5 /PROD=potassium channel, subfamily K, member 5(TASK-2)

			/DB_XREF=gi:4504850 /UG=Hs.127007 potassium channel, subfamily K, member 5 (TASK-2) /FL=gb:AF084830.1 gb:NM_003740.1
219631_at_HG-U133A	FLJ12929	hypothetical protein FLJ12929	gb:NM_024937.1 /DEF=Homo sapiens hypothetical protein FLJ12929 (FLJ12929), mRNA. /FEA=mRNA /GEN=FLJ12929 /PROD=hypothetical protein FLJ12929 /DB_XREF=gi:13376412 /UG=Hs.278956 hypothetical protein FLJ12929 /FL=gb:NM_024937.1
219634_at_HG-U133A	C4ST	chondroitin 4-sulfotransferase	gb:NM_018413.1 /DEF=Homo sapiens chondroitin 4-sulfotransferase (C4ST), mRNA. /FEA=mRNA /GEN=C4ST /PROD=chondroitin 4-sulfotransferase /DB_XREF=gi:8923757 /UG=Hs.287402 chondroitin 4-sulfotransferase /FL=gb:AB042326.1 gb:NM_018413.1 gb:AF239820.1
219641_at_HG-U133A	FLJ10103	hypothetical protein FLJ10103	gb:NM_017996.1 /DEF=Homo sapiens hypothetical protein FLJ10103 (FLJ10103), mRNA. /FEA=mRNA /GEN=FLJ10103 /PROD=hypothetical protein FLJ10103 /DB_XREF=gi:8922230 /UG=Hs.42140 hypothetical protein FLJ10103 /FL=gb:BC001242.1 gb:NM_017996.1
219654_at_HG-U133A	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	gb:NM_014241.1 /DEF=Homo sapiens protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (PTPLA), mRNA. /FEA=mRNA /GEN=PTPLA /PROD=protein tyrosine phosphatase-like (prolineinstead of catalytic arginine), member a /DB_XREF=gi:7657481 /UG=Hs.114062 protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a /FL=gb:AF114494.1 gb:NM_014241.1
219667_s_at_HG-U133A	BANK	hypothetical protein FLJ20706	gb:NM_017935.1 /DEF=Homo sapiens hypothetical protein FLJ20706 (FLJ20706), mRNA. /FEA=mRNA /GEN=FLJ20706 /PROD=hypothetical protein FLJ20706 /DB_XREF=gi:8923635 /UG=Hs.193736 hypothetical protein FLJ20706 /FL=gb:NM_017935.1
219690_at_HG-U133A	FLJ22573	hypothetical protein FLJ22573	gb:NM_024660.1 /DEF=Homo sapiens hypothetical protein FLJ22573 (FLJ22573), mRNA. /FEA=mRNA /GEN=FLJ22573 /PROD=hypothetical protein FLJ22573 /DB_XREF=gi:13375912 /UG=Hs.62406 hypothetical protein FLJ22573 /FL=gb:NM_024660.1

219734_at_HG-U133A	FLJ20174	hypothetical protein FLJ20174	gb:NM_017699.1 /DEF=Homo sapiens hypothetical protein FLJ20174 (FLJ20174), mRNA. /FEA=mRNA /GEN=FLJ20174 /PROD=hypothetical protein FLJ20174 /DB_XREF=gi:8923170 /UG=Hs.114556 hypothetical protein FLJ20174 /FL=gb:NM_017699.1
219753_at_HG-U133A	STAG3	stromal antigen 3	gb:NM_012447.1 /DEF=Homo sapiens stromal antigen 3 (STAG3), mRNA. /FEA=mRNA /GEN=STAG3 /PROD=stromal antigen 3 /DB_XREF=gi:6912685 /UG=Hs.20132 stromal antigen 3 /FL=gb:NM_012447.1
219763_at_HG-U133A	KIAA1608	KIAA1608 protein	gb:NM_024820.1 /DEF=Homo sapiens KIAA1608 protein (KIAA1608), mRNA. /FEA=mRNA /GEN=KIAA1608 /PROD=hypothetical protein FLJ21129 /DB_XREF=gi:13449264 /UG=Hs.300842 KIAA1608 protein /FL=gb:NM_024820.1
219788_at_HG-U133A	PILR	paired immunoglobulin-like receptor alpha	gb:NM_013439.1 /DEF=Homo sapiens paired immunoglobulin-like receptor alpha (PILR(ALPHA)), mRNA. /FEA=mRNA /GEN=PILR(ALPHA) /PROD=paired immunoglobulin-like receptor alpha /DB_XREF=gi:7305384 /UG=Hs.122591 paired immunoglobulin-like receptor alpha /FL=gb:AF161080.1 gb:NM_013439.1
219789_at_HG-U133A	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	Consensus includes gb:AI628360 /FEA=EST /DB_XREF=gi:4665160 /DB_XREF=est:ty75e10.x1 /CLONE=IMAGE:2284938 /UG=Hs.123655 natriuretic peptide receptor Cguanylate cyclase C (atrionatriuretic peptide receptor C) /FL=gb:M59305.1 gb:AF025998.1 gb:NM_000908.1
219793_at_HG-U133A	SNX16	sorting nexin 16	gb:NM_022133.1 /DEF=Homo sapiens sorting nexin 16 (SNX16), mRNA. /FEA=mRNA /GEN=SNX16 /PROD=sorting nexin 16 /DB_XREF=gi:11545864 /UG=Hs.128645 sorting nexin 16 /FL=gb:AF305779.1 gb:NM_022133.1
219812_at_HG-U133A	MGC2463	hypothetical protein MGC2463	gb:NM_024070.1 /DEF=Homo sapiens hypothetical protein MGC2463 (MGC2463), mRNA. /FEA=mRNA /GEN=MGC2463 /PROD=hypothetical protein MGC2463 /DB_XREF=gi:13129051 /UG=Hs.323634 hypothetical protein MGC2463 /FL=gb:BC001129.1 gb:NM_024070.1
219820_at_HG-U133A	NTT5	NTT5 protein	gb:NM_014037.1 /DEF=Homo sapiens NTT5 protein (NTT5), mRNA.

			/FEA=mRNA /GEN=NTT5 /PROD=NTT5 protein /DB_XREF=gi:7662517 /UG=Hs.59260 NTT5 protein /FL=gb:AF265578.1 gb:AL136856.1 gb:AF151977.1 gb:NM_014037.1
219837_s_at_HG-U133A	C17	cytokine-like protein C17	gb:NM_018659.1 /DEF=Homo sapiens cytokine-like protein C17 (C17), mRNA. /FEA=mRNA /GEN=C17 /PROD=cytokine-like protein C17 /DB_XREF=gi:8922107 /UG=Hs.13872 cytokine-like protein C17 /FL=gb:AF193766.1 gb:NM_018659.1
219846_at_HG-U133A	FLJ23040	hypothetical protein FLJ23040	gb:NM_025174.1 /DEF=Homo sapiens hypothetical protein FLJ23040 (FLJ23040), mRNA. /FEA=mRNA /GEN=FLJ23040 /PROD=hypothetical protein FLJ23040 /DB_XREF=gi:13376769 /UG=Hs.169813 hypothetical protein FLJ23040 /FL=gb:NM_025174.1
219868_s_at_HG-U133A	ANKHZN	ANKHZN protein	gb:NM_016376.1 /DEF=Homo sapiens ANKHZN protein (ANKHZN), mRNA. /FEA=mRNA /GEN=ANKHZN /PROD=ANKHZN protein /DB_XREF=gi:7705277 /UG=Hs.284163 ANKHZN protein /FL=gb:AB037360.1 gb:NM_016376.1
219869_s_at_HG-U133A	LOC64116	up-regulated by BCG-CWS	gb:NM_022154.1 /DEF=Homo sapiens up-regulated by BCG-CWS (LOC64116), mRNA. /FEA=mRNA /GEN=LOC64116 /PROD=up-regulated by BCG-CWS /DB_XREF=gi:11545899 /UG=Hs.284205 up-regulated by BCG-CWS /FL=gb:NM_022154.1
219891_at_HG-U133A	FLJ20208	hypothetical protein FLJ20208	gb:NM_017712.1 /DEF=Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA. /FEA=mRNA /GEN=FLJ20208 /PROD=hypothetical protein FLJ20208 /DB_XREF=gi:8923197 /UG=Hs.131776 hypothetical protein FLJ20208 /FL=gb:NM_017712.1
220000_at_HG-U133A	SIGLEC5	sialic acid binding Ig-like lectin 5	gb:NM_003830.1 /DEF=Homo sapiens sialic acid binding Ig-like lectin 5 (SIGLEC5), mRNA. /FEA=mRNA /GEN=SIGLEC5 /PROD=sialic acid binding Ig-like lectin 5 /DB_XREF=gi:4502658 /UG=Hs.117005 sialic acid binding Ig-like lectin 5 /FL=gb:U71383.1 gb:NM_003830.1 gb:AF170484.1
220001_at_HG-U133A	PADI5	peptidyl arginine deiminase, type V	gb:NM_012387.1 /DEF=Homo sapiens peptidyl arginine deiminase, type V (PAD), mRNA. /FEA=mRNA /GEN=PAD /PROD=peptidyl arginine deiminase,

			type V /DB_XREF=gi:6912575 /UG=Hs.117232 peptidyl arginine deiminase, type V /FL=gb:AB017919.1 gb:NM_012387.1
220007_at_HG-U133A	FLJ13984	hypothetical protein FLJ13984	gb:NM_024770.1 /DEF=Homo sapiens hypothetical protein FLJ13984 (FLJ13984), mRNA. /FEA=mRNA /GEN=FLJ13984 /PROD=hypothetical protein FLJ13984 /DB_XREF=gi:13376116 /UG=Hs.135146 hypothetical protein FLJ13984 /FL=gb:NM_024770.1
220050_at_HG-U133A	C9orf9	chromosome 9 open reading frame 9	gb:NM_018956.1 /DEF=Homo sapiens chromosome 9 open reading frame 9 (C9ORF9), mRNA. /FEA=mRNA /GEN=C9ORF9 /PROD=chromosome 9 open reading frame 9 /DB_XREF=gi:9506440 /UG=Hs.62595 chromosome 9 open reading frame 9 /FL=gb:NM_018956.1
220059_at_HG-U133A	BRDG1	BCR downstream signaling 1	gb:NM_012108.1 /DEF=Homo sapiens BCR downstream signaling 1 (BRDG1), mRNA. /FEA=mRNA /GEN=BRDG1 /PROD=BCR downstream signaling 1 /DB_XREF=gi:6912271 /UG=Hs.121128 BCR downstream signaling 1 /FL=gb:AB023483.1 gb:NM_012108.1
220118_at_HG-U133A	TZFP	testis zinc finger protein	gb:NM_014383.1 /DEF=Homo sapiens testis zinc finger protein (TZFP), mRNA. /FEA=mRNA /GEN=TZFP /PROD=testis zinc finger protein /DB_XREF=gi:7657664 /UG=Hs.99430 testis zinc finger protein /FL=gb:AF130255.1 gb:AF165097.1 gb:NM_014383.1
220307_at_HG-U133A	CD244	natural killer cell receptor 2B4	gb:NM_016382.1 /DEF=Homo sapiens natural killer cell receptor 2B4 (CD244), mRNA. /FEA=mRNA /GEN=CD244 /PROD=natural killer cell receptor 2B4 /DB_XREF=gi:7706528 /UG=Hs.157872 natural killer cell receptor 2B4 /FL=gb:AF242540.1 gb:AF105261.1 gb:AF145782.1 gb:AF107761.2 gb:AF117711.1 gb:NM_016382.1
220338_at_HG-U133A	FLJ10244	hypothetical protein FLJ10244	gb:NM_018037.1 /DEF=Homo sapiens hypothetical protein FLJ10244 (FLJ10244), mRNA. /FEA=mRNA /GEN=FLJ10244 /PROD=hypothetical protein FLJ10244 /DB_XREF=gi:8922306 /UG=Hs.274419 hypothetical protein FLJ10244 /FL=gb:NM_018037.1
220564_at_HG-U133A	FLJ11218	hypothetical protein FLJ11218	gb:NM_018363.1 /DEF=Homo sapiens hypothetical protein FLJ11218

			(FLJ11218), mRNA. /FEA=mRNA /GEN=FLJ11218 /PROD=hypothetical protein FLJ11218 /DB_XREF=gi:8922945 /UG=Hs.274413 hypothetical protein FLJ11218 /FL=gb:NM_018363.1
220653_at_HG-U133A	ZIM2	zinc finger, imprinted 2	gb:NM_015363.1 /DEF=Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /FEA=mRNA /GEN=ZIM2 /PROD=zinc finger, imprinted 2 /DB_XREF=gi:7657696 /UG=Hs.201776 zinc finger, imprinted 2 /FL=gb:AF166122.1 gb:NM_015363.1
220744_s_at_HG-U133A	WDR10	WD repeat domain 10	gb:NM_018262.1 /DEF=Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA. /FEA=mRNA /GEN=FLJ10897 /PROD=hypothetical protein FLJ10897 /DB_XREF=gi:8922747 /UG=Hs.70202 WD repeat domain 10 /FL=gb:NM_018262.1
220755_s_at_HG-U133A			gb:NM_016947.1 /DEF=Homo sapiens G8 protein (G8), mRNA. /FEA=mRNA /GEN=G8 /PROD=G8 protein /DB_XREF=gi:8393383 /UG=Hs.109798 G8 protein /FL=gb:NM_016947.1
220764_at_HG-U133A	PPP4R2	protein phosphatase 4 regulatory subunit 2	gb:NM_019853.1 /DEF=Homo sapiens protein phosphatase 4 regulatory subunit 2 (PPP4R2), mRNA. /FEA=mRNA /GEN=PPP4R2 /PROD=protein phosphatase 4 regulatory subunit 2 /DB_XREF=gi:9790172 /UG=Hs.125682 protein phosphatase 4 regulatory subunit 2 /FL=gb:NM_019853.1
220768_s_at_HG-U133A	CSNK1G3	casein kinase 1, gamma 3	gb:NM_004384.1 /DEF=Homo sapiens casein kinase 1, gamma 3 (CSNK1G3), mRNA. /FEA=mRNA /GEN=CSNK1G3 /PROD=casein kinase 1, gamma 3 /DB_XREF=gi:4758079 /UG=Hs.129206 casein kinase 1, gamma 3 /FL=gb:AF049089.1 gb:NM_004384.1
220796_x_at_HG-U133A	FLJ14251	hypothetical protein FLJ14251	gb:NM_024881.1 /DEF=Homo sapiens hypothetical protein FLJ14251 (FLJ14251), mRNA. /FEA=mRNA /GEN=FLJ14251 /PROD=hypothetical protein FLJ14251 /DB_XREF=gi:13376323 /UG=Hs.214178 hypothetical protein FLJ14251 /FL=gb:NM_024881.1
220798_x_at_HG-U133A	FLJ11535	hypothetical protein FLJ11535	gb:NM_024888.1 /DEF=Homo sapiens hypothetical protein FLJ11535 (FLJ11535), mRNA. /FEA=mRNA /GEN=FLJ11535 /PROD=hypothetical protein

			FLJ11535 /DB_XREF=gi:13376338 /UG=Hs.225170 hypothetical protein FLJ11535 /FL=gb:AL136596.1 gb:NM_024888.1
220924_s_at_HG-U133A	SLC38A2	solute carrier family 38, member 2	gb:NM_018976.1 /DEF=Homo sapiens amino acid transporter 2 (KIAA1382), mRNA. /FEA=mRNA /GEN=KIAA1382 /PROD=amino acid transporter 2 /DB_XREF=gi:9506836 /UG=Hs.298275 amino acid transporter 2 /FL=gb:NM_018976.1
220987_s_at_HG-U133A	DKFZP434J037	hypothetical protein DKFZp434J037	gb:NM_030952.1 /DEF=Homo sapiens hypothetical protein DKFZp434J037 (DKFZP434J037), mRNA. /FEA=mRNA /GEN=DKFZP434J037 /PROD=hypothetical protein DKFZp434J037 /DB_XREF=gi:13569921 /FL=gb:NM_030952.1
220999_s_at_HG-U133A	PRO1331	hypothetical protein PRO1331	gb:NM_030778.1 /DEF=Homo sapiens hypothetical protein PRO1331 (PRO1331), mRNA. /FEA=mRNA /GEN=PRO1331 /PROD=hypothetical protein PRO1331 /DB_XREF=gi:13562115 /FL=gb:NM_030778.1
221004_s_at_HG-U133A	ITM3	integral membrane protein 3	gb:NM_030926.1 /DEF=Homo sapiens integral membrane protein 3 (ITM3), mRNA. /FEA=mRNA /GEN=ITM3 /PROD=integral membrane protein 3 /DB_XREF=gi:13569884 /FL=gb:NM_030926.1
221006_s_at_HG-U133A	MY014	hypothetical protein My014	gb:NM_030918.1 /DEF=Homo sapiens hypothetical protein My014 (MY014), mRNA. /FEA=mRNA /GEN=MY014 /PROD=hypothetical protein My014 /DB_XREF=gi:13569876 /FL=gb:NM_030918.1
221011_s_at_HG-U133A	DKFZP566J091	hypothetical protein DKFZp566J091	gb:NM_030915.1 /DEF=Homo sapiens hypothetical protein DKFZp566J091 (DKFZP566J091), mRNA. /FEA=mRNA /GEN=DKFZP566J091 /PROD=hypothetical protein DKFZp566J091 /DB_XREF=gi:13569871 /FL=gb:NM_030915.1
221030_s_at_HG-U133A	DKFZP564B1162	hypothetical protein DKFZp564B1162	gb:NM_031305.1 /DEF=Homo sapiens hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA. /FEA=mRNA /GEN=DKFZP564B1162 /PROD=hypothetical protein DKFZp564B1162 /DB_XREF=gi:13775229 /FL=gb:NM_031305.1
221188_s_at_HG-	CIDEB	cell death-inducing DFFA-like effector b	gb:NM_014430.1 /DEF=Homo sapiens cell death-inducing DFFA-like effector

U133A			b (CIDEB), mRNA. /FEA=mRNA /GEN=CIDEB /PROD=cell death-inducing DFFA-like effector b /DB_XREF=gi:7656978 /UG=Hs.288835 cell death-inducing DFFA-like effector b /FL=gb:AF190901.1 gb:NM_014430.1
221206_at_HG-U133A	FLJ21459	hypothetical protein FLJ21459	gb:NM_024521.1 /DEF=Homo sapiens hypothetical protein FLJ21459 (FLJ21459), mRNA. /FEA=mRNA /GEN=FLJ21459 /PROD=hypothetical protein FLJ21459 /DB_XREF=gi:13375661 /UG=Hs.3769 hypothetical protein FLJ21459 /FL=gb:NM_024521.1
221234_s_at_HG-U133A	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	gb:NM_021813.1 /DEF=Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /FEA=mRNA /GEN=BACH2 /PROD=BTB and CNC homology 1, basic leucine zippertranscription factor 2 /DB_XREF=gi:13540489 /FL=gb:NM_021813.1
221239_s_at_HG-U133A	SPAP1	SH2 domain-containing phosphatase anchor protein 1	gb:NM_030764.1 /DEF=Homo sapiens SH2 domain-containing phosphatase anchor protein 1 (SPAP1), mRNA. /FEA=mRNA /GEN=SPAP1 /PROD=SH2 domain-containing phosphatase anchor protein1 /DB_XREF=gi:13540524 /FL=gb:NM_030764.1
221253_s_at_HG-U133A	MGC3178	thioredoxin related protein	gb:NM_030810.1 /DEF=Homo sapiens hypothetical protein MGC3178 (MGC3178), mRNA. /FEA=mRNA /GEN=MGC3178 /PROD=hypothetical protein MGC3178 /DB_XREF=gi:13540603 /FL=gb:NM_030810.1
221268_s_at_HG-U133A	LOC81537	sphingosine-1-phosphatase	gb:NM_030791.1 /DEF=Homo sapiens sphingosine-1-phosphatase (LOC81537), mRNA. /FEA=mRNA /GEN=LOC81537 /PROD=sphingosine-1-phosphatase /DB_XREF=gi:13540568 /FL=gb:NM_030791.1
221331_x_at_HG-U133A	CTLA4	cytotoxic T-lymphocyte-associated protein 4	gb:NM_005214.1 /DEF=Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA. /FEA=CDS /GEN=CTLA4 /PROD=cytotoxic T-lymphocyte-associated protein 4 /DB_XREF=gi:4885166 /UG=Hs.247824 cytotoxic T-lymphocyte-associated protein 4 /FL=gb:NM_005214.1
221486_at_HG-U133A			gb:AF067170.1 /DEF=Homo sapiens alpha endosulfine mRNA, complete cds. /FEA=mRNA /PROD=alpha endosulfine /DB_XREF=gi:4894373 /UG=Hs.111680 endosulfine alpha /FL=gb:AF067170.1 gb:AF157510.1

221543_s_at_HG-U133A	C8orf2	chromosome 8 open reading frame 2	gb:AL442077.1 /DEF=Homo sapiens mRNA; cDNA DKFZp667H242 (from clone DKFZp667H242); complete cds. /FEA=mRNA /GEN=DKFZp667H242 /PROD=hypothetical protein /DB_XREF=gi:10241715 /UG=Hs.125849 chromosome 8 open reading frame 2 /FL=gb:AL442077.1 gb:NM_007175.1
221555_x_at_HG-U133A	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	Consensus includes gb:AU145941 /FEA=EST /DB_XREF=gi:11007462 /DB_XREF=est:AU145941 /CLONE=HEMBA1006337 /UG=Hs.22116 CDC14 (cell division cycle 14, S. cerevisiae) homolog B /FL=gb:AF064104.1
221558_s_at_HG-U133A	LEF1	lymphoid enhancer-binding factor 1	gb:AF288571.1 /DEF=Homo sapiens lymphoid enhancer factor-1 (LEF1) mRNA, complete cds. /FEA=mRNA /GEN=LEF1 /PROD=lymphoid enhancer factor-1 /DB_XREF=gi:9858157 /UG=Hs.44865 lymphoid enhancer binding factor-1 /FL=gb:AF198532.1 gb:NM_016269.1 gb:AF288571.1
221581_s_at_HG-U133A	WBSCR5	Williams-Beuren syndrome chromosome region 5	gb:AF257135.1 /DEF=Homo sapiens WBSCR15 protein (WBSCR15) mRNA, complete cds. /FEA=mRNA /GEN=WBSCR15 /PROD=WBSCR15 protein /DB_XREF=gi:9651998 /UG=Hs.56607 Williams-Beuren syndrome chromosome region 5 /FL=gb:NM_022040.1 gb:BC001609.1 gb:AF257135.1
221586_s_at_HG-U133A	E2F5	E2F transcription factor 5, p130-binding	gb:U15642.1 /DEF=Human transcription factor E2F-5 mRNA, complete cds. /FEA=mRNA /PROD=E2F-5 /DB_XREF=gi:758415 /UG=Hs.2331 E2F transcription factor 5, p130-binding /FL=gb:NM_001951.2 gb:U15642.1 gb:U31556.1
221601_s_at_HG-U133A	TOSO	regulator of Fas-induced apoptosis	Consensus includes gb:AI084226 /FEA=EST /DB_XREF=gi:3422649 /DB_XREF=est:oy72g09.x1 /CLONE=IMAGE:1671424 /UG=Hs.58831 regulator of Fas-induced apoptosis /FL=gb:AF057557.1 gb:NM_005449.1
221602_s_at_HG-U133A	TOSO	regulator of Fas-induced apoptosis	gb:AF057557.1 /DEF=Homo sapiens anti-Fas-induced apoptosis (TOSO) mRNA, complete cds. /FEA=mRNA /GEN=TOSO /PROD=anti-Fas-induced apoptosis /DB_XREF=gi:3169292 /UG=Hs.58831 regulator of Fas-induced apoptosis /FL=gb:AF057557.1 gb:NM_005449.1
221617_at_HG-U133A			Consensus includes gb:AF077053.1 /DEF=Homo sapiens neuronal cell death-related protein mRNA, complete cds. /FEA=mRNA /PROD=neuronal cell

			death-related protein /DB_XREF=gi:4689153 /UG=Hs.171723 neuronal cell death-related protein /FL=gb:AF077053.1 gb:NM_015975.1 gb:AF220509.1
221642_at_HG-U133A	TREX1	three prime repair exonuclease 1	gb:BC002903.1 /DEF=Homo sapiens, clone MGC:10323, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10323) /DB_XREF=gi:12804100 /UG=Hs.23595 three prime repair exonuclease 1 /FL=gb:BC002903.1
221731_x_at_HG-U133A	CSPG2	chondroitin sulfate proteoglycan 2 (versican)	Consensus includes gb:BF218922 /FEA=EST /DB_XREF=gi:11112418 /DB_XREF=est:601885091F1 /CLONE=IMAGE:4103447 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican)
221739_at_HG-U133A	IL27	interleukin 27	Consensus includes gb:AL524093 /FEA=EST /DB_XREF=gi:12787586 /DB_XREF=est:AL524093 /CLONE=CS0DC002YI04 (5 prime) /UG=Hs.10927 hypothetical protein EUROIMAGE1875335
221755_at_HG-U133A		Homo sapiens mRNA for FLJ00043 protein, partial cds	Consensus includes gb:BG334196 /FEA=EST /DB_XREF=gi:13140634 /DB_XREF=est:602461680F1 /CLONE=IMAGE:4578666 /UG=Hs.325852 Homo sapiens mRNA for FLJ00043 protein, partial cds
221761_at_HG-U133A	ADSS	adenylosuccinate synthase	Consensus includes gb:AA628948 /FEA=EST /DB_XREF=gi:2541335 /DB_XREF=est:af28f07.s1 /CLONE=IMAGE:1032997 /UG=Hs.90011 adenylosuccinate synthase /FL=gb:NM_001126.1
221770_at_HG-U133A	RPE	ribulose-5-phosphate-3-epimerase	Consensus includes gb:BE964473 /FEA=EST /DB_XREF=gi:11767942 /DB_XREF=est:601658180R1 /CLONE=IMAGE:3876354 /UG=Hs.125845 ribulose-5-phosphate-3-epimerase
221778_at_HG-U133A	KIAA1718	KIAA1718 protein	Consensus includes gb:BE217882 /FEA=EST /DB_XREF=gi:8905200 /DB_XREF=est:hv31b02.x1 /CLONE=IMAGE:3174987 /UG=Hs.222707 KIAA1718 protein
221802_s_at_HG-U133A	KIAA1598	KIAA1598 protein	Consensus includes gb:AU157109 /FEA=EST /DB_XREF=gi:11018630 /DB_XREF=est:AU157109 /CLONE=PLACE1006159 /UG=Hs.23740 KIAA1598 protein
221834_at_HG-U133A		Homo sapiens cDNA FLJ31489 fis, clone	Consensus includes gb:AV700132 /FEA=EST /DB_XREF=gi:10302103

		NT2NE2003308	/DB_XREF=est:AV700132 /CLONE=GKCGSE03 /UG=Hs.295923 seven in absentia (Drosophila) homolog 1
221858_at_HG-U133A	KIAA0608	KIAA0608 protein	Consensus includes gb:N34407 /FEA=EST /DB_XREF=gi:1155549 /DB_XREF=est:yy53g10.s1 /CLONE=IMAGE:277314 /UG=Hs.100960 KIAA0608 protein
221865_at_HG-U133A		Homo sapiens clone 23579 mRNA sequence	Consensus includes gb:BF969986 /FEA=EST /DB_XREF=gi:12337201 /DB_XREF=est:602272821F1 /CLONE=IMAGE:4360804 /UG=Hs.170226 Homo sapiens clone 23579 mRNA sequence
221902_at_HG-U133A		ESTs	Consensus includes gb:AL567940 /FEA=EST /DB_XREF=gi:12921802 /DB_XREF=est:AL567940 /CLONE=CS0DF036YK19 (3 prime) /UG=Hs.7967 ESTs
221943_x_at_HG-U133A	RPL38	ribosomal protein L38	Consensus includes gb:AW303136 /FEA=EST /DB_XREF=gi:6712816 /DB_XREF=est:xr59c08.x1 /CLONE=IMAGE:2764430 /UG=Hs.2017 ribosomal protein L38
221969_at_HG-U133A	PAX5	paired box gene 5 (B-cell lineage specific activator protein)	Consensus includes gb:BF510692 /FEA=EST /DB_XREF=gi:11593990 /DB_XREF=est:UI-H-BI4-aof-f-12-0-UI.s1 /CLONE=IMAGE:3084815 /UG=Hs.22030 paired box gene 5 (B-cell lineage specific activator protein)
221980_at_HG-U133A			Consensus includes gb:AL117592.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586H1921 (from clone DKFZp586H1921). /FEA=mRNA /DB_XREF=gi:5912156 /UG=Hs.179765 Homo sapiens mRNA; cDNA DKFZp586H1921 (from clone DKFZp586H1921)
221991_at_HG-U133A	NXPH3	neurexophilin 3	Consensus includes gb:AI937333 /FEA=EST /DB_XREF=gi:5676203 /DB_XREF=est:wp75h10.x1 /CLONE=IMAGE:2467651 /UG=Hs.55069 neurexophilin 3
222062_at_HG-U133A	WSX1	class I cytokine receptor	Consensus includes gb:AI983115 /FEA=EST /DB_XREF=gi:5810334 /DB_XREF=est:wu18b02.x1 /CLONE=IMAGE:2517291 /UG=Hs.132781 class I cytokine receptor
222073_at_HG-U133A	COL4A3	collagen, type IV, alpha 3 (Goodpasture	Consensus includes gb:AI694562 /FEA=EST /DB_XREF=gi:4971902

		antigen)	/DB_XREF=est:wd72g08.x1 /CLONE=IMAGE:2337182 /UG=Hs.150318 ESTs
222108_at_HG-U133A			Consensus includes gb:AC004010 /DEF=Human BAC clone GS1-99H8 /FEA=CDS /DB_XREF=gi:2781385 /UG=Hs.121520 Human BAC clone GS1-99H8
222146_s_at_HG-U133A			Consensus includes gb:AK026674.1 /DEF=Homo sapiens cDNA: FLJ23021 fis, clone LNG01014, highly similar to HUMSEF21B Human SEF2-1B protein (SEF2-1B) mRNA. /FEA=mRNA /DB_XREF=gi:10439577 /UG=Hs.326198 transcription factor 4
222147_s_at_HG-U133A			Consensus includes gb:AL133519 /DEF=Human DNA sequence from clone RP11-122O1 on chromosome 20 Contains a novel gene encoding a protein orthologous to the mouse vesicular inhibitory amino acid transporter (VIAAT), a novel gene similar to the yeast actin-like protein ARP5, 3 CpG islan... /FEA=CDS /DB_XREF=gi:10045268 /UG=Hs.302092 Human DNA sequence from clone RP11-122O1 on chromosome 20 Contains a novel gene encoding a protein orthologous to the mouse vesicular inhibitory amino acid transporter (VIAAT), a novel gene similar to the yeast actin-like protein ARP5, 3 CpG islands, ESTs
222150_s_at_HG-U133A			Consensus includes gb:AK026747.1 /DEF=Homo sapiens cDNA: FLJ23094 fis, clone LNG07379, highly similar to HST000007 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605. /FEA=mRNA /DB_XREF=gi:10439670 /UG=Hs.12969 hypothetical protein
222154_s_at_HG-U133A	DKFZP564A2416	DKFZP564A2416 protein	Consensus includes gb:AK002064.1 /DEF=Homo sapiens cDNA FLJ11202 fis, clone PLACE1007746. /FEA=mRNA /DB_XREF=gi:7023720 /UG=Hs.5297 DKFZP564A2416 protein
222163_s_at_HG-U133A	MGC5347	hypothetical protein MGC5347	Consensus includes gb:BE890973 /FEA=EST /DB_XREF=gi:10349835 /DB_XREF=est:601431962F1 /CLONE=IMAGE:3917319 /UG=Hs.5555 hypothetical protein MGC5347
222166_at_HG-U133A			Consensus includes gb:AK022885.1 /DEF=Homo sapiens cDNA FLJ12823 fis,

			clone NT2RP2002752. /FEA=mRNA /DB_XREF=gi:10434538 /UG=Hs.95867 hypothetical protein EST00098
222203_s_at_HG-U133A			Consensus includes gb:AK023625.1 /DEF=Homo sapiens cDNA FLJ13563 fis, clone PLACE1008111, weakly similar to PROBABLE OXIDOREDUCTASE (EC 1.-.-.-). /FEA=mRNA /DB_XREF=gi:10435607 /UG=Hs.288880 PAN2 protein
222229_x_at_HG-U133A			Consensus includes gb:AL121871 /DEF=Human DNA sequence from clone RP13-258O15 on chromosome Xq21.2-Xq21.33 Contains a pseudogene similar to ribosomal protein L26, STSs and GSSs /FEA=CDS /DB_XREF=gi:6855342 /UG=Hs.272344 Human DNA sequence from clone RP13-258O15 on chromosome Xq21.2-Xq21.33 Contains a pseudogene similar to ribosomal protein L26, STSs and GSSs
222237_s_at_HG-U133A			Consensus includes gb:AC084239 /DEF=Homo sapiens chromosome 19, BAC CTC-512J12 (BC347040), complete sequence /FEA=mRNA_2 /DB_XREF=gi:10864171 /UG=Hs.48589 zinc finger protein 228
222275_at_HG-U133A		ESTs	Consensus includes gb:AI039469 /FEA=EST /DB_XREF=gi:3278663 /DB_XREF=est:ox41a08.s1 /CLONE=IMAGE:1658870 /UG=Hs.27362 ESTs
222282_at_HG-U133A		ESTs	Consensus includes gb:AV761453 /FEA=EST /DB_XREF=gi:10919301 /DB_XREF=est:AV761453 /CLONE=MDSBZA03 /UG=Hs.294014 ESTs
222313_at_HG-U133A		ESTs	Consensus includes gb:AW972359 /FEA=EST /DB_XREF=gi:8162205 /DB_XREF=est:EST384450 /UG=Hs.293334 ESTs
222335_at_HG-U133A		ESTs	Consensus includes gb:BG025063 /FEA=EST /DB_XREF=gi:12411278 /DB_XREF=est:602276406F1 /CLONE=IMAGE:4364304 /UG=Hs.44888 ESTs
222422_s_at_HG-U133B	MGC10924	hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5	Consensus includes gb:AW167859 /FEA=EST /DB_XREF=gi:6399308 /DB_XREF=est:xg55a05.x1 /CLONE=IMAGE:2632208 /UG=Hs.9788 hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5 /FL=gb:BC004317.1 gb:NM_030571.1
222448_s_at_HG-	UMP-CMPK	UMP-CMP kinase	gb:AF112216.1 /DEF=Homo sapiens UMP-CMP kinase mRNA, complete cds.

U133B			/FEA=mRNA /PROD=UMP-CMP kinase /DB_XREF=gi:6563219 /UG=Hs.11463 UMP-CMP kinase /FL=gb:AF259961.1 gb:AF110643.1 gb:AF112216.1 gb:AF070416.1 gb:NM_016308.1
222465_at_HG-U133B	C15orf15	chromosome 15 open reading frame 15	gb:AF165521.1 /DEF=Homo sapiens ribosomal protein L30 isolog (L30) mRNA, complete cds. /FEA=mRNA /GEN=L30 /PROD=ribosomal protein L30 isolog /DB_XREF=gi:9294748 /UG=Hs.284162 60S ribosomal protein L30 isolog /FL=gb:NM_016304.1 gb:AF060926.1 gb:AF212226.1 gb:BC005344.1 gb:AF201949.1 gb:AF165521.1
222477_s_at_HG-U133B	TM7SF3	seven transmembrane protein TM7SF3	gb:BC005176.1 /DEF=Homo sapiens, seven transmembrane protein TM7SF3, clone MGC:847, mRNA, complete cds. /FEA=mRNA /PROD=seven transmembrane protein TM7SF3 /DB_XREF=gi:13477393 /UG=Hs.10071 seven transmembrane protein TM7SF3 /FL=gb:BC005176.1 gb:AB032470.1 gb:NM_016551.1
222492_at_HG-U133B	FLJ21324	hypothetical protein FLJ21324	Consensus includes gb:AW262867 /FEA=EST /DB_XREF=gi:6639683 /DB_XREF=est:xq96d11.x1 /CLONE=IMAGE:2758485 /UG=Hs.4746 hypothetical protein FLJ21324 /FL=gb:NM_021941.1 gb:BC003651.1
222520_s_at_HG-U133B	ESRRBL1	estrogen-related receptor beta like 1	gb:AF139576.1 /DEF=Homo sapiens MHS4R2 (MHS4R2) mRNA, complete cds. /FEA=mRNA /GEN=MHS4R2 /PROD=MHS4R2 /DB_XREF=gi:13171100 /UG=Hs.170318 hypothetical protein FLJ10147 /FL=gb:AF139576.1 gb:AF245220.1 gb:NM_018010.1
222619_at_HG-U133B	ZNF281	zinc finger protein 281	Consensus includes gb:AU150752 /FEA=EST /DB_XREF=gi:11012273 /DB_XREF=est:AU150752 /CLONE=NT2RP2003522 /UG=Hs.59757 zinc finger protein 281 /FL=gb:AF125158.1 gb:NM_012482.1
222680_s_at_HG-U133B	RAMP	RA-regulated nuclear matrix-associated protein	Consensus includes gb:AK001261.1 /DEF=Homo sapiens cDNA FLJ10399 fis, clone NT2RM4000354, weakly similar to LETHAL(2)DENTICLELESS PROTEIN. /FEA=mRNA /DB_XREF=gi:7022404 /UG=Hs.126774 L2DTL protein /FL=gb:AF195765.1 gb:NM_016448.1
222692_s_at_HG-	FLJ23399	hypothetical protein FLJ23399	Consensus includes gb:BF444916 /FEA=EST /DB_XREF=gi:11510054

U133B			/DB_XREF=est:nad19a09.x1 /CLONE=IMAGE:3365681 /UG=Hs.299883 hypothetical protein FLJ23399 /FL=gb:NM_022763.1
222698_s_at_HG-U133B	IMPACT	hypothetical protein IMPACT	gb:AF208694.1 /DEF=Homo sapiens IMPACT (IMPACT) mRNA, complete cds. /FEA=mRNA /GEN=IMPACT /PROD=IMPACT /DB_XREF=gi:11494011 /UG=Hs.284245 hypothetical protein IMPACT /FL=gb:AF208694.1 gb:AB026264.1 gb:NM_018439.1
222862_s_at_HG-U133B	AK5	adenylate kinase 5	Consensus includes gb:BG169832 /FEA=EST /DB_XREF=gi:12676535 /DB_XREF=est:602324480F1 /CLONE=IMAGE:4427755 /UG=Hs.18268 adenylate kinase 5 /FL=gb:AF062595.1 gb:NM_012093.1
222915_s_at_HG-U133B	BANK	hypothetical protein FLJ20706	Consensus includes gb:AA811540 /FEA=EST /DB_XREF=gi:2881151 /DB_XREF=est:ob73e02.s1 /CLONE=IMAGE:1337018 /UG=Hs.193736 hypothetical protein FLJ20706 /FL=gb:NM_017935.1
222916_s_at_HG-U133B			Consensus includes gb:AF116718.1 /DEF=Homo sapiens PRO2900 mRNA, complete cds. /FEA=mRNA /PROD=PRO2900 /DB_XREF=gi:7959934 /UG=Hs.283473 hypothetical protein PRO2900 /FL=gb:AF116718.1 gb:NM_018635.1
222955_s_at_HG-U133B	HT011	uncharacterized hypothalamus protein HT011	gb:AF168713.1 /DEF=Homo sapiens x 004 protein mRNA, complete cds. /FEA=mRNA /PROD=x 004 protein /DB_XREF=gi:9437340 /UG=Hs.267923 uncharacterized hypothalamus protein HT011 /FL=gb:AF220185.1 gb:NM_018472.1 gb:AF168713.1
222976_s_at_HG-U133B	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	gb:BC000771.1 /DEF=Homo sapiens, Similar to tropomyosin 4, clone MGC:3261, mRNA, complete cds. /FEA=mRNA /PROD=Similar to tropomyosin 4 /DB_XREF=gi:12653954 /UG=Hs.85844 neurotrophic tyrosine kinase, receptor, type 1 /FL=gb:BC000771.1
222977_at_HG-U133B	SURF4	surfeit 4	Consensus includes gb:AL518882 /FEA=EST /DB_XREF=gi:12782375 /DB_XREF=est:AL518882 /CLONE=CS0DA011YM11 (3 prime) /UG=Hs.284296 Homo sapiens cDNA: FLJ22993 fis, clone KAT11914 /FL=gb:AF078866.1
222979_s_at_HG-			gb:AF078866.1 /DEF=Homo sapiens SURF-4 mRNA, complete cds.

U133B			/FEA=mRNA /PROD=SURF-4 /DB_XREF=gi:5531846 /UG=Hs.284296 Homo sapiens cDNA: FLJ22993 fis, clone KAT11914 /FL=gb:AF078866.1
222982_x_at_HG-U133B	SLC38A2	solute carrier family 38, member 2	gb:AF298897.1 /DEF=Homo sapiens amino acid transporter system A (ATA2) mRNA, complete cds. /FEA=mRNA /GEN=ATA2 /PROD=amino acid transporter system A /DB_XREF=gi:10945620 /UG=Hs.298275 amino acid transporter 2 /FL=gb:AF298897.1
222996_s_at_HG-U133B	HSPC195	hypothetical protein HSPC195	gb:BC002490.1 /DEF=Homo sapiens, hypothetical protein, clone MGC:915, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:12803342 /UG=Hs.15093 hypothetical protein /FL=gb:BC002490.1 gb:AF151029.1 gb:NM_016463.1
223036_at_HG-U133B	FRSB	phenylalanyl-tRNA synthetase beta-subunit	gb:D84430.1 /DEF=Homo sapiens mRNA for phenylalanyl tRNA synthetase, complete cds. /FEA=mRNA /PROD=phenylalanyl tRNA synthetase /DB_XREF=gi:7768937 /UG=Hs.9081 phenylalanyl-tRNA synthetase beta-subunit /FL=gb:AF042346.1 gb:NM_005687.1 gb:AF161521.1 gb:D84430.1
223044_at_HG-U133B	SLC11A3	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3	gb:AL136944.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586J0624 (from clone DKFZp586J0624); complete cds. /FEA=mRNA /GEN=DKFZp586J0624 /PROD=hypothetical protein /DB_XREF=gi:12053382 /UG=Hs.5944 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 /FL=gb:AL136944.1 gb:AF226614.1 gb:AF231121.1 gb:NM_014585.1 gb:AF215636.1
223054_at_HG-U133B	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	gb:BC001144.1 /DEF=Homo sapiens, ER-associated DNAJ; ER-associated Hsp40 co-chaperone; hDj9; ERj3, clone MGC:1169, mRNA, complete cds. /FEA=mRNA /PROD=ER-associated DNAJ; ER-associated Hsp40co-chaperone; hDj9; ERj3 /DB_XREF=gi:12654614 /UG=Hs.278605 DnaJ (Hsp40) homolog, subfamily B, member 11 /FL=gb:BC001144.1 gb:AB028859.1 gb:AF228505.1 gb:NM_016306.1
223226_x_at_HG-U133B	MGC3181	hypothetical protein MGC3181	gb:BC000274.1 /DEF=Homo sapiens, Similar to single-stranded-DNA-binding protein, clone MGC:3181, mRNA, complete cds. /FEA=mRNA /PROD=Similar

			to single-stranded-DNA-binding protein /DB_XREF=gi:12653022 /UG=Hs.324618 Homo sapiens, Similar to single-stranded-DNA-binding protein, clone MGC:3181, mRNA, complete cds /FL=gb:BC000274.1
223246_s_at_HG-U133B	STRBP	spermatid perinuclear RNA binding protein	gb:BC002693.1 /DEF=Homo sapiens, Similar to spermatid perinuclear RNA-binding protein, clone MGC:3405, mRNA, complete cds. /FEA=mRNA /PROD=Similar to spermatid perinuclear RNA-bindingprotein /DB_XREF=gi:12803714 /UG=Hs.8215 hypothetical protein FLJ11307 /FL=gb:AL136866.1 gb:BC002693.1 gb:AF333337.1 gb:NM_018387.1
223253_at_HG-U133B	UCC1	upregulated in colorectal cancer gene 1	gb:BC000686.1 /DEF=Homo sapiens, UCC1 protein, clone MGC:1185, mRNA, complete cds. /FEA=mRNA /PROD=UCC1 protein /DB_XREF=gi:12653794 /UG=Hs.46721 UCC1 protein /FL=gb:BC000686.1 gb:AY027862.1
223276_at_HG-U133B	NID67	putative small membrane protein NID67	gb:AF313413.1 /DEF=Homo sapiens putative small membrane protein NID67 mRNA, complete cds. /FEA=mRNA /PROD=putative small membrane protein NID67 /DB_XREF=gi:12484085 /UG=Hs.29444 Homo sapiens putative small membrane protein NID67 mRNA, complete cds /FL=gb:AF313413.1
223280_x_at_HG-U133B	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	gb:AF253977.1 /DEF=Homo sapiens HAIRB-iso mRNA, complete cds. /FEA=mRNA /PROD=HAIRB-iso /DB_XREF=gi:12005800 /UG=Hs.17914 membrane-spanning 4-domains, subfamily A, member6 /FL=gb:AF212240.1 gb:AF253977.1 gb:AF261136.1
223287_s_at_HG-U133B	FOXP1	forkhead box P1	gb:AF146696.1 /DEF=Homo sapiens clone pAB195 FOXP1 (FOXP1) mRNA, complete cds. /FEA=mRNA /GEN=FOXP1 /PROD=FOXP1 /DB_XREF=gi:12043713 /UG=Hs.274344 hypothetical protein /FL=gb:AF146696.1 gb:AF151049.1 gb:NM_016477.1
223314_at_HG-U133B	MGC11352	hypothetical protein MGC11352	Consensus includes gb:BF025955 /FEA=EST /DB_XREF=gi:10733667 /DB_XREF=est:601669947F1 /CLONE=IMAGE:3953075 /UG=Hs.101395 hypothetical protein MGC11352 /FL=gb:AL136638.1
223318_s_at_HG-	MGC10974	hypothetical protein MGC10974	gb:BC004393.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 2310045B01

U133B			gene, clone MGC:10974, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 2310045B01 gene /DB_XREF=gi:13325151 /UG=Hs.111099 Homo sapiens, Similar to RIKEN cDNA 2310045B01 gene, clone MGC:10974, mRNA, complete cds /FL=gb:BC004393.1
223321_s_at_HG-U133B	FGFRL1	fibroblast growth factor receptor-like 1	gb:AF312678.1 /DEF=Homo sapiens FGF homologous factor receptor (FHFR) mRNA, complete cds. /FEA=mRNA /GEN=FHFR /PROD=FGF homologous factor receptor /DB_XREF=gi:13183617 /UG=Hs.193326 fibroblast growth factor receptor-like 1 /FL=gb:AF312678.1
223382_s_at_HG-U133B	NIN283	nerve injury gene 283	gb:AL136903.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434E229 (from clone DKFZp434E229); complete cds. /FEA=mRNA /GEN=DKFZp434E229 /PROD=hypothetical protein /DB_XREF=gi:12053302 /UG=Hs.320834 Homo sapiens mRNA; cDNA DKFZp434E229 (from clone DKFZp434E229); complete cds /FL=gb:AL136903.1
223385_at_HG-U133B	CYP2S1	cytochrome P450, subfamily IIS, polypeptide 1	gb:AF335278.1 /DEF=Homo sapiens cytochrome P450 2S1 (CYP2S1) mRNA, complete cds. /FEA=mRNA /GEN=CYP2S1 /PROD=cytochrome P450 2S1 /DB_XREF=gi:13161183 /UG=Hs.98370 cytochrome P450, subfamily IIS, polypeptide 1 /FL=gb:AF335278.1 gb:NM_030622.2
223391_at_HG-U133B	LOC81537	sphingosine-1-phosphatase	Consensus includes gb:BE880703 /FEA=EST /DB_XREF=gi:10329479 /DB_XREF=est:601490317F1 /CLONE=IMAGE:3892493 /UG=Hs.24678 sphingosine-1-phosphatase /FL=gb:AF349315.1
223401_at_HG-U133B	MDS006	x 006 protein	gb:BC001294.1 /DEF=Homo sapiens, Similar to x 006 protein, clone MGC:5294, mRNA, complete cds. /FEA=mRNA /PROD=Similar to x 006 protein /DB_XREF=gi:12654898 /UG=Hs.47668 x 006 protein /FL=gb:BC001294.1
223422_s_at_HG-U133B	DKFZP564B1162	hypothetical protein DKFZp564B1162	Consensus includes gb:AI743534 /FEA=EST /DB_XREF=gi:5111822 /DB_XREF=est:wf72e03.x2 /CLONE=IMAGE:2361148 /UG=Hs.93589 Homo sapiens mRNA; cDNA DKFZp564B1162 (from clone DKFZp564B1162); complete cds /FL=gb:AL136646.1

223449_at_HG-U133B	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	gb:AF225425.1 /DEF=Homo sapiens HT018 mRNA, complete cds. /FEA=mRNA /PROD=HT018 /DB_XREF=gi:9963852 /UG=Hs.108920 HT018 protein /FL=gb:NM_020681.1 gb:AF225425.1
223462_at_HG-U133B	MGC4618	hypothetical protein MGC4618	gb:BC005158.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 3010001K23 gene, clone MGC:4618, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 3010001K23 gene /DB_XREF=gi:13477362 /UG=Hs.89072 Homo sapiens, Similar to RIKEN cDNA 3010001K23 gene, clone MGC:4618, mRNA, complete cds /FL=gb:BC005158.1
223467_at_HG-U133B	RASD1	RAS, dexamethasone-induced 1	gb:AF069506.1 /DEF=Homo sapiens activator of G protein signaling (AGS1) mRNA, complete cds. /FEA=mRNA /GEN=AGS1 /PROD=activator of G protein signaling /DB_XREF=gi:4959037 /UG=Hs.25829 ras-related protein /FL=gb:AF069506.1 gb:AF153192.1 gb:AF172846.1 gb:NM_016084.1
223469_at_HG-U133B	MGC10812	hypothetical protein MGC10812	gb:BC004942.1 /DEF=Homo sapiens, clone MGC:10812, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10812) /DB_XREF=gi:13436298 /UG=Hs.4188 Homo sapiens, clone MGC:10812, mRNA, complete cds /FL=gb:BC004942.1
223471_at_HG-U133B			gb:BC002556.1 /DEF=Homo sapiens, hypothetical protein FLJ22548 similar to gene trap PAT 12, clone MGC:759, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ22548 similar to genetrap PAT 12 /DB_XREF=gi:12803462 /UG=Hs.103267 hypothetical protein FLJ22548 similar to gene trap PAT 12 /FL=gb:NM_022456.1 gb:BC002556.1
223474_at_HG-U133B	C14orf4	chromosome 14 open reading frame 4	Consensus includes gb:AI932310 /FEA=EST /DB_XREF=gi:5671047 /DB_XREF=est:wd26h03.x1 /CLONE=IMAGE:2329301 /UG=Hs.179260 chromosome 14 open reading frame 4 /FL=gb:AF063597.1
223482_at_HG-U133B	TMPIT	transmembrane protein induced by tumor necrosis factor alpha	gb:AF327923.1 /DEF=Homo sapiens transmembrane protein induced by tumor necrosis factor alpha (TMPIT) mRNA, complete cds. /FEA=mRNA /GEN=TMPIT /PROD=transmembrane protein induced by tumor necrosisfactor alpha /DB_XREF=gi:13241760 /UG=Hs.314243 Homo sapiens transmembrane

			protein induced by tumor necrosis factor alpha (TMPIT) mRNA, complete cds /FL=gb:AF327923.1
223498_at_HG-U133B		Homo sapiens, clone IMAGE:3614358, mRNA, partial cds	gb:AB041533.1 /DEF=Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds. /FEA=mRNA /GEN=HCMOGT-1 /PROD=sperm antigen /DB_XREF=gi:10798803 /UG=Hs.15053 Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds /FL=gb:AB041533.1
223514_at_HG-U133B	CARD11	caspase recruitment domain family, member 11	gb:AF322641.1 /DEF=Homo sapiens caspase recruitment domain protein 11 mRNA, complete cds. /FEA=mRNA /PROD=caspase recruitment domain protein 11 /DB_XREF=gi:12382772 /UG=Hs.293867 Homo sapiens caspase recruitment domain protein 11 mRNA, complete cds /FL=gb:AF322641.1
223522_at_HG-U133B	GL012	hypothetical protein GL012	gb:AF251293.1 /DEF=Homo sapiens GL012 mRNA, complete cds. /FEA=mRNA /PROD=GL012 /DB_XREF=gi:12005727 /UG=Hs.21379 hypothetical protein GL012 /FL=gb:AF251293.1
223595_at_HG-U133B	AD031	AD031 protein	gb:AF247167.1 /DEF=Homo sapiens AD031 mRNA, complete cds. /FEA=mRNA /PROD=AD031 /DB_XREF=gi:12005634 /UG=Hs.44004 Homo sapiens AD031 mRNA, complete cds /FL=gb:AF247167.1
223703_at_HG-U133B	CDA017	CDA017 protein	gb:AF267860.1 /DEF=Homo sapiens CDA017 mRNA, complete cds. /FEA=mRNA /PROD=CDA017 /DB_XREF=gi:12006046 /UG=Hs.39780 Homo sapiens CDA017 mRNA, complete cds /FL=gb:AF267860.1
223712_at_HG-U133B	DCOHM	HNF1-alpha dimerization cofactor	gb:AL136721.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566K1946 (from clone DKFZp566K1946); complete cds. /FEA=mRNA /GEN=DKFZp566K1946 /PROD=hypothetical protein /DB_XREF=gi:12052960 /UG=Hs.150186 Homo sapiens mRNA; cDNA DKFZp566K1946 (from clone DKFZp566K1946); complete cds /FL=gb:AL136721.1
223785_at_HG-U133B	FLJ10719	hypothetical protein FLJ10719	gb:BC004277.1 /DEF=Homo sapiens, Similar to hypothetical protein FLJ10719, clone MGC:10837, mRNA, complete cds. /FEA=mRNA /PROD=Similar to hypothetical protein FLJ10719 /DB_XREF=gi:13279100 /UG=Hs.134734 Homo sapiens, Similar to hypothetical protein FLJ10719,

			clone MGC:10837, mRNA, complete cds /FL=gb:BC004277.1
223828_s_at_HG-U133B	LGALS12	lectin, galactoside-binding, soluble, 12 (galectin 12)	gb:AF222694.1 /DEF=Homo sapiens galectin-related inhibitor of proliferation isoform b (GRIP1) mRNA, complete cds. /FEA=mRNA /GEN=GRIP1 /PROD=galectin-related inhibitor of proliferationisoform b /DB_XREF=gi:6979966 /UG=Hs.284183 Homo sapiens galectin-related inhibitor of proliferation isoform a (GRIP1) mRNA, complete cds /FL=gb:AF222694.1 gb:AF222695.1
223839_s_at_HG-U133B			gb:AF132203.1 /DEF=Homo sapiens PRO1933 mRNA, complete cds. /FEA=mRNA /PROD=PRO1933 /DB_XREF=gi:11493551 /UG=Hs.119597 stearoyl-CoA desaturase (delta-9-desaturase) /FL=gb:AF132203.1
223894_s_at_HG-U133B	FTS	fused toes homolog (mouse)	gb:BC001134.1 /DEF=Homo sapiens, hypothetical protein FLJ13258 similar to fused toes, clone MGC:2845, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ13258 similar to fusedtoes /DB_XREF=gi:12654596 /UG=Hs.288929 hypothetical protein FLJ13258 similar to fused toes /FL=gb:BC001134.1
223939_at_HG-U133B	GPR91	G protein-coupled receptor 91	gb:AF348078.1 /DEF=Homo sapiens G-protein coupled receptor 91 (GPR91) mRNA, complete cds. /FEA=mRNA /GEN=GPR91 /PROD=G-protein coupled receptor 91 /DB_XREF=gi:13517982 /UG=Hs.279575 Homo sapiens G-protein coupled receptor 91 (GPR91) mRNA, complete cds /FL=gb:AF348078.1
223981_at_HG-U133B	NIN	ninein (GSK3B interacting protein)	gb:AF223937.1 /DEF=Homo sapiens ninein isotype 1 mRNA, complete cds. /FEA=mRNA /PROD=ninein isotype 1 /DB_XREF=gi:12655859 /UG=Hs.44054 ninein (GSK3B interacting protein) /FL=gb:AF223937.1
223982_s_at_HG-U133B	IPLA2	intracellular membrane-associated calcium-independent phospholipase A2 gamma	gb:AB041261.1 /DEF=Homo sapiens iPLA2 mRNA for calcium-independent phospholipase A2, complete cds. /FEA=mRNA /GEN=iPLA2 /PROD=calcium-independent phospholipase A2 /DB_XREF=gi:7670057 /UG=Hs.44198 intracellular membrane-associated calcium-independent phospholipase A2 gamma /FL=gb:AB041261.1
224044_at_HG-U133B	FLJ11040	hypothetical protein FLJ11040	gb:AL136929.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586D0222 (from

			clone DKFZp586D0222); complete cds. /FEA=mRNA /GEN=DKFZp586D0222 /PROD=hypothetical protein /DB_XREF=gi:12053352 /UG=Hs.14202 hypothetical protein FLJ11040 /FL=gb:AL136929.1
224049_at_HG-U133B	KCNK17	potassium channel, subfamily K, member 17 (TASK-4)	gb:AF339912.1 /DEF=Homo sapiens potassium channel TASK-4 mRNA, complete cds. /FEA=mRNA /PROD=potassium channel TASK-4 /DB_XREF=gi:13507376 /UG=Hs.162282 Homo sapiens potassium channel TASK-4 mRNA, complete cds /FL=gb:AF339912.1
224076_s_at_HG-U133B	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	gb:AF255649.1 /DEF=Homo sapiens DC28 mRNA, complete cds. /FEA=mRNA /PROD=DC28 /DB_XREF=gi:12005822 /UG=Hs.27721 Wolf-Hirschhorn syndrome candidate 1-like 1 /FL=gb:AF255649.1
224221_s_at_HG-U133B	VAV3	vav 3 oncogene	gb:AF118886.1 /DEF=Homo sapiens VAV-3 protein beta isoform (VAV-3) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=VAV-3 /PROD=VAV-3 protein beta isoform /DB_XREF=gi:4416405 /UG=Hs.267659 vav 3 oncogene /FL=gb:AF118886.1
224254_x_at_HG-U133B			gb:AF116695.1 /DEF=Homo sapiens PRO2221 mRNA, complete cds. /FEA=mRNA /PROD=PRO2221 /DB_XREF=gi:7959888 /UG=Hs.296442 hypothetical protein PRO2221 /FL=gb:AF116695.1
224324_at_HG-U133B	B29	B29 protein	gb:AB042647.1 /DEF=Homo sapiens B29 mRNA, complete cds. /FEA=mRNA /GEN=B29 /DB_XREF=gi:13603411 /FL=gb:AB042647.1
224356_x_at_HG-U133B	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	gb:AF237908.1 /DEF=Homo sapiens MS4A6A protein mRNA, complete cds. /FEA=mRNA /PROD=MS4A6A protein /DB_XREF=gi:13649404 /FL=gb:AF237908.1
224389_s_at_HG-U133B	LOC84570	collagen-like Alzheimer amyloid plaque component precursor	gb:AF293341.1 /DEF=Homo sapiens collagen-like Alzheimer amyloid plaque component precursor type II mRNA, complete cds. /FEA=mRNA /PROD=collagen-like Alzheimer amyloid plaque componentprecursor type II /DB_XREF=gi:13625305 /FL=gb:AF293341.1
224404_s_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2	gb:AF343662.1 /DEF=Homo sapiens immunoglobulin receptor translocation associated protein 2a (IRTA2) mRNA, complete cds, alternatively spliced.

			/FEA=mRNA /GEN=IRTA2 /PROD=immunoglobulin receptor translocation associatedprotein 2a /DB_XREF=gi:13591709 /FL=gb:AF343662.1
224405_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2	gb:AF343663.1 /DEF=Homo sapiens immunoglobulin receptor translocation associated protein 2b (IRTA2) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=IRTA2 /PROD=immunoglobulin receptor translocation associatedprotein 2b /DB_XREF=gi:13591711 /FL=gb:AF343663.1
224406_s_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2	gb:AF343664.1 /DEF=Homo sapiens immunoglobulin receptor translocation associated protein 2c (IRTA2) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=IRTA2 /PROD=immunoglobulin receptor translocation associatedprotein 2c /DB_XREF=gi:13591713 /FL=gb:AF343664.1
224407_s_at_HG-U133B	MST4	Mst3 and SOK1-related kinase	gb:AF344882.1 /DEF=Homo sapiens serinethreonine protein kinase MST4 (MST4) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=MST4 /PROD=serinethreonine protein kinase MST4 /DB_XREF=gi:13549066 /FL=gb:AF344882.1
224435_at_HG-U133B	MGC4248	hypothetical protein MGC4248	gb:BC005871.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 5730469M10 gene, clone MGC:4248, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 5730469M10 gene /DB_XREF=gi:13543426 /FL=gb:BC005871.1
224482_s_at_HG-U133B	MGC11316	hypothetical protein MGC11316	gb:BC006240.1 /DEF=Homo sapiens, clone MGC:11316, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:11316) /DB_XREF=gi:13623278 /FL=gb:BC006240.1
224516_s_at_HG-U133B	HSPC195	hypothetical protein HSPC195	gb:BC006428.1 /DEF=Homo sapiens, hypothetical protein, clone MGC:12969, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:13623618 /FL=gb:BC006428.1
224520_s_at_HG-U133B	MGC13168	hypothetical protein MGC13168	gb:BC006440.1 /DEF=Homo sapiens, clone MGC:13168, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:13168) /DB_XREF=gi:13623640 /FL=gb:BC006440.1
224553_s_at_HG-	TNFRSF18	tumor necrosis factor receptor	gb:AF117297.1 /DEF=Homo sapiens TNF receptor superfamily activation-

U133B		superfamily, member 18	inducible protein mRNA, complete cds. /FEA=CDS /PROD=TNF receptor superfamily activation-inducibleprotein /DB_XREF=gi:4378799 /UG=Hs.212680 tumor necrosis factor receptor superfamily, member 18 /FL=gb:AF117297.1
224559_at_HG-U133B			Consensus includes gb:AF001540 /FEA=EST /DB_XREF=gi:2529712 /DB_XREF=est:AF001540 /CLONE=alpha1 /UG=Hs.42346 calcineurin-binding protein calsarcin-1
224570_s_at_HG-U133B		Homo sapiens, clone IMAGE:3882977, mRNA, partial cds	Consensus includes gb:AA166696 /FEA=EST /DB_XREF=gi:1745160 /DB_XREF=est:zo85e03.s1 /CLONE=IMAGE:593692 /UG=Hs.279009 matrix Gla protein
224609_at_HG-U133B	CTL2	CTL2 gene	Consensus includes gb:AI264216 /FEA=EST /DB_XREF=gi:3872419 /DB_XREF=est:qk02h01.x1 /CLONE=IMAGE:1867825 /UG=Hs.105509 CTL2 gene /FL=gb:NM_020428.1
224664_at_HG-U133B		Homo sapiens, RIKEN cDNA 2310005G07 gene, clone MGC:10049 IMAGE:3890955, mRNA, complete cds	Consensus includes gb:BE962336 /FEA=EST /DB_XREF=gi:11765135 /DB_XREF=est:601655601R1 /CLONE=IMAGE:3846049 /UG=Hs.178485 Homo sapiens cDNA FLJ13919 fis, clone Y79AA1000410
224681_at_HG-U133B	GNA12	guanine nucleotide binding protein (G protein) alpha 12	Consensus includes gb:BG028884 /FEA=EST /DB_XREF=gi:12417979 /DB_XREF=est:602292385F1 /CLONE=IMAGE:4387292 /UG=Hs.182874 guanine nucleotide binding protein (G protein) alpha 12 /FL=gb:L01694.1 gb:NM_007353.1
224710_at_HG-U133B	RAB34	RAB34, member RAS oncogene family	Consensus includes gb:AF322067.1 /DEF=Homo sapiens RAB39 (RAB39) mRNA, complete cds. /FEA=CDS /GEN=RAB39 /PROD=RAB39 /DB_XREF=gi:12958664 /UG=Hs.301853 Homo sapiens RAB39 (RAB39) mRNA, complete cds /FL=gb:AF322067.1
224724_at_HG-U133B	KIAA1247	similar to glucosamine-6-sulfatases	Consensus includes gb:AL133001.1 /DEF=Novel human gene on chromosome 20, similar to GLUCOSAMINE-6-SULFATASES. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:6453340 /UG=Hs.43857 similar to glucosamine-6-sulfatases
224727_at_HG-U133B		Homo sapiens mRNA; cDNA	Consensus includes gb:AL045545 /FEA=EST /DB_XREF=gi:5433676

		DKFZp434E2023 (from clone DKFZp434E2023)	/DB_XREF=est:DKFZp434K095_r1 /CLONE=DKFZp434K095 /UG=Hs.250465 Homo sapiens mRNA; cDNA DKFZp434E2023 (from clone DKFZp434E2023)
224735_at_HG-U133B		Homo sapiens cDNA FLJ32189 fis, clone PLACE6002084, weakly similar to CYTOCHROME B561	Consensus includes gb:AA683481 /FEA=EST /DB_XREF=gi:2670079 /DB_XREF=est:zl55b03.s1 /CLONE=IMAGE:505805 /UG=Hs.22546 Homo sapiens cDNA: FLJ22217 fis, clone HRC01591
224739_at_HG-U133B	MG61	porcupine	Consensus includes gb:BE778706 /FEA=EST /DB_XREF=gi:10199993 /DB_XREF=est:601466282F1 /CLONE=IMAGE:3869516 /UG=Hs.5326 amino acid system N transporter 2; porcupine
224764_at_HG-U133B	ARHGAP10	Rho-GTPase activating protein 10	Consensus includes gb:AB037845.1 /DEF=Homo sapiens mRNA for KIAA1424 protein, partial cds. /FEA=mRNA /GEN=KIAA1424 /PROD=KIAA1424 protein /DB_XREF=gi:7243228 /UG=Hs.11611 KIAA1424 protein
224772_at_HG-U133B	MGC14961	hypothetical protein MGC14961	Consensus includes gb:AB032977.1 /DEF=Homo sapiens mRNA for KIAA1151 protein, partial cds. /FEA=mRNA /GEN=KIAA1151 /PROD=KIAA1151 protein /DB_XREF=gi:6382017 /UG=Hs.6298 KIAA1151 protein
224794_s_at_HG-U133B	LOC51148	cerebral cell adhesion molecule	Consensus includes gb:AA654142 /FEA=EST /DB_XREF=gi:2590296 /DB_XREF=est:nt10d06.s1 /CLONE=IMAGE:1192715 /UG=Hs.23954 cerebral cell adhesion molecule /FL=gb:AF177203.1 gb:NM_016174.1
224804_s_at_HG-U133B	FLJ00005	FLJ00005 protein	Consensus includes gb:AU152410 /FEA=EST /DB_XREF=gi:11013931 /DB_XREF=est:AU152410 /CLONE=NT2RP3000901 /UG=Hs.10647 FLJ00005 protein
224811_at_HG-U133B		Homo sapiens cDNA FLJ30652 fis, clone DFNES2000011	Consensus includes gb:BF112093 /FEA=EST /DB_XREF=gi:10941783 /DB_XREF=est:7l40b07.x1 /CLONE=IMAGE:3523908 /UG=Hs.5724 sclerostin
224823_at_HG-U133B		Homo sapiens cDNA: FLJ22300 fis, clone HRC04759	Consensus includes gb:AA526844 /FEA=EST /DB_XREF=gi:2268913 /DB_XREF=est:ni92d10.s1 /CLONE=IMAGE:984307 /UG=Hs.288965 Homo sapiens cDNA: FLJ22300 fis, clone HRC04759
224833_at_HG-U133B	ETS1	v-ets erythroblastosis virus E26	Consensus includes gb:BE218980 /FEA=EST /DB_XREF=gi:8906298

		oncogene homolog 1 (avian)	/DB_XREF=est:hv47a05.x1 /CLONE=IMAGE:3176528 /UG=Hs.18063 Homo sapiens cDNA FLJ10768 fis, clone NT2RP4000150
224837_at_HG-U133B	FOXP1	forkhead box P1	Consensus includes gb:AW080845 /FEA=EST /DB_XREF=gi:6035997 /DB_XREF=est:xc38c08.x1 /CLONE=IMAGE:2586542 /UG=Hs.108327 damage-specific DNA binding protein 1 (127kD)
224838_at_HG-U133B			Consensus includes gb:AK026898.1 /DEF=Homo sapiens cDNA: FLJ23245 fis, clone COL02931. /FEA=mRNA /DB_XREF=gi:10439865 /UG=Hs.108327 damage-specific DNA binding protein 1 (127kD)
224839_s_at_HG-U133B	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	Consensus includes gb:BG328998 /FEA=EST /DB_XREF=gi:13135436 /DB_XREF=est:602428659F1 /CLONE=IMAGE:4558454 /UG=Hs.79265 suppression of tumorigenicity 5
224847_at_HG-U133B		Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572	Consensus includes gb:AW051349 /FEA=EST /DB_XREF=gi:5913619 /DB_XREF=est:wy89g02.x1 /CLONE=IMAGE:2555762 /UG=Hs.180059 Homo sapiens cDNA FLJ20653 fis, clone KAT01739
224848_at_HG-U133B		Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572	Consensus includes gb:AA922068 /FEA=EST /DB_XREF=gi:3069377 /DB_XREF=est:om45d11.s1 /CLONE=IMAGE:1543989 /UG=Hs.180059 Homo sapiens cDNA FLJ20653 fis, clone KAT01739
224872_at_HG-U133B	KIAA1463	KIAA1463 protein	Consensus includes gb:AB040896.1 /DEF=Homo sapiens mRNA for KIAA1463 protein, partial cds. /FEA=mRNA /GEN=KIAA1463 /PROD=KIAA1463 protein /DB_XREF=gi:7959186 /UG=Hs.21104 KIAA1463 protein
224918_x_at_HG-U133B	MGST1	microsomal glutathione S-transferase 1	Consensus includes gb:AI220117 /FEA=EST /DB_XREF=gi:3802320 /DB_XREF=est:qg89h11.x1 /CLONE=IMAGE:1842405 /UG=Hs.790 microsomal glutathione S-transferase 1
224928_at_HG-U133B			Consensus includes gb:AK024846.1 /DEF=Homo sapiens cDNA: FLJ21193 fis, clone COL00110. /FEA=mRNA /DB_XREF=gi:10437253 /UG=Hs.78521 KIAA1717 protein
224932_at_HG-U133B	PRSS2	protease, serine, 2 (trypsin 2)	Consensus includes gb:AI814909 /FEA=EST /DB_XREF=gi:5426124

			/DB_XREF=est:wk68e04.x1 /CLONE=IMAGE:2420574 /UG=Hs.66915 ESTs, Weakly similar to 16.7Kd protein H.sapiens
224935_at_HG-U133B	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	Consensus includes gb:BG165815 /FEA=EST /DB_XREF=gi:12672518 /DB_XREF=est:602344486F1 /CLONE=IMAGE:4454565 /UG=Hs.30376 hypothetical protein
224967_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1287006	Consensus includes gb:W72338 /FEA=EST /DB_XREF=gi:1382943 /DB_XREF=est:zd62a08.s1 /CLONE=IMAGE:345206 /UG=Hs.23703 ESTs
224970_at_HG-U133B	NFIA	nuclear factor I/A	Consensus includes gb:AA419275 /FEA=EST /DB_XREF=gi:2078988 /DB_XREF=est:zv35e01.s1 /CLONE=IMAGE:755640 /UG=Hs.173933 nuclear factor IA
224975_at_HG-U133B	NFIA	nuclear factor I/A	Consensus includes gb:AB037860.1 /DEF=Homo sapiens mRNA for KIAA1439 protein, partial cds. /FEA=mRNA /GEN=KIAA1439 /PROD=KIAA1439 protein /DB_XREF=gi:7243275 /UG=Hs.173933 nuclear factor IA
224976_at_HG-U133B	NFIA	nuclear factor I/A	Consensus includes gb:R37335 /FEA=EST /DB_XREF=gi:794791 /DB_XREF=est:yf56f05.s1 /CLONE=IMAGE:26230 /UG=Hs.173933 nuclear factor IA
224994_at_HG-U133B	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	Consensus includes gb:AA777512 /FEA=EST /DB_XREF=gi:2836991 /DB_XREF=est:zj02g07.s1 /CLONE=IMAGE:449148 /UG=Hs.111460 Homo sapiens cDNA: FLJ21715 fis, clone COL10287, highly similar to AF071569 Homo sapiens multifunctional calciumcalmodulin-dependent protein kinase II delta2 isoform mRNA
225003_at_HG-U133B	MBC3205	hypothetical protein MBC3205	Consensus includes gb:BF343862 /FEA=EST /DB_XREF=gi:11291061 /DB_XREF=est:602015541F1 /CLONE=IMAGE:4150954 /UG=Hs.43621 ESTs
225010_at_HG-U133B			Consensus includes gb:AK024913.1 /DEF=Homo sapiens cDNA: FLJ21260 fis, clone COL01441. /FEA=mRNA /DB_XREF=gi:10437328 /UG=Hs.288862 Homo sapiens cDNA: FLJ21260 fis, clone COL01441
225014_at_HG-U133B		Homo sapiens, clone IMAGE:4247529,	Consensus includes gb:BF508958 /FEA=EST /DB_XREF=gi:11592256

		mRNA, partial cds	/DB_XREF=est:UI-H-BI4-aos-g-12-0-UI.s1 /CLONE=IMAGE:3086038 /UG=Hs.235026 ESTs
225019_at_HG-U133B	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	Consensus includes gb:BF797381 /FEA=EST /DB_XREF=gi:12102435 /DB_XREF=est:602257023F1 /CLONE=IMAGE:4340525 /UG=Hs.111460 Homo sapiens cDNA: FLJ21715 fis, clone COL10287, highly similar to AF071569 Homo sapiens multifunctional calciumcalmodulin-dependent protein kinase II delta2 isoform mRNA
225025_at_HG-U133B	IGSF8	immunoglobulin superfamily, member 8	Consensus includes gb:BC004108.1 /DEF=Homo sapiens, clone IMAGE:3687782, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3687782) /DB_XREF=gi:13278650 /UG=Hs.332012 Homo sapiens, clone IMAGE:3687782, mRNA, partial cds
225051_at_HG-U133B		Homo sapiens, clone IMAGE:3873720, mRNA	Consensus includes gb:AA522435 /FEA=EST /DB_XREF=gi:2264267 /DB_XREF=est:ng30g04.s1 /CLONE=IMAGE:936342 /UG=Hs.268024 Homo sapiens mRNA; cDNA DKFZp434C184 (from clone DKFZp434C184)
225055_at_HG-U133B	FLJ10120	hypothetical protein FLJ10120	Consensus includes gb:AV735241 /FEA=EST /DB_XREF=gi:10852786 /DB_XREF=est:AV735241 /CLONE=cdAAJB04 /UG=Hs.190488 hypothetical protein FLJ10120
225064_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp434N2412 (from clone DKFZp434N2412)	Consensus includes gb:R60018 /FEA=EST /DB_XREF=gi:830713 /DB_XREF=est:yh12b01.s1 /CLONE=IMAGE:42905 /UG=Hs.250535 Homo sapiens mRNA; cDNA DKFZp434N2412 (from clone DKFZp434N2412)
225065_x_at_HG-U133B		Homo sapiens, clone IMAGE:4154219, mRNA, partial cds	Consensus includes gb:AI826279 /FEA=EST /DB_XREF=gi:5446950 /DB_XREF=est:wk33e07.x1 /CLONE=IMAGE:2417220 /UG=Hs.295362 DR1-associated protein 1 (negative cofactor 2 alpha)
225073_at_HG-U133B	HSPC232	hypothetical protein	Consensus includes gb:NM_016488.1 /DEF=Homo sapiens hypothetical protein (HSPC232), mRNA. /FEA=CDS /GEN=HSPC232 /PROD=hypothetical protein HSPC232 /DB_XREF=gi:7705526 /UG=Hs.281428 hypothetical protein /FL=gb:AF151040.1 gb:AF151066.1 gb:NM_016488.1
225080_at_HG-U133B	MYO1C	myosin IC	Consensus includes gb:BG251821 /FEA=EST /DB_XREF=gi:12761637

			/DB_XREF=est:602364436F1 /CLONE=IMAGE:4472864 /UG=Hs.297939 cathepsin B
225085_at_HG-U133B		Homo sapiens, clone MGC:4459 IMAGE:2960564, mRNA, complete cds	Consensus includes gb:AA522888 /FEA=EST /DB_XREF=gi:2263600 /DB_XREF=est:ni41b09.s1 /CLONE=IMAGE:979385 /UG=Hs.96513 ESTs, Highly similar to unnamed protein product H.sapiens
225129_at_HG-U133B	MDS026	uncharacterized hematopoietic stem/progenitor cells protein MDS026	Consensus includes gb:AW170571 /FEA=EST /DB_XREF=gi:6402096 /DB_XREF=est:xn63f11.x1 /CLONE=IMAGE:2698413 /UG=Hs.96144 copine II
225136_at_HG-U133B		Homo sapiens cDNA FLJ32643 fis, clone SYNOV2001212	Consensus includes gb:BF968578 /FEA=EST /DB_XREF=gi:12335793 /DB_XREF=est:602271184F1 /CLONE=IMAGE:4359237 /UG=Hs.18585 ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
225144_at_HG-U133B		ESTs	Consensus includes gb:AI457436 /FEA=EST /DB_XREF=gi:4310305 /DB_XREF=est:tl73e06.x1 /CLONE=IMAGE:2152738 /UG=Hs.28959 ESTs
225175_s_at_HG-U133B	CTL2	CTL2 gene	Consensus includes gb:AI569503 /FEA=EST /DB_XREF=gi:4532877 /DB_XREF=est:tn87h05.x1 /CLONE=IMAGE:2176569 /UG=Hs.105509 CTL2 gene
225230_at_HG-U133B	CEPT1	choline/ethanolaminephosphotransferase	Consensus includes gb:AI735261 /FEA=EST /DB_XREF=gi:5056785 /DB_XREF=est:at08d05.x1 /CLONE=IMAGE:2354505 /UG=Hs.125031 cholineethanolaminephosphotransferase
225246_at_HG-U133B	STIM2	stromal interaction molecule 2	Consensus includes gb:T97323 /FEA=EST /DB_XREF=gi:746668 /DB_XREF=est:ye57b07.s1 /CLONE=IMAGE:121813 /UG=Hs.278894 KIAA1482 protein
225250_at_HG-U133B	STIM2	stromal interaction molecule 2	Consensus includes gb:N48266 /FEA=EST /DB_XREF=gi:1189432 /DB_XREF=est:yz05b10.s1 /CLONE=IMAGE:282139 /UG=Hs.278894 KIAA1482 protein
225270_at_HG-U133B			Consensus includes gb:AL355708.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 44260. /FEA=mRNA /DB_XREF=gi:7799100 /UG=Hs.284169 Homo sapiens mRNA full length insert cDNA clone

			EUROIMAGE 44260
225277_at_HG-U133B		Homo sapiens, Similar to RIKEN cDNA 1100001L14 gene, clone IMAGE:4100291, mRNA, partial cds	Consensus includes gb:AL525780 /FEA=EST /DB_XREF=gi:12789273 /DB_XREF=est:AL525780 /CLONE=CS0DC013YG11 (3 prime) /UG=Hs.9070 Homo sapiens mRNA; cDNA DKFZp434A109 (from clone DKFZp434A109)
225285_at_HG-U133B			Consensus includes gb:AK025615.1 /DEF=Homo sapiens cDNA: FLJ21962 fis, clone HEP05564. /FEA=mRNA /DB_XREF=gi:10438186 /UG=Hs.7567 Homo sapiens cDNA: FLJ21962 fis, clone HEP05564
225305_at_HG-U133B		ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens]	Consensus includes gb:AI826268 /FEA=EST /DB_XREF=gi:5446939 /DB_XREF=est:wk33d06.x1 /CLONE=IMAGE:2417195 /UG=Hs.27769 ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINEACYLCARNITINE CARRIER PROTEIN H.sapiens
225306_s_at_HG-U133B		ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens]	Consensus includes gb:AI826268 /FEA=EST /DB_XREF=gi:5446939 /DB_XREF=est:wk33d06.x1 /CLONE=IMAGE:2417195 /UG=Hs.27769 ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINEACYLCARNITINE CARRIER PROTEIN H.sapiens
225314_at_HG-U133B		ESTs, Weakly similar to unnamed protein product [H.sapiens]	Consensus includes gb:BG291649 /FEA=EST /DB_XREF=gi:13049586 /DB_XREF=est:602385778F1 /CLONE=IMAGE:4514827 /UG=Hs.95835 ESTs, Weakly similar to unnamed protein product H.sapiens
225326_at_HG-U133B	KIAA1311	KIAA1311 protein	Consensus includes gb:AB037732.1 /DEF=Homo sapiens mRNA for KIAA1311 protein, partial cds. /FEA=mRNA /GEN=KIAA1311 /PROD=KIAA1311 protein /DB_XREF=gi:7242976 /UG=Hs.61441 KIAA1311 protein
225327_at_HG-U133B	FLJ10980	hypothetical protein FLJ10980	Consensus includes gb:AB037791.1 /DEF=Homo sapiens mRNA for KIAA1370 protein, partial cds. /FEA=mRNA /GEN=KIAA1370 /PROD=KIAA1370 protein /DB_XREF=gi:7243120 /UG=Hs.29716 hypothetical protein FLJ10980
225330_at_HG-U133B		Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds	Consensus includes gb:AL044092 /FEA=EST /DB_XREF=gi:5432319 /DB_XREF=est:DKFZp434M1328_s1 /CLONE=DKFZp434M1328

			/UG=Hs.293960 ESTs
225331_at_HG-U133B		ESTs	Consensus includes gb:BF941088 /FEA=EST /DB_XREF=gi:12358408 /DB_XREF=est:7d92e07.x1 /CLONE=IMAGE:3280596 /UG=Hs.170307 Ral guanine nucleotide exchange factor RalGPS1A
225344_at_HG-U133B			Consensus includes gb:AL035689 /DEF=Human DNA sequence from clone RP1-187J11 on chromosome 6q11.1-22.33. Contains the gene for a novel protein similar to S. pombe and S. cerevisiae predicted proteins, the gene for a novel protein similar to protein kinase C inhibitors, the 3 end of... /FEA=mRNA_3 /DB_XREF=gi:8218045 /UG=Hs.6966 Human DNA sequence from clone RP1-187J11 on chromosome 6q11.1-22.33. Contains the gene for a novel protein similar to S. pombe and S. cerevisiae predicted proteins, the gene for a novel protein similar to protein kinase C inhibitors, the 3 end of the gen
225386_s_at_HG-U133B	LOC92906	hypothetical protein BC008217	Consensus includes gb:AI559701 /FEA=EST /DB_XREF=gi:4509906 /DB_XREF=est:tq51e03.x1 /CLONE=IMAGE:2212348 /UG=Hs.91684 Homo sapiens mRNA; cDNA DKFZp667I103 (from clone DKFZp667I103)
225406_at_HG-U133B	TSG	twisted gastrulation	Consensus includes gb:AA195009 /FEA=EST /DB_XREF=gi:1784711 /DB_XREF=est:zr35h03.s1 /CLONE=IMAGE:665429 /UG=Hs.247302 twisted gastrulation
225426_at_HG-U133B		ESTs	Consensus includes gb:AW195360 /FEA=EST /DB_XREF=gi:6474436 /DB_XREF=est:xn37d08.x1 /CLONE=IMAGE:2695887 /UG=Hs.7256 integral inner nuclear membrane protein
225452_at_HG-U133B	PPARBP	PPAR binding protein	Consensus includes gb:AI423072 /FEA=EST /DB_XREF=gi:4269003 /DB_XREF=est:tf18b02.x1 /CLONE=IMAGE:2096523 /UG=Hs.10130 ESTs
225469_at_HG-U133B	KRAS2	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	Consensus includes gb:AA015609 /FEA=EST /DB_XREF=gi:1476657 /DB_XREF=est:ze20e11.s1 /CLONE=IMAGE:359564 /UG=Hs.184050 v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog
225510_at_HG-U133B	CHN1	chimerin (chimaerin) 1	Consensus includes gb:BG033561 /FEA=EST /DB_XREF=gi:12425979

			/DB_XREF=est:602302173F1 /CLONE=IMAGE:4403610 /UG=Hs.22660 Homo sapiens cDNA FLJ11658 fis, clone HEMBA1004577
225512_at_HG-U133B		Homo sapiens cDNA FLJ31131 fis, clone IMR322000935	Consensus includes gb:AI005245 /FEA=EST /DB_XREF=gi:3214755 /DB_XREF=est:ot98h02.x1 /CLONE=IMAGE:1624851 /UG=Hs.23853 ESTs
225547_at_HG-U133B		Homo sapiens cDNA FLJ32554 fis, clone SPLEN1000106	Consensus includes gb:BG169443 /FEA=EST /DB_XREF=gi:12676146 /DB_XREF=est:602321129F1 /CLONE=IMAGE:4424526 /UG=Hs.292815 ESTs
225553_at_HG-U133B		Homo sapiens cDNA FLJ12874 fis, clone NT2RP2003769	Consensus includes gb:AL042817 /FEA=EST /DB_XREF=gi:5935584 /DB_XREF=est:DKFZp434F1922_s1 /CLONE=DKFZp434F1922 /UG=Hs.56847 Homo sapiens cDNA FLJ12874 fis, clone NT2RP2003769
225563_at_HG-U133B		ESTs	Consensus includes gb:AI970788 /FEA=EST /DB_XREF=gi:5767614 /DB_XREF=est:wr19g02.x1 /CLONE=IMAGE:2482034 /UG=Hs.30348 ESTs
225565_at_HG-U133B		ESTs, Weakly similar to SFRB_HUMAN SPLICING FACTOR ARGININE/SERINE-RICH 11 [H.sapiens]	Consensus includes gb:AA769455 /FEA=EST /DB_XREF=gi:2820693 /DB_XREF=est:nz41g11.s1 /CLONE=IMAGE:1290404 /UG=Hs.22315 ESTs
225592_at_HG-U133B	NRM	nurim (nuclear envelope membrane protein)	Consensus includes gb:D81048 /FEA=EST /DB_XREF=gi:1178925 /DB_XREF=est:HUM127A03A /CLONE=GEN-127A03 /UG=Hs.57222 nurim (nuclear envelope membrane protein)
225624_at_HG-U133B		Homo sapiens mRNA for FLJ00066 protein, partial cds	Consensus includes gb:AL044019 /FEA=EST /DB_XREF=gi:5432247 /DB_XREF=est:DKFZp434J1128_s1 /CLONE=DKFZp434J1128 /UG=Hs.194478 Homo sapiens mRNA; cDNA DKFZp434O1572 (from clone DKFZp434O1572)
225629_s_at_HG-U133B	KIAA1538	KIAA1538 protein	Consensus includes gb:AI669498 /FEA=EST /DB_XREF=gi:4834272 /DB_XREF=est:wb88e05.x1 /CLONE=IMAGE:2312768 /UG=Hs.35096 KIAA1538 protein
225635_s_at_HG-U133B		Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133	Consensus includes gb:BG535378 /FEA=EST /DB_XREF=gi:13526923 /DB_XREF=est:602563038F1 /CLONE=IMAGE:4688000 /UG=Hs.94109 Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133
225640_at_HG-U133B		Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133	Consensus includes gb:AA875998 /FEA=EST /DB_XREF=gi:2984839 /DB_XREF=est:ob93b09.s1 /CLONE=IMAGE:1338905 /UG=Hs.94109 Homo

			sapiens cDNA FLJ13634 fis, clone PLACE1011133
225653_at_HG-U133B		Homo sapiens, clone IMAGE:3448872, mRNA, partial cds	Consensus includes gb:AV755269 /FEA=EST /DB_XREF=gi:10913117 /DB_XREF=est:AV755269 /CLONE=BMFARD01 /UG=Hs.105664 hypothetical protein FLJ22294
225660_at_HG-U133B	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	Consensus includes gb:W92748 /FEA=EST /DB_XREF=gi:1421920 /DB_XREF=est:zd92h03.s1 /CLONE=IMAGE:356981 /UG=Hs.263395 sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
225670_at_HG-U133B		Homo sapiens cDNA FLJ20667 fis, clone KAIA596	Consensus includes gb:AI384017 /FEA=EST /DB_XREF=gi:4196798 /DB_XREF=est:te35h10.x1 /CLONE=IMAGE:2088739 /UG=Hs.18955 Homo sapiens cDNA FLJ20667 fis, clone KAIA596
225700_at_HG-U133B			Consensus includes gb:AC006042 /DEF=Homo sapiens BAC clone RP11-505D17 from 7p22-p21 /FEA=CDS_2 /DB_XREF=gi:4508120 /UG=Hs.18987 Homo sapiens BAC clone RP11-505D17 from 7p22-p21
225713_at_HG-U133B	KIAA1898	KIAA1898 protein	Consensus includes gb:AV727346 /FEA=EST /DB_XREF=gi:10836767 /DB_XREF=est:AV727346 /CLONE=HTCACC11 /UG=Hs.22410 ESTs
225735_at_HG-U133B			Consensus includes gb:AL110131.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564H122 (from clone DKFZp564H122). /FEA=mRNA /DB_XREF=gi:5817026 /UG=Hs.28783 KIAA1223 protein
225772_s_at_HG-U133B	MGC14288	hypothetical protein MGC14288	Consensus includes gb:BF203664 /FEA=EST /DB_XREF=gi:11097250 /DB_XREF=est:601865696F1 /CLONE=IMAGE:4098670 /UG=Hs.181073 ESTs
225776_at_HG-U133B	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	Consensus includes gb:AW205585 /FEA=EST /DB_XREF=gi:6505059 /DB_XREF=est:UI-H-BI1-afr-a-08-0-UI.s1 /CLONE=IMAGE:2722479 /UG=Hs.20340 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
225782_at_HG-U133B		ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	Consensus includes gb:AW027333 /FEA=EST /DB_XREF=gi:5886089 /DB_XREF=est:wt73d02.x1 /CLONE=IMAGE:2513091 /UG=Hs.35092 ESTs

225790_at_HG-U133B		ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	Consensus includes gb:AL048386 /FEA=EST /DB_XREF=gi:4727526 /DB_XREF=est:DKFZp586F1624_s1 /CLONE=DKFZp586F1624 /UG=Hs.35092 ESTs
225792_at_HG-U133B		Homo sapiens cDNA: FLJ23597 fis, clone LNG15281	Consensus includes gb:AA618420 /FEA=EST /DB_XREF=gi:2505625 /DB_XREF=est:ng03a10.s1 /CLONE=IMAGE:928314 /UG=Hs.299254 Homo sapiens cDNA: FLJ23597 fis, clone LNG15281
225803_at_HG-U133B	FBXO32	F-box only protein 32	Consensus includes gb:AW006123 /FEA=EST /DB_XREF=gi:5854901 /DB_XREF=est:wz92f05.x1 /CLONE=IMAGE:2566305 /UG=Hs.61661 ESTs, Weakly similar to AF174605 1 F-box protein Fbx25 H.sapiens
225804_at_HG-U133B		Homo sapiens, clone MGC:32124 IMAGE:4877960, mRNA, complete cds	Consensus includes gb:BE044480 /FEA=EST /DB_XREF=gi:8361533 /DB_XREF=est:ho46b12.x1 /CLONE=IMAGE:3040415 /UG=Hs.75410 heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
225889_at_HG-U133B		Homo sapiens, Similar to AE-binding protein 2, clone MGC:23151 IMAGE:4843866, mRNA, complete cds	Consensus includes gb:BF475280 /FEA=EST /DB_XREF=gi:11546107 /DB_XREF=est:7q19h05.x1 /CLONE=IMAGE:3698936 /UG=Hs.285833 Homo sapiens cDNA: FLJ22135 fis, clone HEP20858
225897_at_HG-U133B		Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122	Consensus includes gb:AI709406 /FEA=EST /DB_XREF=gi:4999182 /DB_XREF=est:as37d05.x1 /CLONE=IMAGE:2319369 /UG=Hs.330716 Homo sapiens mRNA, 3UTR, up-regulated by BCG-CWS
225902_at_HG-U133B		ESTs, Weakly similar to SFR4_HUMAN SPLICING FACTOR, ARGININE/SERINE-RICH 4 [H.sapiens]	Consensus includes gb:AW194716 /FEA=EST /DB_XREF=gi:6473610 /DB_XREF=est:xn43c08.x1 /CLONE=IMAGE:2696462 /UG=Hs.35274 ESTs
225917_at_HG-U133B	DKFZp762B226	hypothetical protein DKFZp762B226	Consensus includes gb:AA766897 /FEA=EST /DB_XREF=gi:2818135 /DB_XREF=est:nz80c09.s1 /CLONE=IMAGE:1301776 /UG=Hs.122444 ESTs
225927_at_HG-U133B	MAP3K1	mitogen-activated protein kinase kinase kinase 1	Consensus includes gb:AA541479 /FEA=EST /DB_XREF=gi:2287913 /DB_XREF=est:ni89d12.s1 /CLONE=IMAGE:984023 /UG=Hs.170610 ESTs
225959_s_at_HG-U133B	NIN283	nerve injury gene 283	Consensus includes gb:BF432625 /FEA=EST /DB_XREF=gi:11444777 /DB_XREF=est:nac58b01.x1 /CLONE=IMAGE:3406417 /UG=Hs.49657 Homo sapiens mRNA; cDNA DKFZp547N084 (from clone DKFZp547N084)

226005_at_HG-U133B		Homo sapiens, clone IMAGE:4431242, mRNA	Consensus includes gb:BG170762 /FEA=EST /DB_XREF=gi:12677465 /DB_XREF=est:602323878F1 /CLONE=IMAGE:4426914 /UG=Hs.296273 ESTs
226008_at_HG-U133B	HCA4	hepatocellular carcinoma-associated protein HCA4	Consensus includes gb:AA627644 /FEA=EST /DB_XREF=gi:2539739 /DB_XREF=est:nq51d02.s1 /CLONE=IMAGE:1147395 /UG=Hs.94011 ESTs, Weakly similar to MGB4_HUMAN MELANOMA-ASSOCIATED ANTIGEN B4 H.sapiens
226013_at_HG-U133B		Homo sapiens cDNA FLJ13900 fis, clone THYRO1001746	Consensus includes gb:AW451452 /FEA=EST /DB_XREF=gi:6992228 /DB_XREF=est:UI-H-BI3-ali-d-02-0-UI.s1 /CLONE=IMAGE:2736818 /UG=Hs.89474 ADP-ribosylation factor 6
226014_at_HG-U133B	EIF3S5	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	Consensus includes gb:BF115977 /FEA=EST /DB_XREF=gi:10985453 /DB_XREF=est:7n75g02.x1 /CLONE=IMAGE:3570603 /UG=Hs.7811 eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)
226043_at_HG-U133B	AGS3	likely ortholog of rat activator of G-protein signaling 3	Consensus includes gb:AI242661 /FEA=EST /DB_XREF=gi:3838058 /DB_XREF=est:qi18a10.x1 /CLONE=IMAGE:1856826 /UG=Hs.239370 DKFZP727I051 protein
226060_at_HG-U133B	RFT1	putative endoplasmic reticulum multispan transmembrane protein	Consensus includes gb:BF475369 /FEA=EST /DB_XREF=gi:11546196 /DB_XREF=est:naa17f06.x1 /CLONE=IMAGE:3255298 /UG=Hs.324473 mitogen-activated protein kinase 1
226063_at_HG-U133B		Homo sapiens PP3781 mRNA, complete cds	Consensus includes gb:AA481141 /FEA=EST /DB_XREF=gi:2210693 /DB_XREF=est:aa34e11.s1 /CLONE=IMAGE:815180 /UG=Hs.4248 vav 2 oncogene
226066_at_HG-U133B			Consensus includes gb:AL117653.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586C0224 (from clone DKFZp586C0224). /FEA=mRNA /DB_XREF=gi:5912245 /UG=Hs.5884 Homo sapiens mRNA; cDNA DKFZp586C0224 (from clone DKFZp586C0224)
226101_at_HG-U133B		ESTs	Consensus includes gb:AI093546 /FEA=EST /DB_XREF=gi:3432522 /DB_XREF=est:qb08h06.x1 /CLONE=IMAGE:1695707 /UG=Hs.24379 MUM2 protein

226120_at_HG-U133B	LOC123016	hypothetical protein BC001563	Consensus includes gb:AW293939 /FEA=EST /DB_XREF=gi:6700575 /DB_XREF=est:UI-H-BW0-aik-b-11-0-UI.s1 /CLONE=IMAGE:2729444 /UG=Hs.55158 ESTs, Weakly similar to weak similarity to TPR domains C.elegans
226122_at_HG-U133B			Consensus includes gb:AL035086 /DEF=Human DNA sequence from clone 44A20 on chromosome 6q23.1-24.3. Contains a gene for a novel protein similar to MTHFD1 (methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthe... /FEA=mRNA_2 /DB_XREF=gi:4741478 /UG=Hs.51965 KIAA1209 protein
226147_s_at_HG-U133B		Homo sapiens cDNA: FLJ22667 fis, clone HSI08385	Consensus includes gb:AA838075 /FEA=EST /DB_XREF=gi:2913732 /DB_XREF=est:oe93h05.s1 /CLONE=IMAGE:1419225 /UG=Hs.205126 Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
226156_at_HG-U133B	AKT2	v-akt murine thymoma viral oncogene homolog 2	Consensus includes gb:BE866854 /FEA=EST /DB_XREF=gi:10315630 /DB_XREF=est:601442669F1 /CLONE=IMAGE:3847000 /UG=Hs.182278 calmodulin 2 (phosphorylase kinase, delta)
226165_at_HG-U133B	E2F5	E2F transcription factor 5, p130-binding	Consensus includes gb:BF674436 /FEA=EST /DB_XREF=gi:11948331 /DB_XREF=est:602137204F1 /CLONE=IMAGE:4273584 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen)
226188_at_HG-U133B			Consensus includes gb:AK025603.1 /DEF=Homo sapiens cDNA: FLJ21950 fis, clone HEP04949. /FEA=mRNA /DB_XREF=gi:10438171 /UG=Hs.7149 Homo sapiens cDNA: FLJ21950 fis, clone HEP04949
226190_at_HG-U133B		ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]	Consensus includes gb:BG029496 /FEA=EST /DB_XREF=gi:12418592 /DB_XREF=est:602297045F1 /CLONE=IMAGE:4391507 /UG=Hs.57776 ESTs
226210_s_at_HG-U133B		ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	Consensus includes gb:AI291123 /FEA=EST /DB_XREF=gi:3933897 /DB_XREF=est:qm15e11.x1 /CLONE=IMAGE:1881932 /UG=Hs.279789 histone deacetylase 3
226236_at_HG-U133B		ESTs, Weakly similar to A42442 integrin	Consensus includes gb:BF675218 /FEA=EST /DB_XREF=gi:11949113

		beta-1 chain, splice form beta-1-S [H.sapiens]	/DB_XREF=est:602138154F1 /CLONE=IMAGE:4274820 /UG=Hs.3709 low molecular mass ubiquinone-binding protein (9.5kD)
226244_at_HG-U133B		ESTs, Highly similar to AF161403 1 HSPC285 [H.sapiens]	Consensus includes gb:BF059395 /FEA=EST /DB_XREF=gi:10813213 /DB_XREF=est:7k59a05.x1 /CLONE=IMAGE:3479696 /UG=Hs.293815 Homo sapiens HSPC285 mRNA, partial cds
226247_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp434E1515 (from clone DKFZp434E1515)	Consensus includes gb:AI346026 /FEA=EST /DB_XREF=gi:4083232 /DB_XREF=est:qp48b01.x1 /CLONE=IMAGE:1926217 /UG=Hs.287830 Homo sapiens mRNA; cDNA DKFZp434E1515 (from clone DKFZp434E1515)
226250_at_HG-U133B		ESTs	Consensus includes gb:AU144961 /FEA=EST /DB_XREF=gi:11006482 /DB_XREF=est:AU144961 /CLONE=HEMBA1003463 /UG=Hs.104627 Homo sapiens cDNA FLJ10158 fis, clone HEMBA1003463
226252_at_HG-U133B		ESTs	Consensus includes gb:AA058578 /FEA=EST /DB_XREF=gi:1551385 /DB_XREF=est:zf55h02.s1 /CLONE=IMAGE:380883 /UG=Hs.104627 Homo sapiens cDNA FLJ10158 fis, clone HEMBA1003463
226258_at_HG-U133B		ESTs, Weakly similar to T08680 hypothetical protein DKFZp564P0622.1 [H.sapiens]	Consensus includes gb:BG031897 /FEA=EST /DB_XREF=gi:12422649 /DB_XREF=est:602300785F1 /CLONE=IMAGE:4402293 /UG=Hs.12296 ESTs, Weakly similar to T08680 hypothetical protein DKFZp564P0622.1 H.sapiens
226291_at_HG-U133B	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	Consensus includes gb:AB046783.1 /DEF=Homo sapiens mRNA for KIAA1563 protein, partial cds. /FEA=mRNA /GEN=KIAA1563 /PROD=KIAA1563 protein /DB_XREF=gi:10047190 /UG=Hs.27669 KIAA1563 protein
226299_at_HG-U133B	pknbeta	protein kinase PKNbeta	Consensus includes gb:NM_013355.1 /DEF=Homo sapiens protein kinase PKNbeta (pknbeta), mRNA. /FEA=CDS /GEN=pknbeta /PROD=protein kinase PKNbeta /DB_XREF=gi:7019488 /UG=Hs.44101 protein kinase PKNbeta /FL=gb:AB019692.1 gb:NM_013355.1
226301_at_HG-U133B	dJ55C23.6	dJ55C23.6 gene	Consensus includes gb:AV729072 /FEA=EST /DB_XREF=gi:10838493 /DB_XREF=est:AV729072 /CLONE=HTCBBG11 /UG=Hs.43627 SRY (sex determining region Y)-box 22

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226324_s_at_HG-U133B	SLB	selective LIM binding factor, rat homolog	Consensus includes gb:AB033005.1 /DEF=Homo sapiens mRNA for KIAA1179 protein, partial cds. /FEA=mRNA /GEN=KIAA1179 /PROD=KIAA1179 protein /DB_XREF=gi:6330238 /UG=Hs.127401 DKFZP434A163 protein; selective LIM binding factor, rat homolog
226326_at_HG-U133B		Homo sapiens cDNA FLJ31063 fis, clone HSYRA2001105	Consensus includes gb:AI798098 /FEA=EST /DB_XREF=gi:5363581 /DB_XREF=est:wh81c10.x1 /CLONE=IMAGE:2387154 /UG=Hs.11356 ESTs
226342_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp564N1063 (from clone DKFZp564N1063)	Consensus includes gb:AW593244 /FEA=EST /DB_XREF=gi:7280502 /DB_XREF=est:hg11e10.x1 /CLONE=IMAGE:2945322 /UG=Hs.236443 Homo sapiens mRNA; cDNA DKFZp564N1063 (from clone DKFZp564N1063)
226384_at_HG-U133B	HTPAP	HTPAP protein	Consensus includes gb:BE858787 /FEA=EST /DB_XREF=gi:10374184 /DB_XREF=est:7f95d03.x1 /CLONE=IMAGE:3304709 /UG=Hs.8841 ESTs
226408_at_HG-U133B	TEAD2	TEA domain family member 2	Consensus includes gb:AA905942 /FEA=EST /DB_XREF=gi:3041065 /DB_XREF=est:oj83b12.s1 /CLONE=IMAGE:1504895 /UG=Hs.153053 CD37 antigen
226435_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp434F053 (from clone DKFZp434F053)	Consensus includes gb:AU145309 /FEA=EST /DB_XREF=gi:11006830 /DB_XREF=est:AU145309 /CLONE=HEMBA1004460 /UG=Hs.301152 Homo sapiens mRNA; cDNA DKFZp434F053 (from clone DKFZp434F053)
226438_at_HG-U133B			Consensus includes gb:AK025100.1 /DEF=Homo sapiens cDNA: FLJ21447 fis, clone COL04468. /FEA=mRNA /DB_XREF=gi:10437548 /UG=Hs.44241 Homo sapiens cDNA: FLJ21447 fis, clone COL04468
226448_at_HG-U133B		Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete cds	Consensus includes gb:AI130705 /FEA=EST /DB_XREF=gi:3600721 /DB_XREF=est:qc12d05.x1 /CLONE=IMAGE:1709385 /UG=Hs.38516 ESTs, Weakly similar to A46302 PTB-associated splicing factor, long form H.sapiens
226450_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 926491	Consensus includes gb:AV703054 /FEA=EST /DB_XREF=gi:10719384 /DB_XREF=est:AV703054 /CLONE=ADBCMB05 /UG=Hs.98401 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 926491
226454_at_HG-U133B	LOC92979	hypothetical protein BC009489	Consensus includes gb:BF508604 /FEA=EST /DB_XREF=gi:11591902

			/DB_XREF=est:UI-H-BI4-aoo-f-08-0-UI.s1 /CLONE=IMAGE:3085598 /UG=Hs.65377 ESTs, Moderately similar to KIAA1399 protein H.sapiens
226496_at_HG-U133B		Homo sapiens, Similar to hypothetical protein FLJ22611, clone MGC:24716 IMAGE:4277726, mRNA, complete cds	Consensus includes gb:BG291039 /FEA=EST /DB_XREF=gi:13048607 /DB_XREF=est:602386841F1 /CLONE=IMAGE:4515730 /UG=Hs.27774 ESTs, Highly similar to AF161349 1 HSPC086 H.sapiens
226499_at_HG-U133B		ESTs	Consensus includes gb:W72331 /FEA=EST /DB_XREF=gi:1383086 /DB_XREF=est:zd62c11.s1 /CLONE=IMAGE:345236 /UG=Hs.21812 ESTs
226508_at_HG-U133B		Homo sapiens, clone IMAGE:4617948, mRNA	Consensus includes gb:AI042019 /FEA=EST /DB_XREF=gi:3281213 /DB_XREF=est:oy34h10.x1 /CLONE=IMAGE:1667779 /UG=Hs.25328 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
226531_at_HG-U133B	FLJ14466	hypothetical protein FLJ14466	Consensus includes gb:AL530596 /FEA=EST /DB_XREF=gi:12794089 /DB_XREF=est:AL530596 /CLONE=CS0DD008YD03 (5 prime) /UG=Hs.55148 ESTs
226538_at_HG-U133B	MAN2A1	mannosidase, alpha, class 2A, member 1	Consensus includes gb:AV700323 /FEA=EST /DB_XREF=gi:10302294 /DB_XREF=est:AV700323 /CLONE=GKCBSC12 /UG=Hs.63368 ESTs
226545_at_HG-U133B			Consensus includes gb:AL110152.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624). /FEA=mRNA /DB_XREF=gi:5817054 /UG=Hs.94030 Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624)
226546_at_HG-U133B		ESTs	Consensus includes gb:BG477064 /FEA=EST /DB_XREF=gi:13409343 /DB_XREF=est:602524421F1 /CLONE=IMAGE:4642660 /UG=Hs.90286 ESTs
226550_at_HG-U133B		ESTs	Consensus includes gb:AI672159 /FEA=EST /DB_XREF=gi:4851890 /DB_XREF=est:wa04c04.x1 /CLONE=IMAGE:2297094 /UG=Hs.91389 ESTs
226560_at_HG-U133B		ESTs	Consensus includes gb:AA576959 /FEA=EST /DB_XREF=gi:2354433 /DB_XREF=est:nm82d05.s1 /CLONE=IMAGE:1074729 /UG=Hs.13234 ESTs
226590_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1517766	Consensus includes gb:AA910497 /FEA=EST /DB_XREF=gi:3049787 /DB_XREF=est:ok44g07.s1 /CLONE=IMAGE:1516860 /UG=Hs.241334 ESTs

226607_at_HG-U133B	L3MBTL	l(3)mbt-like (Drosophila)	Consensus includes gb:AI498144 /FEA=EST /DB_XREF=gi:4390126 /DB_XREF=est:tm90c01.x1 /CLONE=IMAGE:2165376 /UG=Hs.323795 ESTs
226625_at_HG-U133B	TGFBR3	transforming growth factor, beta receptor III (betaglycan, 300kD)	Consensus includes gb:AW193698 /FEA=EST /DB_XREF=gi:6472397 /DB_XREF=est:xm29e06.x1 /CLONE=IMAGE:2685634 /UG=Hs.79059 transforming growth factor, beta receptor III (betaglycan, 300kD)
226634_at_HG-U133B		Homo sapiens cDNA FLJ12292 fis, clone MAMMA1001812	Consensus includes gb:AA776892 /FEA=EST /DB_XREF=gi:2836223 /DB_XREF=est:ac40c01.s1 /CLONE=IMAGE:858912 /UG=Hs.98613 Homo sapiens cDNA FLJ12292 fis, clone MAMMA1001812
226635_at_HG-U133B		Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133	Consensus includes gb:BG170478 /FEA=EST /DB_XREF=gi:12677181 /DB_XREF=est:602322848F1 /CLONE=IMAGE:4426211 /UG=Hs.94109 Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133
226641_at_HG-U133B		Homo sapiens cDNA FLJ11570 fis, clone HEMBA1003309	Consensus includes gb:AU157224 /FEA=EST /DB_XREF=gi:11018745 /DB_XREF=est:AU157224 /CLONE=PLACE1006780 /UG=Hs.11571 Homo sapiens cDNA FLJ11570 fis, clone HEMBA1003309
226646_at_HG-U133B	KLF2	Kruppel-like factor 2 (lung)	Consensus includes gb:AI831932 /FEA=EST /DB_XREF=gi:5452603 /DB_XREF=est:wh89b08.x1 /CLONE=IMAGE:2387895 /UG=Hs.107740 Kruppel-like factor 2 (lung)
226713_at_HG-U133B		Homo sapiens cDNA FLJ31090 fis, clone IMR321000102	Consensus includes gb:AI247881 /FEA=EST /DB_XREF=gi:3843278 /DB_XREF=est:qh58d08.x1 /CLONE=IMAGE:1848879 /UG=Hs.10198 ESTs
226726_at_HG-U133B	LOC129642	hypothetical protein BC016005	Consensus includes gb:W63676 /FEA=EST /DB_XREF=gi:1371257 /DB_XREF=est:zd30b03.s1 /CLONE=IMAGE:342125 /UG=Hs.15641 ESTs
226734_at_HG-U133B		Homo sapiens cDNA: FLJ23586 fis, clone LNG14376	Consensus includes gb:AW242220 /FEA=EST /DB_XREF=gi:6575974 /DB_XREF=est:xo23g03.x1 /CLONE=IMAGE:2704852 /UG=Hs.306915 Homo sapiens cDNA: FLJ23586 fis, clone LNG14376
226735_at_HG-U133B		Homo sapiens cytomegalovirus partial fusion receptor mRNA, partial cds	Consensus includes gb:AI239899 /FEA=EST /DB_XREF=gi:3835296 /DB_XREF=est:qh38e02.x1 /CLONE=IMAGE:1846970 /UG=Hs.25119 ESTs
226741_at_HG-U133B	LOC51234	hypothetical protein LOC51234	Consensus includes gb:N21320 /FEA=EST /DB_XREF=gi:1126490 /DB_XREF=est:yx53h07.s1 /CLONE=IMAGE:265501 /UG=Hs.250905

			hypothetical protein
226743_at_HG-U133B		Homo sapiens mRNA for FLJ00257 protein	Consensus includes gb:AW003459 /FEA=EST /DB_XREF=gi:5850364 /DB_XREF=est:wq66a10.x1 /CLONE=IMAGE:2476218 /UG=Hs.235709 Homo sapiens mRNA; cDNA DKFZp667B0711 (from clone DKFZp667B0711)
226751_at_HG-U133B	DKFZP566K1924	DKFZP566K1924 protein	Consensus includes gb:AW193693 /FEA=EST /DB_XREF=gi:6472392 /DB_XREF=est:xm29d12.x1 /CLONE=IMAGE:2685623 /UG=Hs.26358 DKFZP566K1924 protein
226783_at_HG-U133B		Homo sapiens cDNA FLJ14014 fis, clone HEMBA1000290	Consensus includes gb:AI762154 /FEA=EST /DB_XREF=gi:5177821 /DB_XREF=est:wh90e02.x1 /CLONE=IMAGE:2388026 /UG=Hs.54982 Homo sapiens cDNA FLJ14014 fis, clone HEMBA1000290
226795_at_HG-U133B		ESTs	Consensus includes gb:AW007739 /FEA=EST /DB_XREF=gi:5856517 /DB_XREF=est:wt68e08.x1 /CLONE=IMAGE:2512646 /UG=Hs.118913 ESTs
226818_at_HG-U133B		Homo sapiens mRNA for FLJ00239 protein	Consensus includes gb:T64884 /FEA=EST /DB_XREF=gi:673929 /DB_XREF=est:yd10b06.s1 /CLONE=IMAGE:66707 /UG=Hs.288581 Homo sapiens cDNA FLJ14296 fis, clone PLACE1008455
226841_at_HG-U133B		Homo sapiens mRNA for FLJ00239 protein	Consensus includes gb:BF590697 /FEA=EST /DB_XREF=gi:11682943 /DB_XREF=est:7h39d02.x1 /CLONE=IMAGE:3318339 /UG=Hs.288581 Homo sapiens cDNA FLJ14296 fis, clone PLACE1008455
226844_at_HG-U133B		ESTs	Consensus includes gb:AI375115 /FEA=EST /DB_XREF=gi:4175105 /DB_XREF=est:tc09e10.x1 /CLONE=IMAGE:2063370 /UG=Hs.293849 ESTs
226876_at_HG-U133B		Homo sapiens, clone IMAGE:4564684, mRNA, partial cds	Consensus includes gb:AI961778 /FEA=EST /DB_XREF=gi:5754491 /DB_XREF=est:wt67d10.x1 /CLONE=IMAGE:2512531 /UG=Hs.124707 ESTs
226878_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1964662	Consensus includes gb:AL581873 /FEA=EST /DB_XREF=gi:12949303 /DB_XREF=est:AL581873 /CLONE=CS0DG006YK17 (3 prime) /UG=Hs.11135 major histocompatibility complex, class II, DN alpha
226905_at_HG-U133B		Homo sapiens, clone IMAGE:4564684, mRNA, partial cds	Consensus includes gb:BG036514 /FEA=EST /DB_XREF=gi:12431757 /DB_XREF=est:602326471F1 /CLONE=IMAGE:4428089 /UG=Hs.187932 ESTs
226936_at_HG-U133B		ESTs	Consensus includes gb:BG492359 /FEA=EST /DB_XREF=gi:13453871

			/DB_XREF=est:602536279F1 /CLONE=IMAGE:4655418 /UG=Hs.35962 ESTs
226939_at_HG-U133B		ESTs	Consensus includes gb:AI202327 /FEA=EST /DB_XREF=gi:3754933 /DB_XREF=est:qs66a07.x1 /CLONE=IMAGE:1943028 /UG=Hs.44833 ESTs
226989_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp434P228 (from clone DKFZp434P228)	Consensus includes gb:BE855765 /FEA=EST /DB_XREF=gi:10367981 /DB_XREF=est:7g12d02.x1 /CLONE=IMAGE:3306243 /UG=Hs.108972 Homo sapiens mRNA; cDNA DKFZp434P228 (from clone DKFZp434P228)
227030_at_HG-U133B		ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]	Consensus includes gb:BG231773 /FEA=EST /DB_XREF=gi:12726899 /DB_XREF=est:naf30b12.x1 /CLONE=IMAGE:4142542 /UG=Hs.318893 ESTs
227038_at_HG-U133B		ESTs	Consensus includes gb:AI963083 /FEA=EST /DB_XREF=gi:5755796 /DB_XREF=est:wt27a06.x1 /CLONE=IMAGE:2508658 /UG=Hs.29567 ESTs
227039_at_HG-U133B	AKAP13	A kinase (PRKA) anchor protein 13	Consensus includes gb:AI674926 /FEA=EST /DB_XREF=gi:4875406 /DB_XREF=est:wc73g12.x1 /CLONE=IMAGE:2324326 /UG=Hs.29893 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 146397
227041_at_HG-U133B		Homo sapiens cDNA FLJ31513 fis, clone NT2RI1000127	Consensus includes gb:BE466145 /FEA=EST /DB_XREF=gi:9511920 /DB_XREF=est:hy10h02.x1 /CLONE=IMAGE:3196947 /UG=Hs.30977 ESTs
227046_at_HG-U133B	C17orf26	chromosome 17 open reading frame 26	Consensus includes gb:BF062384 /FEA=EST /DB_XREF=gi:10821294 /DB_XREF=est:7k77e12.x1 /CLONE=IMAGE:3481462 /UG=Hs.3402 ESTs
227047_x_at_HG-U133B	KIAA1538	KIAA1538 protein	Consensus includes gb:N63748 /FEA=EST /DB_XREF=gi:1211577 /DB_XREF=est:za18f10.s1 /CLONE=IMAGE:292939 /UG=Hs.35096 KIAA1538 protein
227056_at_HG-U133B	KIAA0141	KIAA0141 gene product	Consensus includes gb:AA181172 /FEA=EST /DB_XREF=gi:1764639 /DB_XREF=est:zp69f10.s1 /CLONE=IMAGE:625483 /UG=Hs.63510 KIAA0141 gene product
227065_at_HG-U133B	COL5A2	collagen, type V, alpha 2	Consensus includes gb:AA523105 /FEA=EST /DB_XREF=gi:2263817 /DB_XREF=est:ni44b04.s1 /CLONE=IMAGE:979663 /UG=Hs.82985 collagen, type V, alpha 2
227121_at_HG-U133B		ESTs	Consensus includes gb:BF476076 /FEA=EST /DB_XREF=gi:11546903

			/DB_XREF=est:hr77a10.x1 /CLONE=IMAGE:3134490 /UG=Hs.193784 Homo sapiens mRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)
227145_at_HG-U133B	LOXL4	lysyl oxidase-like 4	Consensus includes gb:AW190565 /FEA=EST /DB_XREF=gi:6465045 /DB_XREF=est:xl40b02.x1 /CLONE=IMAGE:2677131 /UG=Hs.306814 Homo sapiens cDNA: FLJ21889 fis, clone HEP03178
227146_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1644069	Consensus includes gb:AW873348 /FEA=EST /DB_XREF=gi:8007401 /DB_XREF=est:hl92d03.x1 /CLONE=IMAGE:3009413 /UG=Hs.30853 ESTs
227151_at_HG-U133B		Homo sapiens, clone MGC:32065 IMAGE:4869639, mRNA, complete cds	Consensus includes gb:BE464841 /FEA=EST /DB_XREF=gi:9510535 /DB_XREF=est:hs87g04.x1 /CLONE=IMAGE:3144246 /UG=Hs.32365 ESTs, Weakly similar to AF121859 1 sorting nexin 9 H.sapiens
227152_at_HG-U133B		Homo sapiens mRNA for KIAA1551 protein, partial cds	Consensus includes gb:AI979334 /FEA=EST /DB_XREF=gi:5804353 /DB_XREF=est:wu03g02.x1 /CLONE=IMAGE:2515922 /UG=Hs.323822 Homo sapiens mRNA for KIAA1551 protein, partial cds
227167_s_at_HG-U133B		Homo sapiens mesenchymal stem cell protein DSC96 mRNA, partial cds	Consensus includes gb:AW511319 /FEA=EST /DB_XREF=gi:7149397 /DB_XREF=est:hd45c10.x1 /CLONE=IMAGE:2912466 /UG=Hs.61426 ESTs
227173_s_at_HG-U133B	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	Consensus includes gb:AW450901 /FEA=EST /DB_XREF=gi:6991677 /DB_XREF=est:UI-H-BI3-all-d-04-0-UI.s1 /CLONE=IMAGE:2737183 /UG=Hs.88414 BTB and CNC homology 1, basic leucine zipper transcription factor 2
227189_at_HG-U133B	KIAA1599	KIAA1599 protein	Consensus includes gb:AB046819.1 /DEF=Homo sapiens mRNA for KIAA1599 protein, partial cds. /FEA=mRNA /GEN=KIAA1599 /PROD=KIAA1599 protein /DB_XREF=gi:10047272 /UG=Hs.285714 KIAA1599 protein
227198_at_HG-U133B		Homo sapiens cDNA FLJ30555 fis, clone BRAWH2003818	Consensus includes gb:AW085505 /FEA=EST /DB_XREF=gi:6040657 /DB_XREF=est:wy66c12.x1 /CLONE=IMAGE:2553526 /UG=Hs.125019 ESTs, Highly similar to KIAA0886 protein H.sapiens
227206_at_HG-U133B		Homo sapiens cDNA: FLJ21923 fis, clone HEP04081	Consensus includes gb:BE465462 /FEA=EST /DB_XREF=gi:9511237 /DB_XREF=est:hw20e10.x1 /CLONE=IMAGE:3183498 /UG=Hs.108593 Homo

			sapiens cDNA: FLJ21923 fis, clone HEP04081
227212_s_at_HG-U133B		Homo sapiens, Similar to RIKEN cDNA 3321402G02 gene, clone MGC:23929 IMAGE:4807540, mRNA, complete cds	Consensus includes gb:BE544837 /FEA=EST /DB_XREF=gi:9773482 /DB_XREF=est:601078832F1 /CLONE=IMAGE:3464694 /UG=Hs.119960 DKFZP727G051 protein
227224_at_HG-U133B		ESTs	Consensus includes gb:AW003297 /FEA=EST /DB_XREF=gi:5850213 /DB_XREF=est:wq65b01.x1 /CLONE=IMAGE:2476105 /UG=Hs.174104 ESTs
227230_s_at_HG-U133B	KIAA1211	KIAA1211 protein	Consensus includes gb:BE855799 /FEA=EST /DB_XREF=gi:10368049 /DB_XREF=est:7g07a07.x1 /CLONE=IMAGE:3305748 /UG=Hs.205293 KIAA1211 protein
227237_x_at_HG-U133B	KIAA1273	KIAA1273 protein	Consensus includes gb:AW593303 /FEA=EST /DB_XREF=gi:7280561 /DB_XREF=est:hg12g12.x1 /CLONE=IMAGE:2945446 /UG=Hs.23413 KIAA1273 protein
227242_s_at_HG-U133B		Homo sapiens cDNA FLJ31148 fis, clone IMR322001452	Consensus includes gb:BF592034 /FEA=EST /DB_XREF=gi:11684358 /DB_XREF=est:7n98c03.x1 /CLONE=IMAGE:3572716 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF)
227243_s_at_HG-U133B			Consensus includes gb:AL354950 /DEF=Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF) /FEA=mRNA_2 /DB_XREF=gi:9908994 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF)
227249_at_HG-U133B	NUDE1	LIS1-interacting protein NUDE1, rat homolog	Consensus includes gb:AI857685 /FEA=EST /DB_XREF=gi:5511301 /DB_XREF=est:wk96d11.x1 /CLONE=IMAGE:2423253 /UG=Hs.263925 LIS1-interacting protein NUDE1, rat homolog

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227261_at_HG-U133B	KLF12	Kruppel-like factor 12	Consensus includes gb:AA020010 /FEA=EST /DB_XREF=gi:1483683 /DB_XREF=est:ze62f10.s1 /CLONE=IMAGE:363595 /UG=Hs.294018 ESTs
227276_at_HG-U133B	TEM7R	tumor endothelial marker 7-related precursor	Consensus includes gb:AI264121 /FEA=EST /DB_XREF=gi:3872324 /DB_XREF=est:qk03a01.x1 /CLONE=IMAGE:1867848 /UG=Hs.33033 ESTs
227277_at_HG-U133B		ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J. SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:BG530089 /FEA=EST /DB_XREF=gi:13521626 /DB_XREF=est:602558749F1 /CLONE=IMAGE:4696597 /UG=Hs.33074 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
227279_at_HG-U133B	MGC15737	hypothetical protein MGC15737	Consensus includes gb:AA847654 /FEA=EST /DB_XREF=gi:2934172 /DB_XREF=est:oe49e05.s1 /CLONE=IMAGE:1414976 /UG=Hs.39122 ESTs, Weakly similar to CENB MOUSE MAJOR CENTROMERE AUTOANTIGEN B M.musculus
227299_at_HG-U133B	CCNI	cyclin I	Consensus includes gb:AA020986 /FEA=EST /DB_XREF=gi:1484739 /DB_XREF=est:ze65e08.s1 /CLONE=IMAGE:363878 /UG=Hs.79933 cyclin I
227326_at_HG-U133B		ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	Consensus includes gb:BE966768 /FEA=EST /DB_XREF=gi:11772526 /DB_XREF=est:601661268R1 /CLONE=IMAGE:3916097 /UG=Hs.11924 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
227336_at_HG-U133B	DTX1	deltex homolog 1 (Drosophila)	Consensus includes gb:AW576405 /FEA=EST /DB_XREF=gi:7247944 /DB_XREF=est:UI-HF-BN0-ala-c-10-0-UI.s1 /CLONE=IMAGE:3078907 /UG=Hs.124024 deltex (Drosophila) homolog 1 /FL=gb:AF053700.1 gb:NM_004416.1
227353_at_HG-U133B		Homo sapiens, clone MGC:40121 IMAGE:5216355, mRNA, complete cds	Consensus includes gb:BE671663 /FEA=EST /DB_XREF=gi:10032204 /DB_XREF=est:7a55g10.x1 /CLONE=IMAGE:3222690 /UG=Hs.15284 ESTs
227367_at_HG-U133B		ESTs	Consensus includes gb:AW976431 /FEA=EST /DB_XREF=gi:8167659 /DB_XREF=est:EST388540 /UG=Hs.184067 ESTs
227375_at_HG-U133B	DKFZP566D1346	hypothetical protein DKFZp566D1346	Consensus includes gb:AA152232 /FEA=EST /DB_XREF=gi:1721433 /DB_XREF=est:zo04c10.s1 /CLONE=IMAGE:566706 /UG=Hs.22612

			hypothetical protein DKFZp566D1346
227388_at_HG-U133B		Homo sapiens, similar to putative, clone IMAGE:5190302, mRNA, partial cds	Consensus includes gb:AA479016 /FEA=EST /DB_XREF=gi:2205379 /DB_XREF=est:zu39f03.s1 /CLONE=IMAGE:740381 /UG=Hs.26268 ESTs
227393_at_HG-U133B		Homo sapiens cDNA: FLJ23270 fis, clone COL10309, highly similar to HSU33271 Human normal keratinocyte mRNA	Consensus includes gb:AW084755 /FEA=EST /DB_XREF=gi:6039907 /DB_XREF=est:xc57d02.x1 /CLONE=IMAGE:2588355 /UG=Hs.288455 Homo sapiens cDNA: FLJ23270 fis, clone COL10309, highly similar to HSU33271 Human normal keratinocyte mRNA
227396_at_HG-U133B		ESTs	Consensus includes gb:AI631833 /FEA=EST /DB_XREF=gi:4683163 /DB_XREF=est:wa36f12.x1 /CLONE=IMAGE:2300207 /UG=Hs.306163 hypothetical protein AL110115
227407_at_HG-U133B		ESTs	Consensus includes gb:AI341541 /FEA=EST /DB_XREF=gi:4078468 /DB_XREF=est:qq94e07.x1 /CLONE=IMAGE:1939044 /UG=Hs.5324 hypothetical protein
227408_s_at_HG-U133B	MSTP043	MSTP043 protein	Consensus includes gb:AW008976 /FEA=EST /DB_XREF=gi:5857754 /DB_XREF=est:ws75f08.x1 /CLONE=IMAGE:2503815 /UG=Hs.42768 hypothetical protein DKFZp761O0113
227414_at_HG-U133B	DKFZp547E052	hypothetical protein DKFZp547E052	Consensus includes gb:AI889373 /FEA=EST /DB_XREF=gi:5594537 /DB_XREF=est:wm98d06.x1 /CLONE=IMAGE:2443979 /UG=Hs.49359 Homo sapiens mRNA; cDNA DKFZp547E052 (from clone DKFZp547E052)
227415_at_HG-U133B		Homo sapiens cDNA FLJ30865 fis, clone FEBRA2004099	Consensus includes gb:BF109303 /FEA=EST /DB_XREF=gi:10938993 /DB_XREF=est:7l61b10.x1 /CLONE=IMAGE:3525835 /UG=Hs.47094 ESTs
227478_at_HG-U133B		ESTs	Consensus includes gb:BF739885 /FEA=EST /DB_XREF=gi:12066549 /DB_XREF=est:7o40c11.x1 /CLONE=IMAGE:3576573 /UG=Hs.128052 ESTs
227497_at_HG-U133B		Homo sapiens cDNA FLJ11723 fis, clone HEMBA1005314	Consensus includes gb:BE326808 /FEA=EST /DB_XREF=gi:9200584 /DB_XREF=est:hr65b11.x1 /CLONE=IMAGE:3133341 /UG=Hs.196008 Homo sapiens cDNA FLJ11723 fis, clone HEMBA1005314
227525_at_HG-U133B	LOC113263	hypothetical protein BC011254	Consensus includes gb:AA058770 /FEA=EST /DB_XREF=gi:1551643 /DB_XREF=est:zf66a09.s1 /CLONE=IMAGE:381880 /UG=Hs.5510 ESTs

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227527_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp762P1915 (from clone DKFZp762P1915)	Consensus includes gb:AI394529 /FEA=EST /DB_XREF=gi:4224076 /DB_XREF=est:tf77b05.x1 /CLONE=IMAGE:2105265 /UG=Hs.3640 Homo sapiens mRNA; cDNA DKFZp762P1915 (from clone DKFZp762P1915)
227533_at_HG-U133B		ESTs	Consensus includes gb:AA732944 /FEA=EST /DB_XREF=gi:2754303 /DB_XREF=est:zg78d04.s1 /CLONE=IMAGE:399463 /UG=Hs.5415 ESTs
227556_at_HG-U133B	ATP1B1	ATPase, Na+/K+ transporting, beta 1 polypeptide	Consensus includes gb:AI094580 /FEA=EST /DB_XREF=gi:3433556 /DB_XREF=est:oy64c02.s1 /CLONE=IMAGE:1670594 /UG=Hs.78629 ATPase, Na+K+ transporting, beta 1 polypeptide
227568_at_HG-U133B			Consensus includes gb:AF131793.1 /DEF=Homo sapiens clone 25142 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4406621 /UG=Hs.25320 Homo sapiens clone 25142 mRNA sequence
227584_at_HG-U133B		ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:BF339566 /FEA=EST /DB_XREF=gi:11286021 /DB_XREF=est:602039032F1 /CLONE=IMAGE:4186999 /UG=Hs.112461 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
227587_at_HG-U133B	MGC15906	hypothetical protein MGC15906	Consensus includes gb:N46431 /FEA=EST /DB_XREF=gi:1187597 /DB_XREF=est:yy75g12.s1 /CLONE=IMAGE:279430 /UG=Hs.104938 ESTs, Weakly similar to T12492 hypothetical protein DKFZp434C151.1 H.sapiens
227606_s_at_HG-U133B	KIAA1373	KIAA1373 protein	Consensus includes gb:AI638611 /FEA=EST /DB_XREF=gi:4690845 /DB_XREF=est:tt31b11.x1 /CLONE=IMAGE:2242365 /UG=Hs.16229 KIAA1373 protein
227607_at_HG-U133B	KIAA1373	KIAA1373 protein	Consensus includes gb:AI638611 /FEA=EST /DB_XREF=gi:4690845 /DB_XREF=est:tt31b11.x1 /CLONE=IMAGE:2242365 /UG=Hs.16229 KIAA1373 protein
227627_at_HG-U133B	SGKL	serum/glucocorticoid regulated kinase-like	Consensus includes gb:AV690866 /FEA=EST /DB_XREF=gi:10292729 /DB_XREF=est:AV690866 /CLONE=GKCCXF03 /UG=Hs.24131 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens

227646_at_HG-U133B	EBF	early B-cell factor	Consensus includes gb:BG435302 /FEA=EST /DB_XREF=gi:13341808 /DB_XREF=est:602508050F1 /CLONE=IMAGE:4605252 /UG=Hs.32425 ESTs
227670_at_HG-U133B		Homo sapiens cDNA FLJ31529 fis, clone NT2RI2000421, moderately similar to ZINC FINGER PROTEIN 75	Consensus includes gb:N74222 /FEA=EST /DB_XREF=gi:1231507 /DB_XREF=est:za59d08.s1 /CLONE=IMAGE:296847 /UG=Hs.50456 ESTs, Moderately similar to ZN75_HUMAN ZINC FINGER PROTEIN 75 H.sapiens
227680_at_HG-U133B		ESTs	Consensus includes gb:AI057121 /FEA=EST /DB_XREF=gi:3330997 /DB_XREF=est:oz23h05.x1 /CLONE=IMAGE:1676217 /UG=Hs.72087 ESTs
227700_x_at_HG-U133B	FLJ10709	hypothetical protein FLJ10709	Consensus includes gb:AL043161 /FEA=EST /DB_XREF=gi:5935774 /DB_XREF=est:DKFZp434F0123_s1 /CLONE=DKFZp434F0123 /UG=Hs.273357 hypothetical protein FLJ10709
227701_at_HG-U133B			Consensus includes gb:AK024739.1 /DEF=Homo sapiens cDNA: FLJ21086 fis, clone CAS03272. /FEA=mRNA /DB_XREF=gi:10437103 /UG=Hs.28538 Homo sapiens cDNA: FLJ21086 fis, clone CAS03272
227709_at_HG-U133B	RCN1	reticulocalbin 1, EF-hand calcium binding domain	Consensus includes gb:BE670492 /FEA=EST /DB_XREF=gi:10031033 /DB_XREF=est:7e47g06.x1 /CLONE=IMAGE:3285658 /UG=Hs.167791 reticulocalbin 1, EF-hand calcium binding domain
227729_at_HG-U133B		ESTs	Consensus includes gb:AL038092 /FEA=EST /DB_XREF=gi:5407396 /DB_XREF=est:DKFZp566L011_s1 /CLONE=DKFZp566L011 /UG=Hs.107265 ESTs
227744_s_at_HG-U133B	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD)	Consensus includes gb:AW005670 /FEA=EST /DB_XREF=gi:5854448 /DB_XREF=est:wz88f04.x1 /CLONE=IMAGE:2565919 /UG=Hs.303627 heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD)
227749_at_HG-U133B		ESTs	Consensus includes gb:AI703496 /FEA=EST /DB_XREF=gi:4991396 /DB_XREF=est:we24h07.x1 /CLONE=IMAGE:2342077 /UG=Hs.15085 ESTs
227767_at_HG-U133B	CSNK1G3	casein kinase 1, gamma 3	Consensus includes gb:AI073822 /FEA=EST /DB_XREF=gi:3400466 /DB_XREF=est:qa31h03.s1 /CLONE=IMAGE:1688405 /UG=Hs.30164 ESTs
227786_at_HG-U133B	TRAP25	TRAP/Mediator complex component	Consensus includes gb:AI026938 /FEA=EST /DB_XREF=gi:3244454

			/DB_XREF=est:ov82f06.x1 /CLONE=IMAGE:1643843 /UG=Hs.298229 prefoldin 2
227812_at_HG-U133B		Homo sapiens clone HB-2 mRNA sequence	Consensus includes gb:BF432648 /FEA=EST /DB_XREF=gi:11444811 /DB_XREF=est:nac58e04.x1 /CLONE=IMAGE:3406567 /UG=Hs.48376 Homo sapiens clone HB-2 mRNA sequence
227817_at_HG-U133B		ESTs	Consensus includes gb:R51324 /FEA=EST /DB_XREF=gi:813226 /DB_XREF=est:yg72g01.s1 /CLONE=IMAGE:38786 /UG=Hs.6749 ESTs
227829_at_HG-U133B		Homo sapiens cDNA FLJ31267 fis, clone KIDNE2006053, moderately similar to Mus musculus mRNA for acetylglucosaminyltransferase-like protein	Consensus includes gb:AW272738 /FEA=EST /DB_XREF=gi:6659695 /DB_XREF=est:xu22b04.x1 /CLONE=IMAGE:2800879 /UG=Hs.86543 ESTs, Weakly similar to T00256 hypothetical protein KIAA0609 H.sapiens
227867_at_HG-U133B		ESTs, Weakly similar to T18967 hypothetical protein C05G5.5 - Caenorhabditis elegans [C.elegans]	Consensus includes gb:AA005361 /FEA=EST /DB_XREF=gi:1448394 /DB_XREF=est:zh97b01.s1 /CLONE=IMAGE:429193 /UG=Hs.36723 ESTs, Weakly similar to cDNA EST yk414c9.3 comes from this gene C.elegans
227900_at_HG-U133B		ESTs	Consensus includes gb:AV701750 /FEA=EST /DB_XREF=gi:10718080 /DB_XREF=est:AV701750 /CLONE=ADBANA03 /UG=Hs.144139 ESTs
227936_at_HG-U133B		Homo sapiens cDNA FLJ32370 fis, clone PUAEN1000322	Consensus includes gb:AI671172 /FEA=EST /DB_XREF=gi:4850903 /DB_XREF=est:wb14c01.x1 /CLONE=IMAGE:2305632 /UG=Hs.280858 ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 H.sapiens
227988_s_at_HG-U133B	CHAC	chorea acanthocytosis	Consensus includes gb:AW629014 /FEA=EST /DB_XREF=gi:7375804 /DB_XREF=est:hi46e01.x1 /CLONE=IMAGE:2975352 /UG=Hs.65919 ESTs
227998_at_HG-U133B	MGC17528	hypothetical protein MGC17528	Consensus includes gb:AA045184 /FEA=EST /DB_XREF=gi:1523386 /DB_XREF=est:zk66c01.s1 /CLONE=IMAGE:487776 /UG=Hs.738 ribosomal protein L14
227999_at_HG-U133B	LOC170394	hypothetical protein BC011630	Consensus includes gb:AI290476 /FEA=EST /DB_XREF=gi:3933250 /DB_XREF=est:ql98b08.x1 /CLONE=IMAGE:1880343 /UG=Hs.87597 ESTs

228003_at_HG-U133B		ESTs	Consensus includes gb:AW294640 /FEA=EST /DB_XREF=gi:6701276 /DB_XREF=est:UI-H-BW0-ail-c-06-0-UI.s1 /CLONE=IMAGE:2729483 /UG=Hs.95898 ESTs
228007_at_HG-U133B			Consensus includes gb:AL133101.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434O0921 (from clone DKFZp434O0921). /FEA=mRNA /DB_XREF=gi:6453584 /UG=Hs.99508 Homo sapiens mRNA; cDNA DKFZp434O0921 (from clone DKFZp434O0921)
228024_at_HG-U133B	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	Consensus includes gb:AW028100 /FEA=EST /DB_XREF=gi:5886856 /DB_XREF=est:ws63h07.x1 /CLONE=IMAGE:2501917 /UG=Hs.290855 ESTs
228029_at_HG-U133B	KIAA1982	KIAA1982 protein	Consensus includes gb:AW513477 /FEA=EST /DB_XREF=gi:7151555 /DB_XREF=est:xo84f10.x1 /CLONE=IMAGE:2737579 /UG=Hs.22969. ESTs
228055_at_HG-U133B		Homo sapiens napsin 2 precursor, mRNA, partial sequence	Consensus includes gb:AI763426 /FEA=EST /DB_XREF=gi:5179093 /DB_XREF=est:wh92c02.x1 /CLONE=IMAGE:2388194 /UG=Hs.104433 Homo sapiens napsin 2 precursor, mRNA, partial sequence
228058_at_HG-U133B		Homo sapiens, clone MGC:9575 IMAGE:3879368, mRNA, complete cds	Consensus includes gb:AI559190 /FEA=EST /DB_XREF=gi:4509395 /DB_XREF=est:tq42g08.x1 /CLONE=IMAGE:2211518 /UG=Hs.105887 ESTs, Weakly similar to Homolog of rat Zymogen granule membrane protein H.sapiens
228083_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp434I1216 (from clone DKFZp434I1216)	Consensus includes gb:AI433691 /FEA=EST /DB_XREF=gi:4290952 /DB_XREF=est:ti88d06.x1 /CLONE=IMAGE:2139083 /UG=Hs.13768 Homo sapiens mRNA; cDNA DKFZp434I1216 (from clone DKFZp434I1216)
228092_at_HG-U133B		Homo sapiens, Similar to cAMP responsive element modulator, clone MGC:17881 IMAGE:3907190, mRNA, complete cds	Consensus includes gb:AL552470 /FEA=EST /DB_XREF=gi:12891398 /DB_XREF=est:AL552470 /CLONE=CS0DI070YJ22 (5 prime) /UG=Hs.155924 cAMP responsive element modulator
228174_at_HG-U133B		ESTs	Consensus includes gb:AI832363 /FEA=EST /DB_XREF=gi:5454275 /DB_XREF=est:at66c06.x1 /CLONE=IMAGE:2376970 /UG=Hs.48610 ESTs
228176_at_HG-U133B		ESTs, Moderately similar to hypothetical	Consensus includes gb:AA534817 /FEA=EST /DB_XREF=gi:2279070

		protein FLJ20489 [Homo sapiens] [H.sapiens]	/DB_XREF=est:nf81h07.s1 /CLONE=IMAGE:926365 /UG=Hs.55902 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
228183_s_at_HG-U133B	MGC4189	hypothetical protein MGC4189	Consensus includes gb:BF342428 /FEA=EST /DB_XREF=gi:11289441 /DB_XREF=est:602013931F1 /CLONE=IMAGE:4149702 /UG=Hs.78614 complement component 1, q subcomponent binding protein
228193_s_at_HG-U133B	RGC32	RGC32 protein	Consensus includes gb:AI744499 /FEA=EST /DB_XREF=gi:5112787 /DB_XREF=est:wg09a04.x1 /CLONE=IMAGE:2364558 /UG=Hs.76640 RGC32 protein
228211_at_HG-U133B		ESTs	Consensus includes gb:AI693726 /FEA=EST /DB_XREF=gi:4971066 /DB_XREF=est:wd44f03.x1 /CLONE=IMAGE:2331005 /UG=Hs.44367 ESTs
228242_at_HG-U133B		ESTs	Consensus includes gb:BF055201 /FEA=EST /DB_XREF=gi:10809097 /DB_XREF=est:7j76d08.x1 /CLONE=IMAGE:3392367 /UG=Hs.101624 ESTs
228266_s_at_HG-U133B	CGI-142	hepatoma-derived growth factor 2	Consensus includes gb:BE703418 /FEA=EST /DB_XREF=gi:10091160 /DB_XREF=est:MR2-NN1111-070800-008-a03 /UG=Hs.127842 CGI-142
228298_at_HG-U133B	LOC91523	hypothetical protein BC008360	Consensus includes gb:BF056901 /FEA=EST /DB_XREF=gi:10810797 /DB_XREF=est:7k11d11.x1 /CLONE=IMAGE:3444140 /UG=Hs.181261 ESTs
228328_at_HG-U133B		ESTs	Consensus includes gb:AI982758 /FEA=EST /DB_XREF=gi:5809977 /DB_XREF=est:wz28h04.x1 /CLONE=IMAGE:2559415 /UG=Hs.7326 ESTs
228343_at_HG-U133B	POU2F2	POU domain, class 2, transcription factor 2	Consensus includes gb:AA805754 /FEA=EST /DB_XREF=gi:2874504 /DB_XREF=est:ns43e05.s1 /CLONE=IMAGE:1186400 /UG=Hs.333040 ESTs
228345_at_HG-U133B		ESTs	Consensus includes gb:AI745136 /FEA=EST /DB_XREF=gi:5113424 /DB_XREF=est:tr19f03.x1 /CLONE=IMAGE:2218781 /UG=Hs.34656 ESTs
228361_at_HG-U133B		Homo sapiens, Similar to hypothetical protein PRO1722, clone MGC:15692 IMAGE:3351479, mRNA, complete cds	Consensus includes gb:AL561296 /FEA=EST /DB_XREF=gi:12908585 /DB_XREF=est:AL561296 /CLONE=CS0DL010YF15 (5 prime) /UG=Hs.49047 ESTs
228377_at_HG-U133B	KIAA1384	KIAA1384 protein	Consensus includes gb:AB037805.1 /DEF=Homo sapiens mRNA for KIAA1384 protein, partial cds. /FEA=mRNA /GEN=KIAA1384

			/PROD=KIAA1384 protein /DB_XREF=gi:7243148 /UG=Hs.88442 _KIAA1384 protein
228379_at_HG-U133B		ESTs	Consensus includes gb:AW071847 /FEA=EST /DB_XREF=gi:6026772 /DB_XREF=est:ws54d05.x1 /CLONE=IMAGE:2501001 /UG=Hs.75968 thymosin, beta 4, X chromosome
228390_at_HG-U133B		ESTs	Consensus includes gb:AA489100 /FEA=EST /DB_XREF=gi:2218702 /DB_XREF=est:aa56h10.s1 /CLONE=IMAGE:824995 /UG=Hs.184430 ESTs
228408_s_at_HG-U133B	FLJ10498	hypothetical protein FLJ10498	Consensus includes gb:AI738666 /FEA=EST /DB_XREF=gi:5100647 /DB_XREF=est:wi11g03.x1 /CLONE=IMAGE:2389972 /UG=Hs.109045 hypothetical protein FLJ10498
228410_at_HG-U133B	GAB3	GRB2-associated binding protein 3	Consensus includes gb:AA495984 /FEA=EST /DB_XREF=gi:2229305 /DB_XREF=est:zw06d08.s1 /CLONE=IMAGE:768495 /UG=Hs.102630 ESTs
228424_at_HG-U133B	NAALADASEL	N-acetylated alpha-linked acidic dipeptidase-like; ILEAL DIPEPTIDYLPEPTIDASE	Consensus includes gb:AW170591 /FEA=EST /DB_XREF=gi:6402116 /DB_XREF=est:xn64c01.x1 /CLONE=IMAGE:2698464 /UG=Hs.13967 ESTs, Highly similar to NAALADase L protein H.sapiens
228471_at_HG-U133B		ESTs	Consensus includes gb:AA744636 /FEA=EST /DB_XREF=gi:2783400 /DB_XREF=est:ny79e02.s1 /CLONE=IMAGE:1284506 /UG=Hs.145053 ESTs
228476_at_HG-U133B	KIAA1407	KIAA1407 protein	Consensus includes gb:AW193515 /FEA=EST /DB_XREF=gi:6472214 /DB_XREF=est:xm17c03.x1 /CLONE=IMAGE:2684452 /UG=Hs.15370 KIAA1407 protein
228485_s_at_HG-U133B	CDW92	CDw92 antigen	Consensus includes gb:AW165999 /FEA=EST /DB_XREF=gi:6397524 /DB_XREF=est:xf43e09.x1 /CLONE=IMAGE:2620840 /UG=Hs.179902 transporter-like protein
228496_s_at_HG-U133B	CRIM1	cysteine-rich motor neuron 1	Consensus includes gb:AW243081 /FEA=EST /DB_XREF=gi:6576874 /DB_XREF=est:xm92b10.x1 /CLONE=IMAGE:2691643 /UG=Hs.19280 cysteine-rich motor neuron 1
228497_at_HG-U133B	DKFZp761G0313	hypothetical protein DKFZp761G0313	Consensus includes gb:AI279062 /FEA=EST /DB_XREF=gi:3917296 /DB_XREF=est:qm23a06.x1 /CLONE=IMAGE:1882642 /UG=Hs.21710

			hypothetical protein DKFZp761G0313
228518_at_HG-U133B	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marker)	Consensus includes gb:AW575313 /FEA=EST /DB_XREF=gi:7246852 /DB_XREF=est:UI-HF-BL0-acs-c-12-0-UI.s1 /CLONE=IMAGE:3060095 /UG=Hs.278586 KIAA1108 protein
228551_at_HG-U133B			Consensus includes gb:AL137364.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone DKFZp434E0626). /FEA=mRNA /DB_XREF=gi:6807885 /UG=Hs.30957 Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone DKFZp434E0626)
228555_at_HG-U133B		ESTs	Consensus includes gb:AA029441 /FEA=EST /DB_XREF=gi:1496854 /DB_XREF=est:ze96c08.s1 /CLONE=IMAGE:366830 /UG=Hs.32553 ESTs
228570_at_HG-U133B		ESTs	Consensus includes gb:BF510581 /FEA=EST /DB_XREF=gi:11593879 /DB_XREF=est:UI-H-BI4-apk-b-03-0-UI.s1 /CLONE=IMAGE:3087676 /UG=Hs.5027 ESTs
228592_at_HG-U133B		ESTs	Consensus includes gb:AW474852 /FEA=EST /DB_XREF=gi:7044958 /DB_XREF=est:xy07d08.x1 /CLONE=IMAGE:2852463 /UG=Hs.86693 ESTs
228599_at_HG-U133B		ESTs	Consensus includes gb:AI862674 /FEA=EST /DB_XREF=gi:5526781 /DB_XREF=est:wj27f01.x1 /CLONE=IMAGE:2404057 /UG=Hs.86693 ESTs
228652_at_HG-U133B		ESTs, Weakly similar to Z189_HUMAN ZINC FINGER PROTEIN 189 [H.sapiens]	Consensus includes gb:AI279532 /FEA=EST /DB_XREF=gi:3917766 /DB_XREF=est:ql51f03.x1 /CLONE=IMAGE:1875869 /UG=Hs.109540 ESTs, Weakly similar to Z189_HUMAN ZINC FINGER PROTEIN 189 H.sapiens
228660_x_at_HG-U133B	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	Consensus includes gb:AA523537 /FEA=EST /DB_XREF=gi:2264249 /DB_XREF=est:ng30e03.s1 /CLONE=IMAGE:936316 /UG=Hs.117612 hypothetical protein PRO2353
228693_at_HG-U133B		Homo sapiens cDNA FLJ31090 fis, clone IMR321000102	Consensus includes gb:AI681307 /FEA=EST /DB_XREF=gi:4891489 /DB_XREF=est:tx45g07.x1 /CLONE=IMAGE:2272572 /UG=Hs.166674 ESTs
228708_at_HG-U133B		Homo sapiens clone 25194 mRNA sequence	Consensus includes gb:BF438386 /FEA=EST /DB_XREF=gi:11450903 /DB_XREF=est:7q08g08.x1 /CLONE=IMAGE:3677007 /UG=Hs.25318 Homo

			sapiens clone 25194 mRNA sequence
228737_at_HG-U133B	C20orf100	chromosome 20 open reading frame 100	Consensus includes gb:AA211909 /FEA=EST /DB_XREF=gi:1810563 /DB_XREF=est:zq85a03.s1 /CLONE=IMAGE:648364 /UG=Hs.26608 ESTs
228766_at_HG-U133B		ESTs, Weakly similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precusor [Homo sapiens] [H.sapiens]	Consensus includes gb:AW299226 /FEA=EST /DB_XREF=gi:6708903 /DB_XREF=est:xs48a10.x1 /CLONE=IMAGE:2772858 /UG=Hs.325823 ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
228827_at_HG-U133B		Homo sapiens clone 25023 mRNA sequence	Consensus includes gb:AI217416 /FEA=EST /DB_XREF=gi:3797231 /DB_XREF=est:qh22h01.x1 /CLONE=IMAGE:1845457 /UG=Hs.90858 Homo sapiens clone 25023 mRNA sequence
228834_at_HG-U133B	TOB1	transducer of ERBB2, 1	Consensus includes gb:BF240286 /FEA=EST /DB_XREF=gi:11154209 /DB_XREF=est:601905816F1 /CLONE=IMAGE:4133978 /UG=Hs.178137 transducer of ERBB2, 1
228904_at_HG-U133B		ESTs	Consensus includes gb:AW510657 /FEA=EST /DB_XREF=gi:7148735 /DB_XREF=est:hc89b09.x1 /CLONE=IMAGE:2907161 /UG=Hs.156044 ESTs
228916_at_HG-U133B		Homo sapiens cDNA FLJ32343 fis, clone PROST2006260, weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 4	Consensus includes gb:BE857467 /FEA=EST /DB_XREF=gi:10371522 /DB_XREF=est:7f97h11.x1 /CLONE=IMAGE:3304965 /UG=Hs.24380 ESTs
228984_at_HG-U133B	KIAA1394	KIAA1394 protein	Consensus includes gb:AB037815.1 /DEF=Homo sapiens mRNA for KIAA1394 protein, partial cds. /FEA=mRNA /GEN=KIAA1394 /PROD=KIAA1394 protein /DB_XREF=gi:7243168 /UG=Hs.32156 KIAA1394 protein
228988_at_HG-U133B	ZNF6	zinc finger protein 6 (CMPX1)	Consensus includes gb:AU157017 /FEA=EST /DB_XREF=gi:11018538 /DB_XREF=est:AU157017 /CLONE=PLACE1005740 /UG=Hs.323950 zinc finger protein 6 (CMPX1)
229001_at_HG-U133B		Homo sapiens mRNA for FLJ00089 protein, partial cds	Consensus includes gb:BE259127 /FEA=EST /DB_XREF=gi:9129625 /DB_XREF=est:601115521F1 /CLONE=IMAGE:3356236 /UG=Hs.39911 Homo

			sapiens mRNA for FLJ00089 protein, partial cds
229003_x_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1622425	Consensus includes gb:AI095583 /FEA=EST /DB_XREF=gi:3434559 /DB_XREF=est:qb24a02.x1 /CLONE=IMAGE:1697162 /UG=Hs.38509 ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR H.sapiens
229061_s_at_HG-U133B	SLC25A13	solute carrier family 25, member 13 (citrin)	Consensus includes gb:AW268880 /FEA=EST /DB_XREF=gi:6655910 /DB_XREF=est:xv48f03.x1 /CLONE=IMAGE:2816381 /UG=Hs.9599 solute carrier family 25, member 13 (citrin)
229070_at_HG-U133B	MGC12335	hypothetical protein MGC12335	Consensus includes gb:AA470369 /FEA=EST /DB_XREF=gi:2197678 /DB_XREF=est:ne10a12.s1 /CLONE=IMAGE:880798 /UG=Hs.72115 ESTs
229072_at_HG-U133B		ESTs	Consensus includes gb:BF968097 /FEA=EST /DB_XREF=gi:12335312 /DB_XREF=est:602269272F1 /CLONE=IMAGE:4357504 /UG=Hs.26339 ESTs
229138_at_HG-U133B		ESTs	Consensus includes gb:AV747166 /FEA=EST /DB_XREF=gi:10905014 /DB_XREF=est:AV747166 /CLONE=NPCATH06 /UG=Hs.59698 ESTs
229168_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp434K0621 (from clone DKFZp434K0621); partial cds	Consensus includes gb:AI690433 /FEA=EST /DB_XREF=gi:4901735 /DB_XREF=est:tx87f11.x1 /CLONE=IMAGE:2276589 /UG=Hs.55407 Homo sapiens mRNA; cDNA DKFZp434K0621 (from clone DKFZp434K0621); partial cds
229194_at_HG-U133B		ESTs, Weakly similar to JC4296 ring finger protein - fruit fly [D.melanogaster]	Consensus includes gb:AL045882 /FEA=EST /DB_XREF=gi:5433989 /DB_XREF=est:DKFZp434J086_s1 /CLONE=DKFZp434J086 /UG=Hs.126695 ESTs
229232_at_HG-U133B		ESTs, Moderately similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precusor [Homo sapiens] [H.sapiens]	Consensus includes gb:AW135740 /FEA=EST /DB_XREF=gi:6139873 /DB_XREF=est:UI-H-BI1-acf-a-08-0-UI.s1 /CLONE=IMAGE:2714007 /UG=Hs.194071 ESTs, Weakly similar to unnamed protein product H.sapiens
229253_at_HG-U133B	CTMP	C-terminal modulator protein	Consensus includes gb:AI184512 /FEA=EST /DB_XREF=gi:3735150 /DB_XREF=est:qf29e10.x1 /CLONE=IMAGE:1751466 /UG=Hs.266155 ESTs
229280_s_at_HG-			Consensus includes gb:AK026189.1 /DEF=Homo sapiens cDNA: FLJ22536

U133B			fis, clone HRC13155. /FEA=mRNA /DB_XREF=gi:10438959 /UG=Hs.43266 Homo sapiens cDNA: FLJ22536 fis, clone HRC13155
229302_at_HG-U133B		ESTs	Consensus includes gb:AA058832 /FEA=EST /DB_XREF=gi:1551675 /DB_XREF=est:zf65f12.s1 /CLONE=IMAGE:381839 /UG=Hs.40808 ESTs
229310_at_HG-U133B	KIAA1921	KIAA1921 protein	Consensus includes gb:BE465475 /FEA=EST /DB_XREF=gi:9511250 /DB_XREF=est:hw20g02.x1 /CLONE=IMAGE:3183506 /UG=Hs.272572 hemoglobin, alpha 2
229344_x_at_HG-U133B	KIAA1238	KIAA1238 protein	Consensus includes gb:AW135012 /FEA=EST /DB_XREF=gi:6138558 /DB_XREF=est:UI-H-BI1-abt-d-05-0-UI.s1 /CLONE=IMAGE:2712993 /UG=Hs.236463 KIAA1238 protein
229362_at_HG-U133B		ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic [H.sapiens]	Consensus includes gb:AA878516 /FEA=EST /DB_XREF=gi:2987481 /DB_XREF=est:oj19b08.s1 /CLONE=IMAGE:1492599 /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic H.sapiens
229368_s_at_HG-U133B	ZNF216	zinc finger protein 216	Consensus includes gb:AI658995 /FEA=EST /DB_XREF=gi:4762565 /DB_XREF=est:tu23c12.x1 /CLONE=IMAGE:2251894 /UG=Hs.3776 zinc finger protein 216
229383_at_HG-U133B		ESTs	Consensus includes gb:AI707896 /FEA=EST /DB_XREF=gi:4997672 /DB_XREF=est:as34a10.x1 /CLONE=IMAGE:2319066 /UG=Hs.107369 ESTs
229420_at_HG-U133B	RPL23A	ribosomal protein L23a	Consensus includes gb:AI557425 /FEA=EST /DB_XREF=gi:4489788 /DB_XREF=est:PT2.1_7_B11.r /UG=Hs.184776 ribosomal protein L23a
229487_at_HG-U133B		ESTs	Consensus includes gb:W73890 /FEA=EST /DB_XREF=gi:1382285 /DB_XREF=est:zd65h02.s1 /CLONE=IMAGE:345555 /UG=Hs.120785 ESTs
229513_at_HG-U133B			Consensus includes gb:AK025613.1 /DEF=Homo sapiens cDNA: FLJ21960 fis, clone HEP05517. /FEA=mRNA /DB_XREF=gi:10438184 /UG=Hs.287687 Homo sapiens cDNA: FLJ21960 fis, clone HEP05517
229575_at_HG-U133B		ESTs	Consensus includes gb:AW271460 /FEA=EST /DB_XREF=gi:6658490 /DB_XREF=est:xs14g08.x1 /CLONE=IMAGE:2769662 /UG=Hs.122642 ESTs
229621_x_at_HG-		Homo sapiens cDNA FLJ31148 fis, clone	Consensus includes gb:N93227 /FEA=EST /DB_XREF=gi:1265536

U133B		IMR322001452	/DB_XREF=est:zb29d08.s1 /CLONE=IMAGE:305007 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF)
229637_at_HG-U133B		ESTs	Consensus includes gb:AA166891 /FEA=EST /DB_XREF=gi:1745055 /DB_XREF=est:zq39d08.s1 /CLONE=IMAGE:632079 /UG=Hs.25768 ESTs
229659_s_at_HG-U133B		Homo sapiens cDNA: FLJ22667 fis, clone HSI08385	Consensus includes gb:BE501712 /FEA=EST /DB_XREF=gi:9704120 /DB_XREF=est:hw34c04.x1 /CLONE=IMAGE:3184806 /UG=Hs.205126 Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
229681_at_HG-U133B		ESTs	Consensus includes gb:AW449289 /FEA=EST /DB_XREF=gi:6990065 /DB_XREF=est:UI-H-BI3-akh-f-09-0-UI.s1 /CLONE=IMAGE:2734241 /UG=Hs.17551 ESTs
229711_s_at_HG-U133B	MGC5370	hypothetical protein MGC5370	Consensus includes gb:AA902480 /FEA=EST /DB_XREF=gi:3037603 /DB_XREF=est:ok70h12.s1 /CLONE=IMAGE:1519367 /UG=Hs.332938 carboxypeptidase M
229722_at_HG-U133B	HSPC072	HSPC072 protein	Consensus includes gb:BF115733 /FEA=EST /DB_XREF=gi:10985209 /DB_XREF=est:7n64a10.x1 /CLONE=IMAGE:3569202 /UG=Hs.87329 HSPC072 protein
229745_x_at_HG-U133B		Homo sapiens, Similar to thymus expressed gene 3, clone MGC:15476 IMAGE:2967514, mRNA, complete cds	Consensus includes gb:AI468629 /FEA=EST /DB_XREF=gi:4330719 /DB_XREF=est:th83g03.x1 /CLONE=IMAGE:2125300 /UG=Hs.134185 ESTs, Weakly similar to 5E5 RAT 5E5 ANTIGEN R.norvegicus
229750_at_HG-U133B		ESTs	Consensus includes gb:BF510728 /FEA=EST /DB_XREF=gi:11594026 /DB_XREF=est:UI-H-BI4-aoh-c-07-0-UI.s1 /CLONE=IMAGE:3084685 /UG=Hs.143087 ESTs
229779_at_HG-U133B		ESTs	Consensus includes gb:BF476080 /FEA=EST /DB_XREF=gi:11546907 /DB_XREF=est:hr77b03.x1 /CLONE=IMAGE:3134477 /UG=Hs.119471 ESTs
229790_at_HG-U133B	TERF2	telomeric repeat binding factor 2	Consensus includes gb:AW006832 /FEA=EST /DB_XREF=gi:5855610 /DB_XREF=est:wt07h12.x1 /CLONE=IMAGE:2506823 /UG=Hs.100030 telomeric

			repeat binding factor 2
229817_at_HG-U133B	DKFZP434M098	DKFZP434M098 protein	Consensus includes gb:AI452715 /FEA=EST /DB_XREF=gi:4287293 /DB_XREF=est:tj56f10.x1 /CLONE=IMAGE:2145547 /UG=Hs.93738 DKFZP434M098 protein
229833_at_HG-U133B		ESTs, Highly similar to A38283 arachidonate 12-lipoxygenase [H.sapiens]	Consensus includes gb:BF507533 /FEA=EST /DB_XREF=gi:11590842 /DB_XREF=est:UI-H-BW1-amr-f-06-0-UI.s1 /CLONE=IMAGE:3070979 /UG=Hs.33728 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
229844_at_HG-U133B		ESTs	Consensus includes gb:AI699465 /FEA=EST /DB_XREF=gi:4987365 /DB_XREF=est:wa70f09.x1 /CLONE=IMAGE:2301545 /UG=Hs.59368 ESTs
229848_at_HG-U133B	ZNF10	zinc finger protein 10 (KOX 1)	Consensus includes gb:W72653 /FEA=EST /DB_XREF=gi:1382473 /DB_XREF=est:zd67c09.s1 /CLONE=IMAGE:345712 /UG=Hs.91226 ESTs
229872_s_at_HG-U133B	KIAA0493	KIAA0493 protein	Consensus includes gb:AA532655 /FEA=EST /DB_XREF=gi:2276909 /DB_XREF=est:nj17d09.s1 /CLONE=IMAGE:986609 /UG=Hs.295901 KIAA0493 protein
229923_at_HG-U133B			Consensus includes gb:AK026322.1 /DEF=Homo sapiens cDNA: FLJ22669 fis, clone HSI08594. /FEA=mRNA /DB_XREF=gi:10439147 /UG=Hs.44653 Homo sapiens cDNA: FLJ22669 fis, clone HSI08594
229934_at_HG-U133B		ESTs	Consensus includes gb:N39230 /FEA=EST /DB_XREF=gi:1162437 /DB_XREF=est:yy50c03.s1 /CLONE=IMAGE:276964 /UG=Hs.38218 ESTs
229937_x_at_HG-U133B		ESTs	Consensus includes gb:AI681260 /FEA=EST /DB_XREF=gi:4891442 /DB_XREF=est:tx45c07.x1 /CLONE=IMAGE:2272524 /UG=Hs.149924 ESTs
230110_at_HG-U133B		ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:AV713773 /FEA=EST /DB_XREF=gi:10795290 /DB_XREF=est:AV713773 /CLONE=DCBALC05 /UG=Hs.210792 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
230245_s_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp667L0210 (from clone	Consensus includes gb:AI926479 /FEA=EST /DB_XREF=gi:5662443 /DB_XREF=est:wo45b06.x1 /CLONE=IMAGE:2458259 /UG=Hs.181297 ESTs

		DKFZp667L0210)	
230292_at_HG-U133B		Homo sapiens cDNA FLJ25310 fis, clone SYN00991	Consensus includes gb:AA868809 /FEA=EST /DB_XREF=gi:2964254 /DB_XREF=est:al49h02.s1 /CLONE=IMAGE:1460691 /UG=Hs.25447 ESTs
230363_s_at_HG-U133B	SAC2	Sac domain-containing inositol phosphatase 2	Consensus includes gb:BE858808 /FEA=EST /DB_XREF=gi:10374225 /DB_XREF=est:7f95h05.x1 /CLONE=IMAGE:3304761 /UG=Hs.52463 KIAA0966 protein
230405_at_HG-U133B	RAD50	RAD50 homolog (S. cerevisiae)	Consensus includes gb:AI143416 /FEA=EST /DB_XREF=gi:3665225 /DB_XREF=est:qa55a10.s1 /CLONE=IMAGE:1690650 /UG=Hs.41587 RAD50 (S. cerevisiae) homolog
230441_at_HG-U133B		ESTs, Weakly similar to T17233 hypothetical protein DKFZp434I216.1 [H.sapiens]	Consensus includes gb:AI890356 /FEA=EST /DB_XREF=gi:5595520 /DB_XREF=est:wm84c05.x1 /CLONE=IMAGE:2442632 /UG=Hs.127804 ESTs, Weakly similar to T17233 hypothetical protein DKFZp434I216.1 H.sapiens
230489_at_HG-U133B	CD5	CD5 antigen (p56-62)	Consensus includes gb:AI797836 /FEA=EST /DB_XREF=gi:5363393 /DB_XREF=est:wh79f02.x1 /CLONE=IMAGE:2386971 /UG=Hs.58685 CD5 antigen (p56-62)
230499_at_HG-U133B		ESTs	Consensus includes gb:AA805622 /FEA=EST /DB_XREF=gi:2874372 /DB_XREF=est:oc19b11.s1 /CLONE=IMAGE:1341309 /UG=Hs.121572 ESTs
230526_at_HG-U133B	FLJ20015	hypothetical protein FLJ20015	Consensus includes gb:BF515959 /FEA=EST /DB_XREF=gi:11601138 /DB_XREF=est:UI-H-BW1-aoa-g-12-0-UI.s1 /CLONE=IMAGE:3084119 /UG=Hs.62529 ESTs
230551_at_HG-U133B		ESTs	Consensus includes gb:AI692426 /FEA=EST /DB_XREF=gi:4969766 /DB_XREF=est:wd69c09.x1 /CLONE=IMAGE:2336848 /UG=Hs.107331 ESTs
230588_s_at_HG-U133B	MCPR	anaphase-promoting complex 1; meiotic checkpoint regulator	Consensus includes gb:AA906142 /FEA=EST /DB_XREF=gi:3041265 /DB_XREF=est:oj93e12.s1 /CLONE=IMAGE:1505902 /UG=Hs.40137 anaphase-promoting complex 1; meiotic checkpoint regulator
230636_s_at_HG-U133B	BTEB1	basic transcription element binding protein 1	Consensus includes gb:AI458659 /FEA=EST /DB_XREF=gi:4311238 /DB_XREF=est:tk13b12.x1 /CLONE=IMAGE:2150879 /UG=Hs.150557 basic transcription element binding protein 1

230648_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp667L0210 (from clone DKFZp667L0210)	Consensus includes gb:AI377398 /FEA=EST /DB_XREF=gi:4187251 /DB_XREF=est:tc35a11.x1 /CLONE=IMAGE:2066588 /UG=Hs.181297 ESTs
230650_at_HG-U133B		Homo sapiens cDNA FLJ12909 fis, clone NT2RP2004400	Consensus includes gb:AU151107 /FEA=EST /DB_XREF=gi:11012628 /DB_XREF=est:AU151107 /CLONE=NT2RP2004400 /UG=Hs.152460 Homo sapiens cDNA FLJ12909 fis, clone NT2RP2004400
230659_at_HG-U133B	KIAA0212	KIAA0212 gene product	Consensus includes gb:AW139300 /FEA=EST /DB_XREF=gi:6144018 /DB_XREF=est:UI-H-BI1-ada-b-05-0-UI.s1 /CLONE=IMAGE:2715992 /UG=Hs.154332 KIAA0212 gene product
230689_at_HG-U133B		ESTs	Consensus includes gb:AA825243 /FEA=EST /DB_XREF=gi:2898542 /DB_XREF=est:oe59g06.s1 /CLONE=IMAGE:1415962 /UG=Hs.163426 ESTs
230713_at_HG-U133B		ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	Consensus includes gb:BF115786 /FEA=EST /DB_XREF=gi:10985262 /DB_XREF=est:7n64h03.x1 /CLONE=IMAGE:3569524 /UG=Hs.182185 ESTs
230743_at_HG-U133B		Homo sapiens, clone MGC:10077 IMAGE:3896690, mRNA, complete cds	Consensus includes gb:AI743312 /FEA=EST /DB_XREF=gi:5111600 /DB_XREF=est:wg91c09.x1 /CLONE=IMAGE:2372464 /UG=Hs.183096 ESTs
230753_at_HG-U133B		ESTs	Consensus includes gb:R12665 /FEA=EST /DB_XREF=gi:765741 /DB_XREF=est:yf40a04.s1 /CLONE=IMAGE:129294 /UG=Hs.11594 ESTs
230768_at_HG-U133B		ESTs	Consensus includes gb:BE672541 /FEA=EST /DB_XREF=gi:10033082 /DB_XREF=est:7b68g10.x1 /CLONE=IMAGE:3233442 /UG=Hs.58753 ESTs
230775_s_at_HG-U133B	KIAA0610	KIAA0610 protein	Consensus includes gb:BF590192 /FEA=EST /DB_XREF=gi:11682516 /DB_XREF=est:nab21a11.x1 /CLONE=IMAGE:3266229 /UG=Hs.118087 KIAA0610 protein
230793_at_HG-U133B	FLJ20048	hypothetical protein FLJ20048	Consensus includes gb:BE671038 /FEA=EST /DB_XREF=gi:10031579 /DB_XREF=est:7e45c02.x1 /CLONE=IMAGE:3285410 /UG=Hs.116470 hypothetical protein FLJ20048
230795_at_HG-U133B	H4F2	H4 histone, family 2	Consensus includes gb:AI828075 /FEA=EST /DB_XREF=gi:5448746 /DB_XREF=est:wk31e04.x1 /CLONE=IMAGE:2413950 /UG=Hs.55468 ESTs

230802_at_HG-U133B	DKFZP564B1162	hypothetical protein DKFZp564B1162	Consensus includes gb:AI761947 /FEA=EST /DB_XREF=gi:5177614 /DB_XREF=est:wh50b09.x1 /CLONE=IMAGE:2384153 /UG=Hs.131587 ESTs, Weakly similar to Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053 H.sapiens
230803_s_at_HG-U133B	DKFZP564B1162	hypothetical protein DKFZp564B1162	Consensus includes gb:AI761947 /FEA=EST /DB_XREF=gi:5177614 /DB_XREF=est:wh50b09.x1 /CLONE=IMAGE:2384153 /UG=Hs.131587 ESTs, Weakly similar to Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053 H.sapiens
230834_at_HG-U133B		ESTs	Consensus includes gb:BE348656 /FEA=EST /DB_XREF=gi:9260509 /DB_XREF=est:ht73g08.x1 /CLONE=IMAGE:3152414 /UG=Hs.114516 ESTs
230877_at_HG-U133B	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marker)	Consensus includes gb:AI492643 /FEA=EST /DB_XREF=gi:4393646 /DB_XREF=est:qz18a10.x1 /CLONE=IMAGE:2021850 /UG=Hs.284277 Homo sapiens immunoglobulin mu chain antibody MO30 (IgM) mRNA, complete cds
230917_at_HG-U133B		ESTs	Consensus includes gb:AW611685 /FEA=EST /DB_XREF=gi:7316871 /DB_XREF=est:hg86a01.x1 /CLONE=IMAGE:2952456 /UG=Hs.6179 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 17 (72kD)
230939_at_HG-U133B		ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]	Consensus includes gb:AI075039 /FEA=EST /DB_XREF=gi:3401683 /DB_XREF=est:ov13f01.x1 /CLONE=IMAGE:1637209 /UG=Hs.130352 ESTs
230960_at_HG-U133B		ESTs	Consensus includes gb:AI740721 /FEA=EST /DB_XREF=gi:5109009 /DB_XREF=est:wg17d08.x1 /CLONE=IMAGE:2365359 /UG=Hs.128292 ESTs
230983_at_HG-U133B		Homo sapiens mRNA for FLJ00140 protein	Consensus includes gb:BE646461 /FEA=EST /DB_XREF=gi:9970772 /DB_XREF=est:7e87b12.x1 /CLONE=IMAGE:3292127 /UG=Hs.137319 ESTs
230986_at_HG-U133B		Homo sapiens cDNA FLJ30065 fis, clone ADRGL2000328	Consensus includes gb:AI821447 /FEA=EST /DB_XREF=gi:5440526 /DB_XREF=est:yp24d10.x5 /CLONE=IMAGE:188371 /UG=Hs.141120 ESTs
230988_at_HG-U133B		ESTs	Consensus includes gb:AU149490 /FEA=EST /DB_XREF=gi:11011011 /DB_XREF=est:AU149490 /CLONE=NT2RM4002430 /UG=Hs.15155 ESTs
230997_at_HG-U133B		ESTs, Weakly similar to T29012	Consensus includes gb:AI872303 /FEA=EST /DB_XREF=gi:5546352

		hypothetical protein ZK328.7 - Caenorhabditis elegans [C.elegans]	/DB_XREF=est:wm57d10.x1 /CLONE=IMAGE:2440051 /UG=Hs.131816 ESTs, Weakly similar to weak similarity to SP:YAD5 CLOAB C.elegans
231002_s_at_HG-U133B	NUP88	nucleoporin 88kD	Consensus includes gb:AA778438 /FEA=EST /DB_XREF=gi:2837769 /DB_XREF=est:zf39g12.s1 /CLONE=IMAGE:379366 /UG=Hs.172108 nucleoporin 88kD
231050_at_HG-U133B	HRLP5	H-rev107-like protein 5	Consensus includes gb:AW771586 /FEA=EST /DB_XREF=gi:7703643 /DB_XREF=est:hn58g02.x1 /CLONE=IMAGE:3032114 /UG=Hs.12388 ESTs
231069_at_HG-U133B		ESTs, Weakly similar to T45117 hU1-70K protein [H.sapiens]	Consensus includes gb:AI768895 /FEA=EST /DB_XREF=gi:5235404 /DB_XREF=est:wh71f11.x1 /CLONE=IMAGE:2386221 /UG=Hs.295727 ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B WARNING ENTRY !!! H.sapiens
231093_at_HG-U133B	FCRH3	Fc receptor-like protein 3	Consensus includes gb:BF514552 /FEA=EST /DB_XREF=gi:11599731 /DB_XREF=est:UI-H-BW1-ang-b-12-0-UI.s1 /CLONE=IMAGE:3081959 /UG=Hs.123296 ESTs
231101_at_HG-U133B	PPP2R5E	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	Consensus includes gb:AI689803 /FEA=EST /DB_XREF=gi:4901097 /DB_XREF=est:tx25h09.x1 /CLONE=IMAGE:2270657 /UG=Hs.122684 ESTs
231118_at_HG-U133B		Homo sapiens cDNA FLJ25124 fis, clone CBR06414	Consensus includes gb:AW511401 /FEA=EST /DB_XREF=gi:7149479 /DB_XREF=est:hd89e02.x1 /CLONE=IMAGE:2916698 /UG=Hs.133081 ESTs, Weakly similar to T08700 hypothetical protein DKFZp564G013.1 H.sapiens
231181_at_HG-U133B		ESTs	Consensus includes gb:AI683621 /FEA=EST /DB_XREF=gi:4893803 /DB_XREF=est:tw52g09.x1 /CLONE=IMAGE:2263360 /UG=Hs.88651 ESTs
231215_at_HG-U133B		ESTs	Consensus includes gb:AI733145 /FEA=EST /DB_XREF=gi:5054258 /DB_XREF=est:ol91d05.x5 /CLONE=IMAGE:1536969 /UG=Hs.126962 ESTs
231241_at_HG-U133B		ESTs, Moderately similar to PCAF associated factor 65 beta [Homo sapiens] [H.sapiens]	Consensus includes gb:AW469714 /FEA=EST /DB_XREF=gi:7039820 /DB_XREF=est:hd33d10.x1 /CLONE=IMAGE:2911315 /UG=Hs.155635 ESTs, Moderately similar to PCAF associated factor 65 beta H.sapiens
231259_s_at_HG-U133B	CCND2	cyclin D2	Consensus includes gb:BE467688 /FEA=EST /DB_XREF=gi:9513463 /DB_XREF=est:hz67h08.x1 /CLONE=IMAGE:3213087 /UG=Hs.75586 cyclin D2

231269_at_HG-U133B	DJ467N11.1	dJ467N11.1 protein	Consensus includes gb:AU153330 /FEA=EST /DB_XREF=gi:11014851 /DB_XREF=est:AU153330 /CLONE=NT2RP3002911 /UG=Hs.143917 dJ467N11.1 protein /FL=gb:NM_022091.1
231277_x_at_HG-U133B		ESTs	Consensus includes gb:H29590 /FEA=EST /DB_XREF=gi:900500 /DB_XREF=est:ym61a05.s1 /CLONE=IMAGE:52642 /UG=Hs.14822 ESTs
231310_at_HG-U133B		ESTs	Consensus includes gb:BF057073 /FEA=EST /DB_XREF=gi:10810969 /DB_XREF=est:7k15e01.x1 /CLONE=IMAGE:3444552 /UG=Hs.113170 ESTs
231332_at_HG-U133B		ESTs, Moderately similar to 2109260A B cell growth factor [H.sapiens]	Consensus includes gb:AW295037 /FEA=EST /DB_XREF=gi:6701673 /DB_XREF=est:UI-H-BI2-ahs-g-10-0-UI.s1 /CLONE=IMAGE:2728122 /UG=Hs.254986 ESTs
231406_at_HG-U133B		ESTs	Consensus includes gb:AW205664 /FEA=EST /DB_XREF=gi:6505138 /DB_XREF=est:UI-H-BI1-afr-h-07-0-UI.s1 /CLONE=IMAGE:2722813 /UG=Hs.129568 ESTs
231418_at_HG-U133B	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	Consensus includes gb:AI808597 /FEA=EST /DB_XREF=gi:5395163 /DB_XREF=est:wf56d02.x1 /CLONE=IMAGE:2359587 /UG=Hs.89751 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)
231472_at_HG-U133B		ESTs	Consensus includes gb:BE464323 /FEA=EST /DB_XREF=gi:9510098 /DB_XREF=est:hx88c09.x1 /CLONE=IMAGE:3194896 /UG=Hs.124087 ESTs
231538_at_HG-U133B	FLJ23499	hypothetical protein FLJ23499	Consensus includes gb:BG150085 /FEA=EST /DB_XREF=gi:12662115 /DB_XREF=est:nad51d05.x1 /CLONE=IMAGE:3406905 /UG=Hs.17546 hypothetical protein FLJ23499
231552_at_HG-U133B		ESTs	Consensus includes gb:AW451785 /FEA=EST /DB_XREF=gi:6992561 /DB_XREF=est:UI-H-BI3-alk-a-10-0-UI.s1 /CLONE=IMAGE:2737050 /UG=Hs.235240 ESTs
231567_s_at_HG-U133B	TSP-NY	testis-specific protein TSP-NY	Consensus includes gb:AI027946 /FEA=EST /DB_XREF=gi:3245255 /DB_XREF=est:ov84b04.x1 /CLONE=IMAGE:1643983 /UG=Hs.97643 Homo sapiens testis-specific protein TSP-NY mRNA, complete cds

231647_s_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2	Consensus includes gb:AW241983 /FEA=EST /DB_XREF=gi:6575737 /DB_XREF=est:xn77f04.x1 /CLONE=IMAGE:2700511 /UG=Hs.191958 ESTs
231656_x_at_HG-U133B	OSBPL10	oxysterol binding protein-like 10	Consensus includes gb:AW593467 /FEA=EST /DB_XREF=gi:7280725 /DB_XREF=est:hg16f07.x1 /CLONE=IMAGE:2945797 /UG=Hs.321622 hypothetical protein FLJ20363
231736_x_at_HG-U133B	MGST1	microsomal glutathione S-transferase 1	Consensus includes gb:NM_020300.1 /DEF=Homo sapiens microsomal glutathione S-transferase 1 (MGST1), mRNA. /FEA=CDS /GEN=MGST1 /PROD=microsomal glutathione S-transferase 1 /DB_XREF=gi:9945305 /UG=Hs.790 microsomal glutathione S-transferase 1 /FL=gb:NM_020300.1
231775_at_HG-U133B	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	Consensus includes gb:W65310 /FEA=EST /DB_XREF=gi:1373636 /DB_XREF=est:zd33e01.r1 /CLONE=IMAGE:342456 /UG=Hs.249190 tumor necrosis factor receptor superfamily, member 10a /FL=gb:U90875.1 gb:NM_003844.1
231793_s_at_HG-U133B	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	Consensus includes gb:AA448956 /FEA=EST /DB_XREF=gi:2162976 /DB_XREF=est:zx07b10.r1 /CLONE=IMAGE:785755 /UG=Hs.111460 Homo sapiens cDNA: FLJ21715 fis, clone COL10287, highly similar to AF071569 Homo sapiens multifunctional calciumcalmodulin-dependent protein kinase II delta2 isoform mRNA /FL=gb:AF071569.1
231794_at_HG-U133B	CTLA4	cytotoxic T-lymphocyte-associated protein 4	Consensus includes gb:BG536887 /FEA=EST /DB_XREF=gi:13528433 /DB_XREF=est:602564631F1 /CLONE=IMAGE:4689582 /UG=Hs.247824 cytotoxic T-lymphocyte-associated protein 4 /FL=gb:L15006.1
231837_at_HG-U133B	USP28	ubiquitin specific protease 28	Consensus includes gb:AB040948.1 /DEF=Homo sapiens mRNA for KIAA1515 protein, partial cds. /FEA=mRNA /GEN=KIAA1515 /PROD=KIAA1515 protein /DB_XREF=gi:7959296 /UG=Hs.142856 KIAA1515 protein
231854_at_HG-U133B		Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391	Consensus includes gb:W63579 /FEA=EST /DB_XREF=gi:1371152 /DB_XREF=est:zb99a10.r1 /CLONE=IMAGE:320922 /UG=Hs.120905 Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391

231870_s_at_HG-U133B	LOC51068	CGI-07 protein	Consensus includes gb:BG291007 /FEA=EST /DB_XREF=gi:13048543 /DB_XREF=est:602386804F1 /CLONE=IMAGE:4515864 /UG=Hs.181022 CGI-07 protein
231873_at_HG-U133B		Homo sapiens cDNA FLJ13364 fis, clone PLACE1000292	Consensus includes gb:AL046696 /FEA=EST /DB_XREF=gi:5434759 /DB_XREF=est:DKFZp434C099_r1 /CLONE=DKFZp434C099 /UG=Hs.315284 Homo sapiens cDNA FLJ13364 fis, clone PLACE1000292
231887_s_at_HG-U133B	KIAA1274	KIAA protein (similar to mouse paladin)	Consensus includes gb:AB033100.1 /DEF=Homo sapiens mRNA for KIAA1274 protein, partial cds. /FEA=mRNA /GEN=KIAA1274 /PROD=KIAA1274 protein /DB_XREF=gi:6331286 /UG=Hs.300646 KIAA protein (similar to mouse paladin)
231897_at_HG-U133B			Consensus includes gb:AL135787 /DEF=Human DNA sequence from clone RP11-16L21 on chromosome 9. Contains the gene for NADP-dependent leukotriene B4 12-hydroxydehydrogenase, the gene for a novel DnaJ domain protein similar to Drosophila, C. elegans and Arabidopsis predicted proteins, t... /FEA=mRNA_1 /DB_XREF=gi:9588110 /UG=Hs.297143 Human DNA sequence from clone RP11-16L21 on chromosome 9. Contains the gene for NADP-dependent leukotriene B4 12-hydroxydehydrogenase, the gene for a novel DnaJ domain protein similar to Drosophila, C. elegans and Arabidopsis predicted proteins, the GNG10
231926_at_HG-U133B			Consensus includes gb:AK023744.1 /DEF=Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15. /FEA=mRNA /DB_XREF=gi:10435769 /UG=Hs.318510 Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15
231945_at_HG-U133B	KIAA1275	KIAA1275 protein	Consensus includes gb:AK001570.1 /DEF=Homo sapiens cDNA FLJ10708 fis, clone NT2RP3000868, weakly similar to Human ovarian cancer downregulated myosin heavy chain homolog mRNA. /FEA=mRNA

			/DB_XREF=gi:7022904 /UG=Hs.102796 KIAA1275 protein
231969_at_HG-U133B	DKFZp762K222	hypothetical protein DKFZp762K222	Consensus includes gb:AB037813.1 /DEF=Homo sapiens mRNA for KIAA1392 protein, partial cds. /FEA=mRNA /GEN=KIAA1392 /PROD=KIAA1392 protein /DB_XREF=gi:7243164 /UG=Hs.159200 hypothetical protein DKFZp762K222
231981_at_HG-U133B			Consensus includes gb:AK001889.1 /DEF=Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114. /FEA=mRNA /DB_XREF=gi:7023437 /UG=Hs.35156 Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114
231982_at_HG-U133B			Consensus includes gb:AF161441.1 /DEF=Homo sapiens HSPC323 mRNA, partial cds. /FEA=mRNA /PROD=HSPC323 /DB_XREF=gi:6841295 /UG=Hs.130714 Homo sapiens HSPC323 mRNA, partial cds
232027_at_HG-U133B			Consensus includes gb:AL049548 /DEF=Human DNA sequence from clone 398G3 on chromosome 6q25.1-25.3. Contains the 3part of the gene for the ortholog of rat CPG2, part of a novel gene, ESTs, STSs and GSSs /FEA=mRNA /DB_XREF=gi:4902741 /UG=Hs.241420 Homo sapiens mRNA for KIAA1756 protein, partial cds
232035_at_HG-U133B	H4FH	H4 histone family, member H	Consensus includes gb:BE740761 /FEA=EST /DB_XREF=gi:10154753 /DB_XREF=est:601593557F1 /CLONE=IMAGE:3947415 /UG=Hs.93758 H4 histone family, member H
232060_at_HG-U133B			Consensus includes gb:AK000776.1 /DEF=Homo sapiens cDNA FLJ20769 fis, clone COL06674. /FEA=mRNA /DB_XREF=gi:7021073 /UG=Hs.128753 Homo sapiens cDNA FLJ20769 fis, clone COL06674
232080_at_HG-U133B	KIAA1301	KIAA1301 protein	Consensus includes gb:AL390186.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434N1131 (from clone DKFZp434N1131). /FEA=mRNA /GEN=DKFZp434N1131 /PROD=hypothetical protein /DB_XREF=gi:9368899 /UG=Hs.8707 KIAA1301 protein
232112_at_HG-U133B		ESTs, Weakly similar to KIAA0351 [H.sapiens]	Consensus includes gb:AW504453 /FEA=EST /DB_XREF=gi:7142120 /DB_XREF=est:UI-HF-BN0-alq-c-04-0-UI.r1 /CLONE=IMAGE:3080431

			/UG=Hs.220745 Human DNA sequence from clone RP4-595C2 on chromosome 1q24.1-25.3 Contains ESTs, STSs and GSSs. Contains the 3 part of the gene for two isoforms of the KIAA0351 protein and the gene for angiopoietin Y1
232125_at_HG-U133B		Homo sapiens cDNA FLJ12166 fis, clone MAMMA1000616	Consensus includes gb:AU147419 /FEA=EST /DB_XREF=gi:11008940 /DB_XREF=est:AU147419 /CLONE=MAMMA1000616 /UG=Hs.202577 Homo sapiens cDNA FLJ12166 fis, clone MAMMA1000616
232127_at_HG-U133B			Consensus includes gb:AK021494.1 /DEF=Homo sapiens cDNA FLJ11432 fis, clone HEMBA1001099. /FEA=mRNA /DB_XREF=gi:10432689 /UG=Hs.166486 Homo sapiens cDNA FLJ11432 fis, clone HEMBA1001099
232201_at_HG-U133B	NKD2	naked cuticle homolog 2 (Drosophila)	Consensus includes gb:BC004940.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 2210403L10 gene, clone IMAGE:3609702, mRNA, partial cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 2210403L10 gene /DB_XREF=gi:13436292 /UG=Hs.240951 Homo sapiens, Similar to RIKEN cDNA 2210403L10 gene, clone IMAGE:3609702, mRNA, partial cds
232204_at_HG-U133B	EBF	early B-cell factor	Consensus includes gb:AF208502.1 /DEF=Homo sapiens early B-cell transcription factor (EBF) mRNA, partial cds. /FEA=mRNA /GEN=EBF /PROD=early B-cell transcription factor /DB_XREF=gi:6630993 /UG=Hs.185708 early B-cell factor
232210_at_HG-U133B		Homo sapiens cDNA FLJ14056 fis, clone HEMBB1000335	Consensus includes gb:AU146384 /FEA=EST /DB_XREF=gi:11007905 /DB_XREF=est:AU146384 /CLONE=HEMBB1000335 /UG=Hs.206868 Homo sapiens cDNA FLJ14056 fis, clone HEMBB1000335
232231_at_HG-U133B			Consensus includes gb:AL353944.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761J1112 (from clone DKFZp761J1112). /FEA=mRNA /DB_XREF=gi:7669984 /UG=Hs.50115 Homo sapiens mRNA; cDNA DKFZp761J1112 (from clone DKFZp761J1112)
232234_at_HG-U133B	C20orf24	chromosome 20 open reading frame 24	Consensus includes gb:AA305476 /FEA=EST /DB_XREF=gi:1957823 /DB_XREF=est:EST176483 /UG=Hs.184062 putative Rab5-interacting protein

232614_at_HG-U133B		Homo sapiens cDNA FLJ12049 fis, clone HEMBB1001996	Consensus includes gb:AU146963 /FEA=EST /DB_XREF=gi:11008484 /DB_XREF=est:AU146963 /CLONE=HEMBB1001996 /UG=Hs.171395 Homo sapiens cDNA FLJ12049 fis, clone HEMBB1001996
232636_at_HG-U133B			Consensus includes gb:AL080239 /DEF=Human DNA sequence from clone GS1-256O22 on chromosome Xq26.3-28 Contains part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG Island /FEA=CDS /DB_XREF=gi:5531259 /UG=Hs.272284 Human DNA sequence from clone GS1-256O22 on chromosome Xq26.3-28 Contains part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG Island
232641_at_HG-U133B			Consensus includes gb:AC004908 /DEF=Homo sapiens PAC clone RP5-855D21 /FEA=CDS_3 /DB_XREF=gi:4156179 /UG=Hs.249181 Homo sapiens PAC clone RP5-855D21
232739_at_HG-U133B			Consensus includes gb:AK025419.1 /DEF=Homo sapiens cDNA: FLJ21766 fis, clone COLF7179. /FEA=mRNA /DB_XREF=gi:10437927 /UG=Hs.318722 Homo sapiens cDNA: FLJ21766 fis, clone COLF7179
232841_at_HG-U133B			Consensus includes gb:AK026750.1 /DEF=Homo sapiens cDNA: FLJ23097 fis, clone LNG07418. /FEA=mRNA /DB_XREF=gi:10439673 /UG=Hs.152432 Homo sapiens cDNA: FLJ23097 fis, clone LNG07418
232950_s_at_HG-U133B	NIR3	PYK2 N-terminal domain-interacting receptor 3	Consensus includes gb:AB040890.1 /DEF=Homo sapiens mRNA for KIAA1457 protein, partial cds. /FEA=mRNA /GEN=KIAA1457 /PROD=KIAA1457 protein /DB_XREF=gi:7959174 /UG=Hs.272759 KIAA1457 protein
233072_at_HG-U133B	KIAA1857	netrin G2	Consensus includes gb:AI348745 /FEA=EST /DB_XREF=gi:4085951 /DB_XREF=est:ta92e12.x2 /CLONE=IMAGE:2051566 /UG=Hs.163642 Homo sapiens clone 25187 and 25188 mRNA sequences, partial cds
233106_at_HG-U133B		Homo sapiens cDNA FLJ12375 fis, clone	Consensus includes gb:AU148054 /FEA=EST /DB_XREF=gi:11009575

		MAMMA1002475	/DB_XREF=est:AU148054 /CLONE=MAMMA1002475 /UG=Hs.288797 Homo sapiens cDNA FLJ12375 fis, clone MAMMA1002475
233137_at_HG-U133B			Consensus includes gb:AF143887.1 /DEF=Homo sapiens clone IMAGE:121687 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4895032 /UG=Hs.18119 Homo sapiens clone IMAGE:121687 mRNA sequence
233138_at_HG-U133B		Homo sapiens cDNA FLJ13412 fis, clone PLACE1001745	Consensus includes gb:AU155968 /FEA=EST /DB_XREF=gi:11017489 /DB_XREF=est:AU155968 /CLONE=PLACE1001745 /UG=Hs.178533 Homo sapiens cDNA FLJ13412 fis, clone PLACE1001745
233177_s_at_HG-U133B	KIAA1184	KIAA1184 protein	Consensus includes gb:AB033010.1 /DEF=Homo sapiens mRNA for KIAA1184 protein, partial cds. /FEA=mRNA /GEN=KIAA1184 /PROD=KIAA1184 protein /DB_XREF=gi:6330254 /UG=Hs.100747 KIAA1184 protein
233195_at_HG-U133B			Consensus includes gb:AL117535.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434F062 (from clone DKFZp434F062). /FEA=mRNA /DB_XREF=gi:5912064 /UG=Hs.150874 Homo sapiens mRNA; cDNA DKFZp434F062 (from clone DKFZp434F062)
233261_at_HG-U133B		Homo sapiens cDNA FLJ11741 fis, clone HEMBA1005506	Consensus includes gb:AU145682 /FEA=EST /DB_XREF=gi:11007203 /DB_XREF=est:AU145682 /CLONE=HEMBA1005506 /UG=Hs.293916 Homo sapiens cDNA FLJ11741 fis, clone HEMBA1005506
233328_x_at_HG-U133B			Consensus includes gb:AL121673 /DEF=Human DNA sequence from clone RP11-305P22 on chromosome 20 Contains ESTs, STSs, GSSs and 7 CpG islands. Contains three novel genes and a novel gene for a helix-loop-helix DNA binding protein /FEA=mRNA_7 /DB_XREF=gi:9650752 /UG=Hs.34487 hypothetical protein FLJ23412
233483_at_HG-U133B		Homo sapiens mRNA for FLJ00050 protein, partial cds	Consensus includes gb:AK024458.1 /DEF=Homo sapiens mRNA for FLJ00050 protein, partial cds. /FEA=mRNA /GEN=FLJ00050 /PROD=FLJ00050 protein /DB_XREF=gi:10440429 /UG=Hs.193857 Homo sapiens mRNA for FLJ00050 protein, partial cds

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233500_x_at_HG-U133B	LLT1	lectin-like NK cell receptor	Consensus includes gb:AF285089.1 /DEF=Homo sapiens clone 7B C-type lectin (CLAX) mRNA, partial cds. /FEA=mRNA /GEN=CLAX /PROD=C-type lectin /DB_XREF=gi:9837291 /UG=Hs.136748 lectin-like NK cell receptor
233520_s_at_HG-U133B			Consensus includes gb:AL359338.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2068071. /FEA=mRNA /DB_XREF=gi:8574097 /UG=Hs.50794 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2068071
233555_s_at_HG-U133B			Consensus includes gb:AL034418 /DEF=Human DNA sequence from clone RP5-1049G16 on chromosome 20q12-13.2. Contains the 3 end of the NCOA3 gene for nuclear receptor coactivator 3 (thyroid hormone receptor activator molecule TRAM-1, Receptor-Associated Coactivator RAC3, Amplified In Br... /FEA=mRNA_4 /DB_XREF=gi:11546048 /UG=Hs.43857 similar to glucosamine-6-sulfatases
233559_s_at_HG-U133B	FENS-1	phosphoinositide-binding protein SR1	Consensus includes gb:AK023415.1 /DEF=Homo sapiens cDNA FLJ13353 fis, clone OVARC1002182, weakly similar to BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN). /FEA=mRNA /DB_XREF=gi:10435344 /UG=Hs.44743 KIAA1435 protein
233589_x_at_HG-U133B			Consensus includes gb:AK000392.1 /DEF=Homo sapiens cDNA FLJ20385 fis, clone KAIA4085. /FEA=mRNA /DB_XREF=gi:7020451 /UG=Hs.169758 hypothetical protein FLJ20245
233613_x_at_HG-U133B		Homo sapiens cDNA FLJ13436 fis, clone PLACE1002598, weakly similar to OLIGORIBONUCLEASE (EC 3.1.-.-)	Consensus includes gb:AU156209 /FEA=EST /DB_XREF=gi:11017730 /DB_XREF=est:AU156209 /CLONE=PLACE1002598 /UG=Hs.296737 Homo sapiens cDNA FLJ13436 fis, clone PLACE1002598, weakly similar to OLIGORIBONUCLEASE (EC 3.1.-.-)
233813_at_HG-U133B			Consensus includes gb:AK026900.1 /DEF=Homo sapiens cDNA: FLJ23247 fis, clone COL03425. /FEA=mRNA /DB_XREF=gi:10439867 /UG=Hs.288651 Homo sapiens cDNA: FLJ23247 fis, clone COL03425
233845_at_HG-U133B		Homo sapiens clone HQ0452 PRO0452	Consensus includes gb:AF090925.1 /DEF=Homo sapiens clone HQ0452

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		mRNA, partial cds	PRO0452 mRNA, partial cds. /FEA=mRNA /PROD=PRO0452 /DB_XREF=gi:6690216 /UG=Hs.283921 Homo sapiens clone HQ0452 PRO0452 mRNA, partial cds
233955_x_at_HG-U133B	HSPC195	hypothetical protein HSPC195	Consensus includes gb:AK001782.1 /DEF=Homo sapiens cDNA FLJ10920 fis, clone OVARC1000384. /FEA=mRNA /DB_XREF=gi:7023268 /UG=Hs.15093 hypothetical protein
234005_x_at_HG-U133B	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	Consensus includes gb:AK022692.1 /DEF=Homo sapiens cDNA FLJ12630 fis, clone NT2RM4001836. /FEA=mRNA /DB_XREF=gi:10434236 /UG=Hs.26996 KIAA1278 protein
234032_at_HG-U133B			Consensus includes gb:AF119847.1 /DEF=Homo sapiens PRO1550 mRNA, partial cds. /FEA=mRNA /PROD=PRO1550 /DB_XREF=gi:7770130 /UG=Hs.283940 Homo sapiens PRO1550 mRNA, partial cds
234107_s_at_HG-U133B			Consensus includes gb:AL121780 /DEF=Human DNA sequence from clone RP11-555E18 on chromosome 20 Contains the 3 end of the gene for a novel protein similar to bacterial histidyl-tRNA synthetase, ESTs, STSs and GSSs /FEA=mRNA /DB_XREF=gi:10334636 /UG=Hs.306024 FK506-binding protein 3 (25kD)
234132_at_HG-U133B			Consensus includes gb:AK021831.1 /DEF=Homo sapiens cDNA FLJ11769 fis, clone HEMBA1005755. /FEA=mRNA /DB_XREF=gi:10433098 /UG=Hs.306614 Homo sapiens cDNA FLJ11769 fis, clone HEMBA1005755
234140_s_at_HG-U133B	STIM2	stromal interaction molecule 2	Consensus includes gb:AK023369.1 /DEF=Homo sapiens cDNA FLJ13307 fis, clone OVARC1001419, weakly similar to Homo sapiens GOK (STIM1) mRNA. /FEA=mRNA /DB_XREF=gi:10435274 /UG=Hs.306644 Homo sapiens cDNA FLJ13307 fis, clone OVARC1001419, weakly similar to Homo sapiens GOK (STIM1) mRNA
234362_s_at_HG-U133B	CTLA4	cytotoxic T-lymphocyte-associated protein 4	Consensus includes gb:U90273.1 /DEF=Homo sapiens CTLA-4 mRNA, partial cds. /FEA=mRNA /GEN=CTLA-4 /PROD=CTLA-4 /DB_XREF=gi:4099840 /UG=Hs.247824 cytotoxic T-lymphocyte-associated protein 4

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234584_s_at_HG-U133B	ATE1	arginyltransferase 1	Consensus includes gb:AF079098.1 /DEF=Homo sapiens arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds. /FEA=mRNA /GEN=ATE1 /PROD=arginine-tRNA-protein transferase 1-1p /DB_XREF=gi:3806093 /UG=Hs.301497 arginyltransferase 1
234643_x_at_HG-U133B			Consensus includes gb:AK025451.1 /DEF=Homo sapiens cDNA: FLJ21798 fis, clone HEP00573. /FEA=mRNA /DB_XREF=gi:10437968 /UG=Hs.306812 Homo sapiens cDNA: FLJ21798 fis, clone HEP00573
234660_s_at_HG-U133B	DIS3	mitotic control protein dis3 homolog	Consensus includes gb:AL080158.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434L194 (from clone DKFZp434L194); partial cds. /FEA=mRNA /GEN=DKFZp434L194 /PROD=hypothetical protein /DB_XREF=gi:5262618 /UG=Hs.323346 KIAA1008 protein
234682_at_HG-U133B			Consensus includes gb:AL079341 /DEF=Human DNA sequence from clone RP1-319M7 on chromosome 6p21.1-21.3 Contains a gene for a protein similar to KIAA0952 protein, a novel pseudogene, STSs, GSSs and a CpG island /FEA=CDS /DB_XREF=gi:8655533 /UG=Hs.307123 Human DNA sequence from clone RP1-319M7 on chromosome 6p21.1-21.3 Contains a gene for a protein similar to KIAA0952 protein, a novel pseudogene, STSs, GSSs and a CpG island
234725_s_at_HG-U133B	SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Consensus includes gb:AK026133.1 /DEF=Homo sapiens cDNA: FLJ22480 fis, clone HRC10841. /FEA=mRNA /DB_XREF=gi:10438886 /UG=Hs.9598 hypothetical protein from EUROIMAGE 1955967
234726_s_at_HG-U133B			Consensus includes gb:AK025482.1 /DEF=Homo sapiens cDNA: FLJ21829 fis, clone HEP01461. /FEA=mRNA /DB_XREF=gi:10438011 /UG=Hs.79353 hypothetical protein FLJ13576
234764_x_at_HG-U133B			Consensus includes gb:U96394.1 /DEF=Human anti-streptococcalanti-myosin immunoglobulin lambda light chain variable region mRNA, partial cds. /FEA=mRNA /PROD=anti-streptococcalanti-myosin immunoglobulinlambda light

			chain variable region /DB_XREF=gi:2352087 /UG=Hs.307341 Human anti-streptococcalanti-myosin immunoglobulin lambda light chain variable region mRNA, partial cds
234839_at_HG-U133B			Consensus includes gb:AL049277.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564I103 (from clone DKFZp564I103). /FEA=mRNA /DB_XREF=gi:4500031 /UG=Hs.274502 Homo sapiens mRNA; cDNA DKFZp564I103 (from clone DKFZp564I103)
234862_at_HG-U133B			Consensus includes gb:AL096770 /DEF=Human DNA sequence from clone RP11-150A6 on chromosome 6. Contains four genes for novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) proteins, a DDX6 (DEADH (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54kD)) ps... /FEA=CDS_3 /DB_XREF=gi:10198644 /UG=Hs.272282 Human DNA sequence from clone RP11-150A6 on chromosome 6. Contains four genes for novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) proteins, a DDX6 (DEADH (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54kD)) pseudogene
235023_at_HG-U133B		Homo sapiens cDNA FLJ32182 fis, clone PLACE6001823	Consensus includes gb:AA828371 /FEA=EST /DB_XREF=gi:2901470 /DB_XREF=est:ob60g12.s1 /CLONE=IMAGE:1335814 /UG=Hs.292896 ESTs
235051_at_HG-U133B		Homo sapiens cDNA FLJ31090 fis, clone IMR321000102	Consensus includes gb:BF696931 /FEA=EST /DB_XREF=gi:11982339 /DB_XREF=est:602129695F1 /CLONE=IMAGE:4286422 /UG=Hs.55098 ESTs
235052_at_HG-U133B		ESTs, Weakly similar to I38598 zinc finger protein ZNF132 [H.sapiens]	Consensus includes gb:AV758821 /FEA=EST /DB_XREF=gi:10916669 /DB_XREF=est:AV758821 /CLONE=BMFAWC02 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 H.sapiens
235061_at_HG-U133B		Homo sapiens cDNA FLJ30116 fis, clone BRACE1000042, weakly similar to PROTEIN PHOSPHATASE 2C ABI2 (EC 3.1.3.16)	Consensus includes gb:AV706522 /FEA=EST /DB_XREF=gi:10723801 /DB_XREF=est:AV706522 /CLONE=ADBDAF07 /UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235101_at_HG-U133B	KIAA1014	KIAA1014 protein	Consensus includes gb:AV683244 /FEA=EST /DB_XREF=gi:10285107

			/DB_XREF=est:AV683244 /CLONE=GKCASH01 /UG=Hs.195602 ESTs
235124_at_HG-U133B		Homo sapiens, clone IMAGE:4592052, mRNA, partial cds	Consensus includes gb:BE502930 /FEA=EST /DB_XREF=gi:9705338 /DB_XREF=est:hz81c07.x1 /CLONE=IMAGE:3214380 /UG=Hs.153400 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235259_at_HG-U133B		Homo sapiens, clone MGC:29898 IMAGE:4992139, mRNA, complete cds	Consensus includes gb:AA398590 /FEA=EST /DB_XREF=gi:2051832 /DB_XREF=est:zt75b06.s1 /CLONE=IMAGE:728147 /UG=Hs.97415 ESTs, Weakly similar to E04F6.2 gene product C.elegans
235263_at_HG-U133B	DKFZP434A0131	DKFZp434A0131 protein	Consensus includes gb:BF530545 /FEA=EST /DB_XREF=gi:11617908 /DB_XREF=est:602071803F1 /CLONE=IMAGE:4214760 /UG=Hs.271853 ESTs, Moderately similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235278_at_HG-U133B		ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]	Consensus includes gb:BF032500 /FEA=EST /DB_XREF=gi:10740212 /DB_XREF=est:601453326F1 /CLONE=IMAGE:3856854 /UG=Hs.136585 ESTs
235287_at_HG-U133B		Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572	Consensus includes gb:AW192700 /FEA=EST /DB_XREF=gi:6471399 /DB_XREF=est:xl48h09.x1 /CLONE=IMAGE:2677985 /UG=Hs.253015 ESTs
235291_s_at_HG-U133B		Homo sapiens cDNA FLJ32255 fis, clone PROST1000226	Consensus includes gb:BE875232 /FEA=EST /DB_XREF=gi:10324008 /DB_XREF=est:601488533F1 /CLONE=IMAGE:3890600 /UG=Hs.268180 ESTs
235331_x_at_HG-U133B		ESTs, Weakly similar to JC4296 ring finger protein - fruit fly [D.melanogaster]	Consensus includes gb:AI341142 /FEA=EST /DB_XREF=gi:4078069 /DB_XREF=est:qx89e09.x1 /CLONE=IMAGE:2009704 /UG=Hs.197484 ESTs
235353_at_HG-U133B	KIAA0746	KIAA0746 protein	Consensus includes gb:AI887866 /FEA=EST /DB_XREF=gi:5593030 /DB_XREF=est:tk05c07.x1 /CLONE=IMAGE:2150124 /UG=Hs.127335 ESTs
235359_at_HG-U133B		ESTs, Weakly similar to S42799 garp precursor [H.sapiens]	Consensus includes gb:AA534416 /FEA=EST /DB_XREF=gi:2278669 /DB_XREF=est:nf76c11.s1 /CLONE=IMAGE:925844 /UG=Hs.162185 ESTs
235372_at_HG-U133B	FREB	Fc receptor homolog expressed in B cells	Consensus includes gb:AW575245 /FEA=EST /DB_XREF=gi:7246784 /DB_XREF=est:UI-HF-BK0-aaw-h-09-0-UI.s1 /CLONE=IMAGE:3055360 /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma H.sapiens

235385_at_HG-U133B	FLJ20668	hypothetical protein FLJ20668	Consensus includes gb:AI935334 /FEA=EST /DB_XREF=gi:5674204 /DB_XREF=est:wo82b12.x1 /CLONE=IMAGE:2461823 /UG=Hs.122406 ESTs
235400_at_HG-U133B	FREB	Fc receptor homolog expressed in B cells	Consensus includes gb:AL560266 /FEA=EST /DB_XREF=gi:12906564 /DB_XREF=est:AL560266 /CLONE=CS0DG007YG20 (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma H.sapiens
235401_s_at_HG-U133B	FREB	Fc receptor homolog expressed in B cells	Consensus includes gb:AL560266 /FEA=EST /DB_XREF=gi:12906564 /DB_XREF=est:AL560266 /CLONE=CS0DG007YG20 (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma H.sapiens
235414_at_HG-U133B		ESTs, Weakly similar to S47072 finger protein HZF10, Krueppel-related [H.sapiens]	Consensus includes gb:BF432571 /FEA=EST /DB_XREF=gi:11444722 /DB_XREF=est:nac56h08.x1 /CLONE=IMAGE:3406695 /UG=Hs.164102 ESTs, Moderately similar to S47072 finger protein HZF10, Krueppel-related H.sapiens
235421_at_HG-U133B		ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	Consensus includes gb:AV713062 /FEA=EST /DB_XREF=gi:10732381 /DB_XREF=est:AV713062 /CLONE=DCAADD12 /UG=Hs.122431 ESTs
235422_at_HG-U133B	FALZ	fetal Alzheimer antigen	Consensus includes gb:AA977218 /FEA=EST /DB_XREF=gi:3154664 /DB_XREF=est:oq25h05.s1 /CLONE=IMAGE:1587417 /UG=Hs.118142 ESTs
235428_at_HG-U133B		ESTs	Consensus includes gb:H78106 /FEA=EST /DB_XREF=gi:1056195 /DB_XREF=est:yu83g09.s1 /CLONE=IMAGE:240448 /UG=Hs.104480 ESTs
235444_at_HG-U133B		ESTs	Consensus includes gb:AI417897 /FEA=EST /DB_XREF=gi:4261401 /DB_XREF=est:tg55b06.x1 /CLONE=IMAGE:2112659 /UG=Hs.235860 ESTs
235446_at_HG-U133B		ESTs	Consensus includes gb:AW856618 /FEA=EST /DB_XREF=gi:7952311 /DB_XREF=est:RC3-CT0297-060100-012-e08 /UG=Hs.293702 ESTs
235459_at_HG-U133B		ESTs	Consensus includes gb:BF114745 /FEA=EST /DB_XREF=gi:10984221 /DB_XREF=est:7j66h07.x1 /CLONE=IMAGE:3391453 /UG=Hs.136316 ESTs
235483_at_HG-U133B		Homo sapiens cDNA FLJ30906 fis, clone FEBRA2006055	Consensus includes gb:AA858058 /FEA=EST /DB_XREF=gi:2946360 /DB_XREF=est:ob14a03.s1 /CLONE=IMAGE:1323628 /UG=Hs.180711 ESTs
235502_at_HG-U133B		ESTs	Consensus includes gb:BF030448 /FEA=EST /DB_XREF=gi:10738160

			/DB_XREF=est:601558546F1 /CLONE=IMAGE:3828250 /UG=Hs.79204 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235521_at_HG-U133B	HOXA3	homeo box A3	Consensus includes gb:AW137982 /FEA=EST /DB_XREF=gi:6142300 /DB_XREF=est:UI-H-BI1-acl-b-07-0-UI.s1 /CLONE=IMAGE:2714461 /UG=Hs.222446 ESTs
235604_x_at_HG-U133B		ESTs, Weakly similar to Z208_HUMAN ZINC FINGER PROTEIN 208 [H.sapiens]	Consensus includes gb:AI758697 /FEA=EST /DB_XREF=gi:5152422 /DB_XREF=est:ty23e06.x1 /CLONE=IMAGE:2279938 /UG=Hs.256801 ESTs
235647_at_HG-U133B		ESTs	Consensus includes gb:AI298279 /FEA=EST /DB_XREF=gi:3958015 /DB_XREF=est:qm92a06.x1 /CLONE=IMAGE:1896178 /UG=Hs.293411 ESTs
235674_at_HG-U133B		ESTs	Consensus includes gb:AW575183 /FEA=EST /DB_XREF=gi:7246722 /DB_XREF=est:UI-HF-BK0-aas-f-07-0-UI.s1 /CLONE=IMAGE:3054876 /UG=Hs.13849 ESTs
235692_at_HG-U133B		ESTs	Consensus includes gb:AW024527 /FEA=EST /DB_XREF=gi:5878057 /DB_XREF=est:wv04h07.x1 /CLONE=IMAGE:2528605 /UG=Hs.31922 ESTs
235706_at_HG-U133B	CPM	carboxypeptidase M	Consensus includes gb:AW663908 /FEA=EST /DB_XREF=gi:7456447 /DB_XREF=est:hi73d08.x1 /CLONE=IMAGE:2977935 /UG=Hs.241569 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235719_at_HG-U133B		ESTs	Consensus includes gb:BE326857 /FEA=EST /DB_XREF=gi:9200633 /DB_XREF=est:hr65h06.x1 /CLONE=IMAGE:3133403 /UG=Hs.99237 ESTs
235749_at_HG-U133B			Consensus includes gb:AI057619 /FEA=EST /DB_XREF=gi:3331485 /DB_XREF=est:oy31f09.x1 /CLONE=IMAGE:1667465 /UG=Hs.133423 ESTs, Highly similar to T42654 hypothetical protein DKFZp434G1115.1 H.sapiens
235753_at_HG-U133B		ESTs	Consensus includes gb:AI492051 /FEA=EST /DB_XREF=gi:4393054 /DB_XREF=est:tg06h08.x1 /CLONE=IMAGE:2108031 /UG=Hs.196169 ESTs
235818_at_HG-U133B		ESTs	Consensus includes gb:AI498747 /FEA=EST /DB_XREF=gi:4390729

			/DB_XREF=est:tm64h07.x1 /CLONE=IMAGE:2162941 /UG=Hs.133355 ESTs
235823_at_HG-U133B		Homo sapiens cDNA FLJ32102 fis, clone OCBBF2001196	Consensus includes gb:AI763000 /FEA=EST /DB_XREF=gi:5178667 /DB_XREF=est:wi05h10.x1 /CLONE=IMAGE:2389411 /UG=Hs.120155 ESTs
235982_at_HG-U133B	FCRH1	Fc receptor-like protein 1	Consensus includes gb:AA677057 /FEA=EST /DB_XREF=gi:2657579 /DB_XREF=est:zj59f11.s1 /CLONE=IMAGE:454605 /UG=Hs.180644 ESTs
236019_at_HG-U133B		ESTs	Consensus includes gb:AI076335 /FEA=EST /DB_XREF=gi:3405513 /DB_XREF=est:oz04a05.x1 /CLONE=IMAGE:1674320 /UG=Hs.19440 ESTs
236190_at_HG-U133B		ESTs	Consensus includes gb:BF516337 /FEA=EST /DB_XREF=gi:11601516 /DB_XREF=est:UI-H-BW1-anz-h-12-0-UI.s1 /CLONE=IMAGE:3084166 /UG=Hs.115772 ESTs, Weakly similar to unknown D.melanogaster
236226_at_HG-U133B		ESTs	Consensus includes gb:AW294080 /FEA=EST /DB_XREF=gi:6700716 /DB_XREF=est:UI-H-BI2-ahg-a-04-0-UI.s1 /CLONE=IMAGE:2726670 /UG=Hs.126808 ESTs
236248_x_at_HG-U133B		ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	Consensus includes gb:AI859834 /FEA=EST /DB_XREF=gi:5513439 /DB_XREF=est:wm21a08.x1 /CLONE=IMAGE:2436566 /UG=Hs.155512 ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
236265_at_HG-U133B		Homo sapiens, clone IMAGE:3887266, mRNA	Consensus includes gb:BF438799 /FEA=EST /DB_XREF=gi:11451316 /DB_XREF=est:nab54b05.x1 /CLONE=IMAGE:3269696 /UG=Hs.88013 ESTs
236280_at_HG-U133B		ESTs	Consensus includes gb:AI225238 /FEA=EST /DB_XREF=gi:3807951 /DB_XREF=est:qx12c04.x1 /CLONE=IMAGE:2001126 /UG=Hs.176920 ESTs
236293_at_HG-U133B		ESTs	Consensus includes gb:BE676335 /FEA=EST /DB_XREF=gi:10036876 /DB_XREF=est:7f27d12.x1 /CLONE=IMAGE:3295895 /UG=Hs.283313 ESTs
236301_at_HG-U133B		Homo sapiens, clone IMAGE:3866403, mRNA	Consensus includes gb:AA789123 /FEA=EST /DB_XREF=gi:2849243 /DB_XREF=est:aa66f03.s1 /CLONE=IMAGE:825917 /UG=Hs.46645 ESTs
236341_at_HG-U133B	CTLA4	cytotoxic T-lymphocyte-associated protein 4	Consensus includes gb:AI733018 /FEA=EST /DB_XREF=gi:5054131 /DB_XREF=est:oh60h01.x5 /CLONE=IMAGE:1471441 /UG=Hs.313929 ESTs
236378_at_HG-U133B		ESTs, Weakly similar to CIB_HUMAN	Consensus includes gb:BF681360 /FEA=EST /DB_XREF=gi:11955255

		SNK INTERACTING PROTEIN 2-28 [H.sapiens]	/DB_XREF=est:602156549F1 /CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Weakly similar to A Chain A, Homology-Based Model Of Calcium-Saturated Cib H.sapiens
236458_at_HG-U133B		ESTs	Consensus includes gb:BE875072 /FEA=EST /DB_XREF=gi:10323848 /DB_XREF=est:601485941F1 /CLONE=IMAGE:3888275 /UG=Hs.9002 ESTs
236535_at_HG-U133B	FLJ22116	hypothetical protein FLJ22116	Consensus includes gb:AW069285 /FEA=EST /DB_XREF=gi:6024283 /DB_XREF=est:cr43f07.x1 /CLONE=HBMSC_cr43f07 /UG=Hs.159452 ESTs
236557_at_HG-U133B		ESTs, Weakly similar to Z295_HUMAN ZINC FINGER PROTEIN 295 [H.sapiens]	Consensus includes gb:AW085625 /FEA=EST /DB_XREF=gi:6040777 /DB_XREF=est:xb41d11.x1 /CLONE=IMAGE:2578869 /UG=Hs.186838 ESTs, Weakly similar to Z295_HUMAN ZINC FINGER PROTEIN 295 H.sapiens
236606_at_HG-U133B		ESTs	Consensus includes gb:N50912 /FEA=EST /DB_XREF=gi:1192078 /DB_XREF=est:yy93a05.s1 /CLONE=IMAGE:281072 /UG=Hs.47150 ESTs
236648_at_HG-U133B		ESTs	Consensus includes gb:AI684467 /FEA=EST /DB_XREF=gi:4895761 /DB_XREF=est:wa82d04.x1 /CLONE=IMAGE:2302663 /UG=Hs.144057 ESTs
236656_s_at_HG-U133B		ESTs	Consensus includes gb:AW014647 /FEA=EST /DB_XREF=gi:5863404 /DB_XREF=est:UI-H-BI0p-abd-b-12-0-UI.s1 /CLONE=IMAGE:2711375 /UG=Hs.265499 ESTs
236707_at_HG-U133B	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	Consensus includes gb:AA521016 /FEA=EST /DB_XREF=gi:2261559 /DB_XREF=est:aa70f04.s1 /CLONE=IMAGE:826303 /UG=Hs.185375 ESTs
236728_at_HG-U133B		ESTs	Consensus includes gb:AW070437 /FEA=EST /DB_XREF=gi:6025435 /DB_XREF=est:xa11b11.x1 /CLONE=IMAGE:2567997 /UG=Hs.26330 ESTs
236787_at_HG-U133B		ESTs	Consensus includes gb:AW591809 /FEA=EST /DB_XREF=gi:7278974 /DB_XREF=est:xx85d08.x1 /CLONE=IMAGE:2850447 /UG=Hs.126630 ESTs
236796_at_HG-U133B		ESTs	Consensus includes gb:AI052447 /FEA=EST /DB_XREF=gi:3308438 /DB_XREF=est:oz07g04.x1 /CLONE=IMAGE:1674678 /UG=Hs.118659 ESTs
236837_x_at_HG-U133B		ESTs	Consensus includes gb:BE669806 /FEA=EST /DB_XREF=gi:10030347 /DB_XREF=est:7e25b04.x1 /CLONE=IMAGE:3283471 /UG=Hs.129137 ESTs
236854_at_HG-U133B		ESTs	Consensus includes gb:AA743694 /FEA=EST /DB_XREF=gi:2784510

			/DB_XREF=est:ny92d07.s1 /CLONE=IMAGE:1285741 /UG=Hs.48984 ESTs
236892_s_at_HG-U133B	HOXB6	homeo box B6	Consensus includes gb:BF590528 /FEA=EST /DB_XREF=gi:11682852 /DB_XREF=est:7h36h10.x1 /CLONE=IMAGE:3318115 /UG=Hs.269918 ESTs
236908_at_HG-U133B		ESTs	Consensus includes gb:BE550429 /FEA=EST /DB_XREF=gi:9792121 /DB_XREF=est:7a25b09.x1 /CLONE=IMAGE:3219737 /UG=Hs.143905 ESTs
236914_at_HG-U133B		ESTs	Consensus includes gb:AW080028 /FEA=EST /DB_XREF=gi:6035180 /DB_XREF=est:xe11g09.x1 /CLONE=IMAGE:2606848 /UG=Hs.131601 ESTs
236979_at_HG-U133B		ESTs	Consensus includes gb:AI821801 /FEA=EST /DB_XREF=gi:5440880 /DB_XREF=est:nr06c07.x5 /CLONE=IMAGE:1161036 /UG=Hs.168974 ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens -
237006_at_HG-U133B		ESTs	Consensus includes gb:AA703523 /FEA=EST /DB_XREF=gi:2713441 /DB_XREF=est:zj12h12.s1 /CLONE=IMAGE:450119 /UG=Hs.24128 ESTs
237068_at_HG-U133B		ESTs	Consensus includes gb:AI871655 /FEA=EST /DB_XREF=gi:5545704 /DB_XREF=est:we28g08.x1 /CLONE=IMAGE:2342462 /UG=Hs.200815 ESTs
237291_at_HG-U133B		ESTs	Consensus includes gb:AI695007 /FEA=EST /DB_XREF=gi:4982907 /DB_XREF=est:we45c09.x1 /CLONE=IMAGE:2344048 /UG=Hs.159362 ESTs
237337_at_HG-U133B		ESTs	Consensus includes gb:AI539318 /FEA=EST /DB_XREF=gi:4453453 /DB_XREF=est:te45f03.x1 /CLONE=IMAGE:2089661 /UG=Hs.115580 ESTs
237411_at_HG-U133B	LOC153516	hypothetical protein BC010563	Consensus includes gb:N71063 /FEA=EST /DB_XREF=gi:1227643 /DB_XREF=est:za86a11.s1 /CLONE=IMAGE:299420 /UG=Hs.38173 ESTs
237431_at_HG-U133B		ESTs	Consensus includes gb:AW449838 /FEA=EST /DB_XREF=gi:6990614 /DB_XREF=est:UI-H-BI3-akm-d-12-0-UI.s1 /CLONE=IMAGE:2734894 /UG=Hs.97562 ESTs
237864_at_HG-U133B		ESTs	Consensus includes gb:AI990122 /FEA=EST /DB_XREF=gi:5837003 /DB_XREF=est:ws29d06.x1 /CLONE=IMAGE:2498603 /UG=Hs.196988 ESTs
238012_at_HG-U133B		ESTs	Consensus includes gb:AI620209 /FEA=EST /DB_XREF=gi:4629335 /DB_XREF=est:tu54d10.x1 /CLONE=IMAGE:2254867 /UG=Hs.37916 ESTs

238022_at_HG-U133B		ESTs	Consensus includes gb:AA954994 /FEA=EST /DB_XREF=gi:3118689 /DB_XREF=est:op24f03.s1 /CLONE=IMAGE:1577789 /UG=Hs.237396 ESTs
238026_at_HG-U133B	RPL35A	ribosomal protein L35a	Consensus includes gb:AI458020 /FEA=EST /DB_XREF=gi:4312038 /DB_XREF=est:tj66e05.x1 /CLONE=IMAGE:2146496 /UG=Hs.293287 ESTs
238039_at_HG-U133B		ESTs, Moderately similar to A53959 thromboxane A-2 receptor, endothelial [H.sapiens]	Consensus includes gb:BG180437 /FEA=EST /DB_XREF=gi:12687140 /DB_XREF=est:602331329F1 /CLONE=IMAGE:4432615 /UG=Hs.27167 ESTs
238055_at_HG-U133B			Consensus includes gb:BG505277 /FEA=EST /DB_XREF=gi:13466794 /DB_XREF=est:602551757F1 /CLONE=IMAGE:4663982 /UG=Hs.100501 ESTs, Highly similar to AT1C_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IC H.sapiens
238057_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp451H032 (from clone DKFZp451H032)	Consensus includes gb:AW195800 /FEA=EST /DB_XREF=gi:6475020 /DB_XREF=est:xn41b09.x1 /CLONE=IMAGE:2696249 /UG=Hs.149401 ESTs
238066_at_HG-U133B	RBP7	retinoid binding protein 7	Consensus includes gb:AI733027 /FEA=EST /DB_XREF=gi:5054140 /DB_XREF=est:oj14a06.x5 /CLONE=IMAGE:1492114 /UG=Hs.292718 ESTs, Weakly similar to RET2_HUMAN RETINOL-BINDING PROTEIN II, CELLULAR H.sapiens
238155_at_HG-U133B		ESTs	Consensus includes gb:AI638235 /FEA=EST /DB_XREF=gi:4690469 /DB_XREF=est:tt12a04.x1 /CLONE=IMAGE:2240526 /UG=Hs.171689 ESTs
238208_at_HG-U133B		ESTs	Consensus includes gb:N53978 /FEA=EST /DB_XREF=gi:1195144 /DB_XREF=est:yv60h12.s1 /CLONE=IMAGE:247175 /UG=Hs.113106 ESTs
238304_at_HG-U133B		ESTs	Consensus includes gb:R45137 /FEA=EST /DB_XREF=gi:823491 /DB_XREF=est:yg39f12.s1 /CLONE=IMAGE:34825 /UG=Hs.21868 ESTs
238365_s_at_HG-U133B		ESTs, Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus]	Consensus includes gb:AI638342 /FEA=EST /DB_XREF=gi:4690576 /DB_XREF=est:tt09g10.x1 /CLONE=IMAGE:2240322 /UG=Hs.158272 ESTs
238367_s_at_HG-		ESTs, Weakly similar to CA13 MOUSE	Consensus includes gb:AW015512 /FEA=EST /DB_XREF=gi:5864269

U133B		COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus]	/DB_XREF=est:UI-H-BI0p-aau-a-12-0-UI.s1 /CLONE=IMAGE:2710558 /UG=Hs.158272 ESTs
238376_at_HG-U133B		Homo sapiens cDNA FLJ30967 fis, clone HEART2000309, weakly similar to PTB-ASSOCIATED SPLICING FACTOR	Consensus includes gb:AI436581 /FEA=EST /DB_XREF=gi:4282842 /DB_XREF=est:ti03d04.x1 /CLONE=IMAGE:2129383 /UG=Hs.169738 ESTs
238392_at_HG-U133B		ESTs	Consensus includes gb:AW301504 /FEA=EST /DB_XREF=gi:6711181 /DB_XREF=est:xs78a03.x1 /CLONE=IMAGE:2775724 /UG=Hs.145480 ESTs
238516_at_HG-U133B	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	Consensus includes gb:BF247383 /FEA=EST /DB_XREF=gi:11162750 /DB_XREF=est:601858146F1 /CLONE=IMAGE:4068634 /UG=Hs.126351 ESTs
238583_at_HG-U133B		ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN CGI-131 [H.sapiens]	Consensus includes gb:BG023974 /FEA=EST /DB_XREF=gi:12409070 /DB_XREF=est:602303676F1 /CLONE=IMAGE:4394946 /UG=Hs.133878 ESTs, Weakly similar to AF151889 1 CGI-131 protein H.sapiens
238587_at_HG-U133B	MGC15437	nm23-phosphorylated unknown substrate	Consensus includes gb:AI927919 /FEA=EST /DB_XREF=gi:5663883 /DB_XREF=est:wp03d11.x1 /CLONE=IMAGE:2463765 /UG=Hs.187625 ESTs
238593_at_HG-U133B		ESTs	Consensus includes gb:AW962511 /FEA=EST /DB_XREF=gi:8152347 /DB_XREF=est:EST374584 /UG=Hs.152003 ESTs
238604_at_HG-U133B		ESTs	Consensus includes gb:AA768884 /FEA=EST /DB_XREF=gi:2820122 /DB_XREF=est:nz82e07.s1 /CLONE=IMAGE:1301988 /UG=Hs.140489 ESTs
238651_at_HG-U133B		ESTs	Consensus includes gb:BF512491 /FEA=EST /DB_XREF=gi:11597593 /DB_XREF=est:UI-H-BI3-alw-h-01-0-UI.s1 /CLONE=IMAGE:3069144 /UG=Hs.23096 ESTs
238652_at_HG-U133B		ESTs	Consensus includes gb:AW419203 /FEA=EST /DB_XREF=gi:6947135 /DB_XREF=est:xu31b03.x1 /CLONE=IMAGE:2801741 /UG=Hs.313541 ESTs
238686_at_HG-U133B	FBXO3	F-box only protein 3	Consensus includes gb:AA130258 /FEA=EST /DB_XREF=gi:1691420 /DB_XREF=est:zl29c04.r1 /CLONE=IMAGE:503334 /UG=Hs.332421 ESTs
238750_at_HG-U133B		ESTs	Consensus includes gb:AW083576 /FEA=EST /DB_XREF=gi:6038728 /DB_XREF=est:xc18g08.x1 /CLONE=IMAGE:2584670 /UG=Hs.218707 ESTs
238752_at_HG-U133B		ESTs	Consensus includes gb:AA780295 /FEA=EST /DB_XREF=gi:2839626

			/DB_XREF=est:af55h01.s1 /CLONE=IMAGE:1035601 /UG=Hs.122155 ESTs
238756_at_HG-U133B		ESTs	Consensus includes gb:AI860012 /FEA=EST /DB_XREF=gi:5513628 /DB_XREF=est:wm22g09.x1 /CLONE=IMAGE:2436736 /UG=Hs.41294 ESTs
238790_at_HG-U133B		ESTs, Weakly similar to lectin-like NK cell receptor [Homo sapiens] [H.sapiens]	Consensus includes gb:BE738988 /FEA=EST /DB_XREF=gi:10152980 /DB_XREF=est:601556050F1 /CLONE=IMAGE:3825757 /UG=Hs.156100 ESTs, Weakly similar to c-type lectin DCL1 M.musculus
238791_at_HG-U133B		ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	Consensus includes gb:AA282536 /FEA=EST /DB_XREF=gi:1925451 /DB_XREF=est:zs90d12.s1 /CLONE=IMAGE:704759 /UG=Hs.267124 ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
238824_at_HG-U133B		Homo sapiens cDNA FLJ30581 fis, clone BRAWH2007069	Consensus includes gb:BF844863 /FEA=EST /DB_XREF=gi:12200793 /DB_XREF=est:MR1-HT1136-221200-009-g07 /UG=Hs.145569 ESTs
238856_s_at_HG-U133B		Homo sapiens, clone MGC:17708 IMAGE:3868595, mRNA, complete cds	Consensus includes gb:BG108346 /FEA=EST /DB_XREF=gi:12602192 /DB_XREF=est:602280355F1 /CLONE=IMAGE:4368180 /UG=Hs.72045 ESTs
239054_at_HG-U133B		ESTs, Weakly similar to 810024G URF 2 [H.sapiens]	Consensus includes gb:BE348277 /FEA=EST /DB_XREF=gi:9260130 /DB_XREF=est:hw21g08.x1 /CLONE=IMAGE:3183614 /UG=Hs.144616 ESTs, Weakly similar to NADH dehydrogenase subunit 2 H.sapiens
239071_at_HG-U133B		ESTs	Consensus includes gb:AI972451 /FEA=EST /DB_XREF=gi:5769367 /DB_XREF=est:wr39h05.x1 /CLONE=IMAGE:2490105 /UG=Hs.173904 ESTs
239122_at_HG-U133B	IL24	interleukin 24	Consensus includes gb:AI638155 /FEA=EST /DB_XREF=gi:4690389 /DB_XREF=est:ts97a11.x1 /CLONE=IMAGE:2239196 /UG=Hs.176430 ESTs
239152_at_HG-U133B		ESTs	Consensus includes gb:AW263526 /FEA=EST /DB_XREF=gi:6640342 /DB_XREF=est:xn80d07.x1 /CLONE=IMAGE:2700781 /UG=Hs.243023 ESTs
239214_at_HG-U133B		ESTs	Consensus includes gb:AA806831 /FEA=EST /DB_XREF=gi:2876407 /DB_XREF=est:oc29b08.s1 /CLONE=IMAGE:1351095 /UG=Hs.123244 ESTs
239229_at_HG-U133B		ESTs	Consensus includes gb:AI342246 /FEA=EST /DB_XREF=gi:4079173 /DB_XREF=est:qt26g09.x1 /CLONE=IMAGE:1949152 /UG=Hs.50125 ESTs
239231_at_HG-U133B		ESTs, Weakly similar to ALUC_HUMAN	Consensus includes gb:BE464819 /FEA=EST /DB_XREF=gi:9510513

		!!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]	/DB_XREF=est:hs87d03.x1 /CLONE=IMAGE:3144197 /UG=Hs.63187 ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! H.sapiens
239263_at_HG-U133B		ESTs	Consensus includes gb:BE905194 /FEA=EST /DB_XREF=gi:10398233 /DB_XREF=est:601499220F1 /CLONE=IMAGE:3901109 /UG=Hs.97855 ESTs
239278_at_HG-U133B		ESTs, Weakly similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]	Consensus includes gb:AI471969 /FEA=EST /DB_XREF=gi:4334059 /DB_XREF=est:tj85a12.x1 /CLONE=IMAGE:2148286 /UG=Hs.182606 ESTs
239279_at_HG-U133B		ESTs	Consensus includes gb:AI862518 /FEA=EST /DB_XREF=gi:5526625 /DB_XREF=est:wj15a03.x1 /CLONE=IMAGE:2402860 /UG=Hs.158094 ESTs
239287_at_HG-U133B		ESTs	Consensus includes gb:AA769410 /FEA=EST /DB_XREF=gi:2820648 /DB_XREF=est:nz38f06.s1 /CLONE=IMAGE:1290083 /UG=Hs.128654 ESTs
239292_at_HG-U133B		ESTs	Consensus includes gb:AA825563 /FEA=EST /DB_XREF=gi:2898875 /DB_XREF=est:od55c12.s1 /CLONE=IMAGE:1371862 /UG=Hs.124786 ESTs
239302_s_at_HG-U133B		ESTs, Moderately similar to I60307 beta-galactosidase, alpha peptide - Escherichia coli [E.coli]	Consensus includes gb:AA931539 /FEA=EST /DB_XREF=gi:3085925 /DB_XREF=est:oo56a09.s1 /CLONE=IMAGE:1570168 /UG=Hs.293056 ESTs
239393_at_HG-U133B		ESTs	Consensus includes gb:AW510927 /FEA=EST /DB_XREF=gi:7149005 /DB_XREF=est:hd41d06.x1 /CLONE=IMAGE:2912075 /UG=Hs.125243 ESTs
239442_at_HG-U133B		ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:BF589179 /FEA=EST /DB_XREF=gi:11681503 /DB_XREF=est:nab28d04.x1 /CLONE=IMAGE:3267126 /UG=Hs.173776 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
239478_x_at_HG-U133B		ESTs	Consensus includes gb:AI761411 /FEA=EST /DB_XREF=gi:5177078 /DB_XREF=est:wg65c03.x1 /CLONE=IMAGE:2369956 /UG=Hs.169812 ESTs
239538_at_HG-U133B		ESTs	Consensus includes gb:BG548811 /FEA=EST /DB_XREF=gi:13547489 /DB_XREF=est:602576251F1 /CLONE=IMAGE:4704372 /UG=Hs.146509 ESTs
239597_at_HG-U133B		ESTs	Consensus includes gb:AA993566 /FEA=EST /DB_XREF=gi:3180111

			/DB_XREF=est:ot96g10.s1 /CLONE=IMAGE:1624674 /UG=Hs.159983 ESTs
239647_at_HG-U133B		ESTs, Weakly similar to chondroitin 4-sulfotransferase [Homo sapiens] [H.sapiens]	Consensus includes gb:AA677272 /FEA=EST /DB_XREF=gi:2657794 /DB_XREF=est:zj61c03.s1 /CLONE=IMAGE:454756 /UG=Hs.117048 ESTs
239651_at_HG-U133B		ESTs	Consensus includes gb:BE671583 /FEA=EST /DB_XREF=gi:10032124 /DB_XREF=est:7e54c10.x1 /CLONE=IMAGE:3286290 /UG=Hs.189394 ESTs
239679_at_HG-U133B		ESTs	Consensus includes gb:AI871160 /FEA=EST /DB_XREF=gi:5545128 /DB_XREF=est:wl79g10.x1 /CLONE=IMAGE:2431170 /UG=Hs.163778 ESTs
239699_s_at_HG-U133B		ESTs	Consensus includes gb:AW195920 /FEA=EST /DB_XREF=gi:6475150 /DB_XREF=est:xn86g08.x1 /CLONE=IMAGE:2701406 /UG=Hs.144252 ESTs
239791_at_HG-U133B	HOXB6	homeo box B6	Consensus includes gb:AI125255 /FEA=EST /DB_XREF=gi:3593769 /DB_XREF=est:qd87h09.x1 /CLONE=IMAGE:1736513 /UG=Hs.269918 ESTs
239824_s_at_HG-U133B	MGC10744	hypothetical protein MGC10744	Consensus includes gb:BF971873 /FEA=EST /DB_XREF=gi:12339088 /DB_XREF=est:602240462F1 /CLONE=IMAGE:4328990 /UG=Hs.25092 ESTs
239835_at_HG-U133B	KIAA1842	KIAA1842 protein	Consensus includes gb:AA669114 /FEA=EST /DB_XREF=gi:2630613 /DB_XREF=est:aa81h02.s1 /CLONE=IMAGE:827379 /UG=Hs.116665 ESTs
239956_at_HG-U133B		ESTs	Consensus includes gb:AW291535 /FEA=EST /DB_XREF=gi:6698171 /DB_XREF=est:UI-H-BI2-agk-b-12-0-UI.s1 /CLONE=IMAGE:2724454 /UG=Hs.254980 ESTs
240061_at_HG-U133B		ESTs	Consensus includes gb:AW664903 /FEA=EST /DB_XREF=gi:7457447 /DB_XREF=est:hi85e04.x1 /CLONE=IMAGE:2979102 /UG=Hs.186649 ESTs
240106_at_HG-U133B		ESTs, Weakly similar to A49175 Motch B protein - mouse [M.musculus]	Consensus includes gb:AI633523 /FEA=EST /DB_XREF=gi:4684853 /DB_XREF=est:th68b11.x1 /CLONE=IMAGE:2123805 /UG=Hs.44705 ESTs
240113_at_HG-U133B		ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:AI732466 /FEA=EST /DB_XREF=gi:5053579 /DB_XREF=est:zn87g06.x5 /CLONE=IMAGE:565210 /UG=Hs.193133 ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
240201_at_HG-U133B		ESTs	Consensus includes gb:AI821995 /FEA=EST /DB_XREF=gi:5441074

			/DB_XREF=est:ok97f07.x5 /CLONE=IMAGE:1521925 /UG=Hs.130173 ESTs
240239_at_HG-U133B	FLJ14779	hypothetical protein FLJ14779	Consensus includes gb:N63953 /FEA=EST /DB_XREF=gi:1211782 /DB_XREF=est:yz81b03.s1 /CLONE=IMAGE:289421 /UG=Hs.243662 ESTs
240269_at_HG-U133B		ESTs	Consensus includes gb:BF590274 /FEA=EST /DB_XREF=gi:11682598 /DB_XREF=est:nab22d01.x1 /CLONE=IMAGE:3266712 /UG=Hs.164923 ESTs
240449_at_HG-U133B	ZNF341	zinc finger protein 341	Consensus includes gb:AW204518 /FEA=EST /DB_XREF=gi:6503990 /DB_XREF=est:UI-H-BI1-aei-g-02-0-UI.s1 /CLONE=IMAGE:2719658 /UG=Hs.244601 ESTs
240572_s_at_HG-U133B		ESTs, Weakly similar to lectin-like NK cell receptor [Homo sapiens] [H.sapiens]	Consensus includes gb:BF436632 /FEA=EST /DB_XREF=gi:11449031 /DB_XREF=est:7p09b02.x1 /CLONE=IMAGE:3645243 /UG=Hs.156100 ESTs, Weakly similar to c-type lectin DCL1 M.musculus
240581_at_HG-U133B		ESTs	Consensus includes gb:AW007727 /FEA=EST /DB_XREF=gi:5856505 /DB_XREF=est:wt68d07.x1 /CLONE=IMAGE:2512621 /UG=Hs.132650 ESTs
240740_at_HG-U133B		ESTs	Consensus includes gb:AW182300 /FEA=EST /DB_XREF=gi:6450760 /DB_XREF=est:xj41a03.x1 /CLONE=IMAGE:2659756 /UG=Hs.112612 ESTs
240785_at_HG-U133B		ESTs	Consensus includes gb:BE671136 /FEA=EST /DB_XREF=gi:10031677 /DB_XREF=est:7e46d12.x1 /CLONE=IMAGE:3285527 /UG=Hs.243602 ESTs
240801_at_HG-U133B	C21orf37	chromosome 21 open reading frame 37	Consensus includes gb:N56968 /FEA=EST /DB_XREF=gi:1200858 /DB_XREF=est:yy56b01.s1 /CLONE=IMAGE:277513 /UG=Hs.46707 chromosome 21 open reading frame 37
240842_at_HG-U133B		ESTs	Consensus includes gb:AA853996 /FEA=EST /DB_XREF=gi:2941534 /DB_XREF=est:aj52a02.s1 /CLONE=IMAGE:1393898 /UG=Hs.269757 ESTs, Weakly similar to B34087 hypothetical protein H.sapiens
241353_s_at_HG-U133B		ESTs	Consensus includes gb:AW471181 /FEA=EST /DB_XREF=gi:7041287 /DB_XREF=est:xv13b04.x1 /CLONE=IMAGE:2812975 /UG=Hs.160874 ESTs
241370_at_HG-U133B		ESTs	Consensus includes gb:AA278233 /FEA=EST /DB_XREF=gi:1920173 /DB_XREF=est:zs77a10.r1 /CLONE=IMAGE:703482 /UG=Hs.100691 ESTs
241383_at_HG-U133B		ESTs	Consensus includes gb:H05959 /FEA=EST /DB_XREF=gi:869511

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			/DB_XREF=est:yl76d05.s1 /CLONE=IMAGE:44004 /UG=Hs.62189 ESTs
241395_at_HG-U133B		ESTs	Consensus includes gb:AL572553 /FEA=EST /DB_XREF=gi:12930934 /DB_XREF=est:AL572553 /CLONE=CS0DI008YD03 (3 prime) /UG=Hs.145990 ESTs
241421_at_HG-U133B		ESTs	Consensus includes gb:N92599 /FEA=EST /DB_XREF=gi:1264908 /DB_XREF=est:zb27d04.s1 /CLONE=IMAGE:304807 /UG=Hs.130694 ESTs
241464_s_at_HG-U133B		ESTs	Consensus includes gb:AI973033 /FEA=EST /DB_XREF=gi:5769859 /DB_XREF=est:wr46g03.x1 /CLONE=IMAGE:2490772 /UG=Hs.126691 ESTs
241483_at_HG-U133B		ESTs	Consensus includes gb:AA156795 /FEA=EST /DB_XREF=gi:1728410 /DB_XREF=est:zl20a03.s1 /CLONE=IMAGE:502444 /UG=Hs.62772 ESTs
241525_at_HG-U133B		ESTs	Consensus includes gb:AV700191 /FEA=EST /DB_XREF=gi:10302162 /DB_XREF=est:AV700191 /CLONE=GKCEKG11 /UG=Hs.132051 ESTs
241734_at_HG-U133B		Homo sapiens cDNA FLJ25286 fis, clone STM06909	Consensus includes gb:AI391443 /FEA=EST /DB_XREF=gi:4217447 /DB_XREF=est:tf96e06.x1 /CLONE=IMAGE:2107138 /UG=Hs.107622 ESTs
241742_at_HG-U133B	PRAM-1	PRAM-1 protein	Consensus includes gb:AW027174 /FEA=EST /DB_XREF=gi:5885930 /DB_XREF=est:wt72c10.x1 /CLONE=IMAGE:2513010 /UG=Hs.239276 ESTs, Weakly similar to FYB_HUMAN FYN-BINDING PROTEIN H.sapiens
241754_at_HG-U133B		ESTs	Consensus includes gb:AA829836 /FEA=EST /DB_XREF=gi:2902935 /DB_XREF=est:od40c07.s1 /CLONE=IMAGE:1370412 /UG=Hs.59504 ESTs
241795_at_HG-U133B		ESTs	Consensus includes gb:AA678073 /FEA=EST /DB_XREF=gi:2658595 /DB_XREF=est:zi12g12.s1 /CLONE=IMAGE:430630 /UG=Hs.129827 ESTs
241810_at_HG-U133B		ESTs	Consensus includes gb:BF509144 /FEA=EST /DB_XREF=gi:11592442 /DB_XREF=est:UI-H-BI4-aov-a-05-0-UI.s1 /CLONE=IMAGE:3086097 /UG=Hs.202088 ESTs
241930_x_at_HG-U133B		ESTs	Consensus includes gb:AA223204 /FEA=EST /DB_XREF=gi:1843755 /DB_XREF=est:zr06c05.s1 /CLONE=IMAGE:650696 /UG=Hs.186898 ESTs
241969_at_HG-U133B	ITM2B	integral membrane protein 2B	Consensus includes gb:AA150242 /FEA=EST /DB_XREF=gi:1721773 /DB_XREF=est:zl07c04.s1 /CLONE=IMAGE:491622 /UG=Hs.323529 ESTs,

			Highly similar to S27963 modulator recognition factor 2 H.sapiens
241975_at_HG-U133B		ESTs	Consensus includes gb:N29850 /FEA=EST /DB_XREF=gi:1148370 /DB_XREF=est:yw94a12.s1 /CLONE=IMAGE:259870 /UG=Hs.44098 ESTs
241985_at_HG-U133B		ESTs	Consensus includes gb:AI814405 /FEA=EST /DB_XREF=gi:5425620 /DB_XREF=est:wj72g03.x1 /CLONE=IMAGE:2408404 /UG=Hs.224569 ESTs
242065_x_at_HG-U133B	KIAA0982	KIAA0982 protein	Consensus includes gb:BG477984 /FEA=EST /DB_XREF=gi:13410263 /DB_XREF=est:602522982F1 /CLONE=IMAGE:4641356 /UG=Hs.147801 ESTs
242104_at_HG-U133B		ESTs, Moderately similar to PRO0478 protein [Homo sapiens] [H.sapiens]	Consensus includes gb:AA826288 /FEA=EST /DB_XREF=gi:2899600 /DB_XREF=est:od03h09.s1 /CLONE=IMAGE:1358177 /UG=Hs.191782 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
242223_at_HG-U133B		ESTs	Consensus includes gb:AA505323 /FEA=EST /DB_XREF=gi:2241460 /DB_XREF=est:nh83c08.s1 /CLONE=IMAGE:965102 /UG=Hs.151609 ESTs
242292_at_HG-U133B		Homo sapiens, similar to melanoma antigen, family A, 11, clone MGC:34827 IMAGE:5199470, mRNA, complete cds	Consensus includes gb:H12084 /FEA=EST /DB_XREF=gi:876904 /DB_XREF=est:ym11g10.s1 /CLONE=IMAGE:47703 /UG=Hs.31110 ESTs, Weakly similar to MAGE-B4 H.sapiens
242329_at_HG-U133B		ESTs	Consensus includes gb:AW071804 /FEA=EST /DB_XREF=gi:6026729 /DB_XREF=est:ws53h03.x1 /CLONE=IMAGE:2500949 /UG=Hs.152541 ESTs
242363_at_HG-U133B		ESTs	Consensus includes gb:BF592008 /FEA=EST /DB_XREF=gi:11684332 /DB_XREF=est:7o35e09.x1 /CLONE=IMAGE:3576280 /UG=Hs.87372 ESTs
242388_x_at_HG-U133B		ESTs	Consensus includes gb:AW576600 /FEA=EST /DB_XREF=gi:7248139 /DB_XREF=est:UI-HF-BR0p-ajy-c-07-0-UI.s1 /CLONE=IMAGE:3076212 /UG=Hs.123581 ESTs
242404_at_HG-U133B		ESTs	Consensus includes gb:AW518888 /FEA=EST /DB_XREF=gi:7156970 /DB_XREF=est:ha45g06.x1 /CLONE=IMAGE:2876698 /UG=Hs.40937 ESTs
242414_at_HG-U133B		ESTs	Consensus includes gb:AW960707 /FEA=EST /DB_XREF=gi:8150391 /DB_XREF=est:EST372778 /UG=Hs.148324 ESTs
242434_at_HG-U133B		Homo sapiens cDNA FLJ31093 fis, clone	Consensus includes gb:AW771952 /FEA=EST /DB_XREF=gi:7704001

		IMR321000161	/DB_XREF=est:hn66h01.x1 /CLONE=IMAGE:3032881 /UG=Hs.191581 ESTs
242448_at_HG-U133B		ESTs, Weakly similar to neuronal thread protein [Homo sapiens] [H.sapiens]	Consensus includes gb:AI800895 /FEA=EST /DB_XREF=gi:5366367 /DB_XREF=est:wg14b02.x1 /CLONE=IMAGE:2365035 /UG=Hs.131929 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
242458_at_HG-U133B		ESTs	Consensus includes gb:AA721230 /FEA=EST /DB_XREF=gi:2737365 /DB_XREF=est:nz72b04.s1 /CLONE=IMAGE:1300975 /UG=Hs.102398 ESTs
242463_x_at_HG-U133B		ESTs, Weakly similar to A32891 finger protein 1, placental [H.sapiens]	Consensus includes gb:AI620827 /FEA=EST /DB_XREF=gi:4629953 /DB_XREF=est:tu86c12.x1 /CLONE=IMAGE:2257942 /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental H.sapiens
242520_s_at_HG-U133B		ESTs	Consensus includes gb:AW511110 /FEA=EST /DB_XREF=gi:7149188 /DB_XREF=est:hd43d06.x1 /CLONE=IMAGE:2912267 /UG=Hs.193754 ESTs
242525_at_HG-U133B		ESTs	Consensus includes gb:AA747436 /FEA=EST /DB_XREF=gi:2787394 /DB_XREF=est:nx88f10.s1 /CLONE=IMAGE:1269355 /UG=Hs.163105 ESTs
242541_at_HG-U133B	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	Consensus includes gb:AV692159 /FEA=EST /DB_XREF=gi:10294022 /DB_XREF=est:AV692159 /CLONE=GKCAOB12 /UG=Hs.301496 ESTs
242633_x_at_HG-U133B		ESTs	Consensus includes gb:AA829635 /FEA=EST /DB_XREF=gi:2902734 /DB_XREF=est:od35a09.s1 /CLONE=IMAGE:1369912 /UG=Hs.186589 ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
242695_at_HG-U133B		ESTs	Consensus includes gb:BF512254 /FEA=EST /DB_XREF=gi:11597433 /DB_XREF=est:UI-H-BW1-amb-a-09-0-UI.s1 /CLONE=IMAGE:3069209 /UG=Hs.126767 ESTs
242729_at_HG-U133B		ESTs, Moderately similar to I38344 titin, cardiac muscle [H.sapiens]	Consensus includes gb:BE551384 /FEA=EST /DB_XREF=gi:9793076 /DB_XREF=est:7b64a09.x1 /CLONE=IMAGE:3232984 /UG=Hs.166999 ESTs, Moderately similar to I38344 titin, cardiac muscle H.sapiens
242738_s_at_HG-U133B		ESTs	Consensus includes gb:BG402859 /FEA=EST /DB_XREF=gi:13296307 /DB_XREF=est:602418552F1 /CLONE=IMAGE:4525500 /UG=Hs.163208 ESTs

242774_at_HG-U133B	SYNE-2	synaptic nuclei expressed gene 2	Consensus includes gb:AI684761 /FEA=EST /DB_XREF=gi:4896055 /DB_XREF=est:wa85h04.x1 /CLONE=IMAGE:2302999 /UG=Hs.201552 ESTs, Weakly similar to T17288 hypothetical protein DKFZp434P1550.1 H.sapiens
242845_at_HG-U133B			Consensus includes gb:AI366780 /FEA=EST /DB_XREF=gi:4136525 /DB_XREF=est:qq41d08.x1 /CLONE=IMAGE:1935087 /UG=Hs.144995 ESTs
242866_x_at_HG-U133B		ESTs	Consensus includes gb:BF509229 /FEA=EST /DB_XREF=gi:11592527 /DB_XREF=est:UI-H-BI4-aow-a-04-0-UI.s1 /CLONE=IMAGE:3086118 /UG=Hs.147381 ESTs
242932_at_HG-U133B		ESTs	Consensus includes gb:AW292329 /FEA=EST /DB_XREF=gi:6698965 /DB_XREF=est:UI-H-BI2-agy-h-05-0-UI.s1 /CLONE=IMAGE:2726240 /UG=Hs.163481 ESTs
242975_s_at_HG-U133B	GNAS	GNAS complex locus	Consensus includes gb:AV753357 /FEA=EST /DB_XREF=gi:10911205 /DB_XREF=est:AV753357 /CLONE=NPDAVC03 /UG=Hs.159354 ESTs
243000_at_HG-U133B		Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572	Consensus includes gb:AW194766 /FEA=EST /DB_XREF=gi:6473684 /DB_XREF=est:xn31a04.x1 /CLONE=IMAGE:2695278 /UG=Hs.209382 ESTs
243020_at_HG-U133B		ESTs	Consensus includes gb:R06738 /FEA=EST /DB_XREF=gi:757358 /DB_XREF=est:yf11a03.s1 /CLONE=IMAGE:126508 /UG=Hs.220823 ESTs
243024_at_HG-U133B		ESTs, Weakly similar to I38598 zinc finger protein ZNF132 [H.sapiens]	Consensus includes gb:AI024029 /FEA=EST /DB_XREF=gi:3239073 /DB_XREF=est:ow70f06.s1 /CLONE=IMAGE:1652195 /UG=Hs.293707 ESTs, Weakly similar to I38598 zinc finger protein ZNF132 H.sapiens
243030_at_HG-U133B		ESTs	Consensus includes gb:AA211369 /FEA=EST /DB_XREF=gi:1810023 /DB_XREF=est:zp51h10.s1 /CLONE=IMAGE:613027 /UG=Hs.269493 ESTs
243154_at_HG-U133B		ESTs	Consensus includes gb:AA215381 /FEA=EST /DB_XREF=gi:1815191 /DB_XREF=est:zr97c09.s1 /CLONE=IMAGE:683632 /UG=Hs.86650 ESTs
243228_at_HG-U133B		ESTs	Consensus includes gb:BF980709 /FEA=EST /DB_XREF=gi:12383456 /DB_XREF=est:602303749F1 /CLONE=IMAGE:4395156 /UG=Hs.32406 ESTs
243362_s_at_HG-U133B	LEF1	lymphoid enhancer-binding factor 1	Consensus includes gb:AA992805 /FEA=EST /DB_XREF=gi:3178539 /DB_XREF=est:ot85a07.s1 /CLONE=IMAGE:1623540 /UG=Hs.171865 ESTs

243363_at_HG-U133B	LEF1	lymphoid enhancer-binding factor 1	Consensus includes gb:AA992805 /FEA=EST /DB_XREF=gi:3178539 /DB_XREF=est:ot85a07.s1 /CLONE=IMAGE:1623540 /UG=Hs.171865 ESTs
243493_at_HG-U133B		ESTs	Consensus includes gb:T97977 /FEA=EST /DB_XREF=gi:747322 /DB_XREF=est:ye58g09.s1 /CLONE=IMAGE:121984 /UG=Hs.60260 ESTs
243538_at_HG-U133B		ESTs	Consensus includes gb:AA738314 /FEA=EST /DB_XREF=gi:2769071 /DB_XREF=est:nx16g04.s1 /CLONE=IMAGE:1256310 /UG=Hs.5840 ESTs
243579_at_HG-U133B	MSI2	musashi homolog 2 (Drosophila)	Consensus includes gb:BF029215 /FEA=EST /DB_XREF=gi:10736927 /DB_XREF=est:601765432F1 /CLONE=IMAGE:3997687 /UG=Hs.173179 ESTs, Weakly similar to JW0079 heterogeneous nuclear ribonucleoprotein homolog JKTBP H.sapiens
243756_at_HG-U133B		ESTs	Consensus includes gb:AI057226 /FEA=EST /DB_XREF=gi:3331092 /DB_XREF=est:oz11c08.x1 /CLONE=IMAGE:1675022 /UG=Hs.120855 ESTs
243764_at_HG-U133B		ESTs	Consensus includes gb:AW085312 /FEA=EST /DB_XREF=gi:6040464 /DB_XREF=est:xe08f05.x1 /CLONE=IMAGE:2606529 /UG=Hs.177164 ESTs
243780_at_HG-U133B		ESTs	Consensus includes gb:AW575863 /FEA=EST /DB_XREF=gi:7247498 /DB_XREF=est:UI-HF-BL0-aci-e-03-0-UI.s1 /CLONE=IMAGE:3059045 /UG=Hs.136232 ESTs
243798_at_HG-U133B		ESTs	Consensus includes gb:AI436580 /FEA=EST /DB_XREF=gi:4282834 /DB_XREF=est:ti03d03.x1 /CLONE=IMAGE:2129381 /UG=Hs.257490 ESTs
243859_at_HG-U133B		ESTs	Consensus includes gb:AW237390 /FEA=EST /DB_XREF=gi:6569779 /DB_XREF=est:xm71b10.x1 /CLONE=IMAGE:2689627 /UG=Hs.250488 ESTs
243932_at_HG-U133B		ESTs	Consensus includes gb:AI286254 /FEA=EST /DB_XREF=gi:3924487 /DB_XREF=est:qu91a02.x1 /CLONE=IMAGE:1979402 /UG=Hs.149809 ESTs
243968_x_at_HG-U133B		ESTs	Consensus includes gb:AI572979 /FEA=EST /DB_XREF=gi:4536353 /DB_XREF=est:tn64g01.x1 /CLONE=IMAGE:2174352 /UG=Hs.174767 ESTs
244147_at_HG-U133B		ESTs	Consensus includes gb:AA777639 /FEA=EST /DB_XREF=gi:2837118 /DB_XREF=est:zi95c04.s1 /CLONE=IMAGE:448518 /UG=Hs.118088 ESTs
244230_at_HG-U133B		ESTs	Consensus includes gb:AW263527 /FEA=EST /DB_XREF=gi:6640343

			/DB_XREF=est:xn80d08.x1 /CLONE=IMAGE:2700783 /UG=Hs.293142 ESTs
244248_at_HG-U133B		ESTs	Consensus includes gb:AI129850 /FEA=EST /DB_XREF=gi:3598364 /DB_XREF=est:qc35a12.x1 /CLONE=IMAGE:1711582 /UG=Hs.133396 ESTs
244257_at_HG-U133B		ESTs	Consensus includes gb:AI363185 /FEA=EST /DB_XREF=gi:4114806 /DB_XREF=est:qy68e05.x1 /CLONE=IMAGE:2017184 /UG=Hs.192121 ESTs
244261_at_HG-U133B		ESTs	Consensus includes gb:AW340139 /FEA=EST /DB_XREF=gi:6836765 /DB_XREF=est:hc93h01.x1 /CLONE=IMAGE:2907601 /UG=Hs.105866 ESTs
244523_at_HG-U133B	MMD	monocyte to macrophage differentiation-associated	Consensus includes gb:AW104453 /FEA=EST /DB_XREF=gi:6075188 /DB_XREF=est:xd78b02.x1 /CLONE=IMAGE:2603691 /UG=Hs.99734 ESTs
244550_at_HG-U133B		ESTs	Consensus includes gb:AA552017 /FEA=EST /DB_XREF=gi:2322269 /DB_XREF=est:ng01g11.s1 /CLONE=IMAGE:928196 /UG=Hs.162245 ESTs
244636_at_HG-U133B		ESTs	Consensus includes gb:AL042699 /FEA=EST /DB_XREF=gi:5422148 /DB_XREF=est:DKFZp434P0421_s1 /CLONE=DKFZp434P0421 /UG=Hs.209222 ESTs
244652_at_HG-U133B		ESTs	Consensus includes gb:AW444868 /FEA=EST /DB_XREF=gi:6986630 /DB_XREF=est:UI-H-BI3-ajz-a-11-0-UI.s1 /CLONE=IMAGE:2733237 /UG=Hs.190129 ESTs
244740_at_HG-U133B		Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds	Consensus includes gb:BE855713 /FEA=EST /DB_XREF=gi:10368199 /DB_XREF=est:7g08d09.x1 /CLONE=IMAGE:3305873 /UG=Hs.23133 ESTs, Weakly similar to A33569 alcohol sulfotransferase R.norvegicus
244876_at_HG-U133B		ESTs	Consensus includes gb:BF112140 /FEA=EST /DB_XREF=gi:10941830 /DB_XREF=est:7l40g11.x1 /CLONE=IMAGE:3524156 /UG=Hs.191950 ESTs
266_s_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region
32541_at_HG-U133A	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	Cluster Incl. S46622:calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] /cds=(286,1794) /gb=S46622 /gi=258000 /ug=Hs.75206 /len=2134
34210_at_HG-U133A	CDW52	CDW52 antigen (CAMPATH-1 antigen)	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-

			301723 /clone_end=3' /gb=N90866 /gi=1444193 /ug=Hs.214742-/len=577
34689_at_HG-U133A	TREX1	three prime repair exonuclease 1	Cluster Incl. AJ243797:Homo sapiens mRNA for deoxyribonuclease III (drn3 gene) /cds=(256,1170) /gb=AJ243797 /gi=5524926 /ug=Hs.23595 /len=1239
34726_at_HG-U133A	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	Cluster Incl. U07139:Human voltage-gated calcium channel beta subunit mRNA, complete cds /cds=(34,1488) /gb=U07139 /gi=463890 /ug=Hs.239447 /len=2532
35666_at_HG-U133A	SEMA3F	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	Cluster Incl. U38276:Human semaphorin III family homolog mRNA, complete cds /cds=(315,2576) /gb=U38276 /gi=1061350 /ug=Hs.32981 /len=3534
35974_at_HG-U133A	LRMP	lymphoid-restricted membrane protein	Cluster Incl. U10485:Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds /cds=(574,2241) /gb=U10485 /gi=505685 /ug=Hs.40202 /len=2417
36004_at_HG-U133A	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	Cluster Incl. AF074382:Homo sapiens IkB kinase gamma subunit (IKK-gamma) mRNA, complete cds /cds=(148,1407) /gb=AF074382 /gi=3641279 /ug=Hs.43505 /len=1976
36566_at_HG-U133A	CTNS	cystinosis, nephropathic	Cluster Incl. AJ222967:Homo sapiens mRNA for cystinosin /cds=(339,1442) /gb=AJ222967 /gi=3036839 /ug=Hs.64837 /len=2611
36612_at_HG-U133A	KIAA0280	KIAA0280 protein	Cluster Incl. D87470:Human mRNA for KIAA0280 gene, partial cds /cds=(0,876) /gb=D87470 /gi=1665822 /ug=Hs.75400 /len=6837
36920_at_HG-U133A	MTM1	myotubular myopathy 1	Cluster Incl. U46024:Homo sapiens myotubularin (MTM1) mRNA, complete cds /cds=(54,1865) /gb=U46024 /gi=1378039 /ug=Hs.75302 /len=3411
37152_at_HG-U133A	PPARD	peroxisome proliferative activated receptor, delta	Cluster Incl. L07592:Human peroxisome proliferator activated receptor mRNA, complete cds /cds=(337,1662) /gb=L07592 /gi=190229 /ug=Hs.106415 /len=3301
37424_at_HG-U133A	HCR	HCR (a-helix coiled-coil rod homologue)	Cluster Incl. AB029343:Homo sapiens HCR (a-helix coiled-coil rod homologue) gene, complete cds /cds=(22,2292) /gb=AB029343 /gi=5360900 /ug=Hs.110746 /len=2445
37831_at_HG-U133A	KIAA0545	KIAA0545 protein	Cluster Incl. AB011117:Homo sapiens mRNA for KIAA0545 protein, partial

			cds /cds=(0,3390) /gb=AB011117 /gi=3043613 /ug=Hs.129943 /len=5520
38149_at_HG-U133A	KIAA0053	KIAA0053 gene product	Cluster Incl. D29642:Human mRNA for KIAA0053 gene, complete cds /cds=(193,2109) /gb=D29642 /gi=473934 /ug=Hs.1528 /len=2739
38269_at_HG-U133A	PKD2	protein kinase D2	Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630) /gb=AL050147 /gi=4884153 /ug=Hs.91146 /len=1837
38340_at_HG-U133A	HIP12	huntingtin interacting protein 12	Cluster Incl. AB014555:Homo sapiens mRNA for KIAA0655 protein, partial cds /cds=(0,3253) /gb=AB014555 /gi=3327123 /ug=Hs.96731 /len=4457
38487_at_HG-U133A	FLJ12442	hypothetical protein FLJ12442	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777
39650_s_at_HG-U133A	KIAA0435	KIAA0435 gene product	Cluster Incl. AB007895:Homo sapiens KIAA0435 mRNA, complete cds /cds=(1195,3528) /gb=AB007895 /gi=2662150 /ug=Hs.31438 /len=5347
39835_at_HG-U133A	SBF1	SET binding factor 1	Cluster Incl. U93181:Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds /cds=(0,5095) /gb=U93181 /gi=3015537 /ug=Hs.112049 /len=5228
40148_at_HG-U133A	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	Cluster Incl. U62325:Human FE65-like protein (hFE65L) mRNA, partial cds /cds=(0,2194) /gb=U62325 /gi=1657751 /ug=Hs.15740 /len=2896
40189_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	Cluster Incl. M93651:Human set gene, complete cds /cds=(3,836) /gb=M93651 /gi=338038 /ug=Hs.145279 /len=2562
41220_at_HG-U133A	MSF	MLL septin-like fusion	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938
41553_at_HG-U133A	C8orf1	chromosome 8 open reading frame 1	Cluster Incl. AI738702:wi22b11.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2390973 /clone_end=3' /gb=AI738702 /gi=5100683 /ug=Hs.40539 /len=650
41577_at_HG-U133A	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	Cluster Incl. AB020630:Homo sapiens mRNA for KIAA0823 protein, partial cds /cds=(0,1239) /gb=AB020630 /gi=4240131 /ug=Hs.45719 /len=5597
41660_at_HG-U133A	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog,	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar

		Drosophila)	to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438
44065_at_HG-U133A	FLJ14827	hypothetical protein FLJ14827	Cluster Incl. AI937468:wp77e05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2467808 /clone_end=3' /gb=AI937468 /gi=5676338 /ug=Hs.235849 /len=516
44563_at_HG-U133A	FLJ10385	hypothetical protein FLJ10385	Cluster Incl. AI858000:wj69b05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2408049 /clone_end=3' /gb=AI858000 /gi=5511616 /ug=Hs.30922 /len=715
44669_at_HG-U133A		ESTs, Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus]	Cluster Incl. N31716:yy15c12.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-271318 /clone_end=3' /gb=N31716 /gi=1152115 /ug=Hs.31754 /len=624
44790_s_at_HG-U133A	FLJ21562	hypothetical protein FLJ21562	Cluster Incl. AI129310:qc48a05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1712816 /clone_end=3' /gb=AI129310 /gi=3597824 /ug=Hs.234923 /len=811
45633_at_HG-U133A	FLJ13912	hypothetical protein FLJ13912	Cluster Incl. AI421812:tf55a07.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2103156 /clone_end=3' /gb=AI421812 /gi=4267743 /ug=Hs.47125 /len=556
46142_at_HG-U133A	FLJ12681	hypothetical protein FLJ12681	Cluster Incl. AI003763:ou91e02.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1635194 /clone_end=3' /gb=AI003763 /gi=3213273 /ug=Hs.58362 /len=594
49306_at_HG-U133A	AD037	AD037 protein	Cluster Incl. AI890191:wm79f05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2442177 /clone_end=3' /gb=AI890191 /gi=5595355 /ug=Hs.239937 /len=674
49485_at_HG-U133A	PRDM4	PR domain containing 4	Cluster Incl. W22625:71E5 Homo sapiens cDNA /clone=(not-directional) /gb=W22625 /gi=1299507 /ug=Hs.21807 /len=632
50221_at_HG-U133A		Homo sapiens, Similar to transcription factor EB, clone IMAGE:3944945, mRNA, partial cds	Cluster Incl. AI524138:th09f03.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2117789 /clone_end=3' /gb=AI524138 /gi=4438273 /ug=Hs.23391 /len=834
50277_at_HG-U133A	GGA1	golgi associated, gamma adaptin ear	Cluster Incl. AW001443:wu31e12.x1 Homo sapiens cDNA, 3' end

		containing, ARF binding protein 1	/clone=IMAGE-990785 /clone_end=3' /gb=AW001443 /gi=5848359 /ug=Hs.239110 /len=490
51192_at_HG-U133A	SSH-3	slingshot 3	Cluster Incl. AA134926:zo23d02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-587715 /clone_end=3' /gb=AA134926 /gi=1696027 /ug=Hs.29173 /len=535
54970_at_HG-U133A	DKFZP761I2123	KIAA1886 protein	Cluster Incl. AA868332:ak40h05.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1408473 /clone_end=3' /gb=AA868332 /gi=2963777 /ug=Hs.77978 /len=481
55093_at_HG-U133A	KIAA1402	KIAA1402 protein	Cluster Incl. AA534198:nj21a11.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-993116 /clone_end=3' /gb=AA534198 /gi=2278214 /ug=Hs.86392 /len=603
56256_at_HG-U133A	LOC51092	CGI-40 protein	Cluster Incl. AA150165:zl06h03.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-491573 /clone_end=5' /gb=AA150165 /gi=1721695 /ug=Hs.20102 /len=576
56919_at_HG-U133A	KIAA1449	WD repeat endosomal protein	Cluster Incl. AI806628:wf14g08.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2350622 /clone_end=3' /gb=AI806628 /gi=5393194 /ug=Hs.109778 /len=557
57588_at_HG-U133A	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	Cluster Incl. R62432:yg52e11.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-36023 /clone_end=3' /gb=R62432 /gi=834311 /ug=Hs.12321 /len=487
58780_s_at_HG-U133A	FLJ10357	hypothetical protein FLJ10357	Cluster Incl. R42449:yg02a07.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-30831 /clone_end=3' /gb=R42449 /gi=817213 /ug=Hs.235831 /len=431
59697_at_HG-U133A		ESTs, Weakly similar to RAB8_HUMAN RAS-RELATED PROTEIN RAB-8 [H.sapiens]	Cluster Incl. AA582932:nn80a11.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1090172 /clone_end=3' /gb=AA582932 /gi=2360292 /ug=Hs.21349 /len=614
635_s_at_HG-U133A	PPP2R5B	protein phosphatase 2, regulatory subunit B (B56), beta isoform	L42374 /FEATURE=mRNA /DEFINITION=HUMPP2ABA Homo sapiens protein phosphatase 2A B56-beta (PP2A) mRNA, complete cds
64942_at_HG-U133A		ESTs	Cluster Incl. AI937160:wp73h02.x1 Homo sapiens cDNA, 3' end

			/clone=IMAGE-2467443 /clone_end=3' /gb=AI937160 /gi=5676030 /ug=Hs.7967 /len=552
74694_s_at_HG-U133A	FLJ23282	hypothetical protein FLJ23282	Cluster Incl. AA907940:ol24e02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1524410 /clone_end=3' /gb=AA907940 /gi=3041944 /ug=Hs.234006 /len=404
77508_r_at_HG-U133A	FLJ23282	hypothetical protein FLJ23282	Cluster Incl. AW001436:wu31e04.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-990769 /clone_end=3' /gb=AW001436 /gi=5848352 /ug=Hs.170253 /len=471
90610_at_HG-U133A	LRRN1	leucine-rich repeat protein, neuronal 1	Cluster Incl. AI654857:wb65b10.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2310523 /clone_end=3' /gb=AI654857 /gi=4738836 /ug=Hs.160115 /len=621
AFFX-M27830_5_at_HG-U133A			M27830 Human 28S ribosomal RNA gene, complete cds (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-M27830_5_at_HG-U133B			M27830 Human 28S ribosomal RNA gene, complete cds (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-M27830_M_at_HG-U133A			M27830 Human 28S ribosomal RNA gene, complete cds (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-r2-Bs-dap-3_at_HG-U133A			Bacillus subtilis /REF=L38424 /DEF=B subtilis dapB, jojF, jojG genes corresponding to nucleotides 2634-3089 of L38424 /LEN=1931 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-r2-Ec-bioD-3_at_HG-U133A			Escherichia coli /REF=J04423 /DEF=E coli bioD gene dethiobiotin synthetase corresponding to nucleotides 5312-5559 of J04423 /LEN=676 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

Table 44

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Table 45:

AffyID	Accession Number	Sequence
1007_s_at	gb|U48705	Human receptor tyrosine kinase DDR gene Homo sapiens TNF receptor-1 associated protein (TRADD) mRNA, 3' end of cdsctggcgggcgtgggaacccaggccccgccgaggcggccaggaggtgagatggcagctgggcaaaatgggcacgaagagtgggtgggcagcgcatacctgtttgtggag tcctcgctggacaaggtggtcctgtcggatgcctacgcgcacccccagcagaaggtggcagtgtacagggctctgcaggctgccttggcagagagcggcgggagcccggacgtg ctgcagatgctgaagatccaccgcagcgacccgcagctgatcgtgcagctgcgattctgcgggcggcagccctgtggccgcttcctccgcgcctaccgcgaggggcgctgcgc gccgcgctgcagaggagcctggcggccgcgctcgcccagcactcggtgccgctgcaactggagctgcgcgccggcgccgagcggctggacgctttgctggcggacgaggagc gctgtttgagttgcatcctagcccagcagcccgaccggctccgggatgaagaactggctgagctggaggatgcgctgcgaaatctgaagtgcggctcgggggcccggggtggcg acggggaggtcgcttcggccccttgcagccccggtgccctctctgtcggaggtgaagccgccgccgccgccgccacctgcccagacttttctgttccagggtcagcctgtagtga atcggccgctgagcctgaaggaccaacagacgttcgcgcgctctgtgggtctcaaatggcgcaaggtggggcgctcactgcagcgaggctgccgggcgctgcgggacccggcg ctggactcgctggcctacgagtacgagcgcgagggactgtacgagcaggccttccagctgctgcggcgcttcgtgcaggccgagggccgccgcgccacgctgcagcgcctggtg gaggcactcgaggagaacgagctcaccagcctggcagaggacttgctgggcctgaccgatcccaatggcggcctggcctagaccaggggtgcagccagcttttggagaacctg gatggccttagggttccttctgcggctattgctgaaccccctgtccatccacgggaccctgaaactccacttggcctatctgctggacctgctggggcagagttgattgccttccccaggag ccagaccactgggggtgcatcattggggattctgcctcaggtactttgatagagtgtggggtgggggggacttgctttggagatcagcctcaccttctcccatcccagaagcggggctt acagccagcccttacagtttcactcatgaagcaccttgatctttggtgtcctggacttcatcctgggtgctgcagatactgcagtgaagtaaaacaggaatcaatcttgcctgcccccag ctcacactcagcgtgggaccccgaatgttaagcaatgataataaagtataacacgg
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SUBSTITUTE SHEET (RULE 26)

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213942_at	gb|AL134303	Consensus includes gb:AL134303 /FEA=EST /DB_XREF=gi:6602490 /DB_XREF=est:DKFZp547K034_r1 /CLONE=DKFZp547K034 /UG=Hs.56186 EGF-like-domain, multiple 3 cctaagctgtggaagacgggcaggaggggctttctcgggcctggattggcgggtttta ctcactctgggcaaactggacatttctgccaccgtgtgcccttgtctcgtggtaaccggc gtccttcagcctgtccccctggcttccacggggctggctgccaggggttgtgctggtgtc aacatggagccccctgcgaccccatcagtggccgatgcctctgccctgccggcttccacg gccacttctgtgagaggggtgtgagccaggttcatttggagagggctgccaccagcgct gtgactgtgacgggggggcaccctgtgaccctgtcaccggtctctgcctttgcccaccag ggcgctcaggagccacctgtaacctggattgcagaaggggccantttgggcccagctgca ccctgcactgtgactgcgggggtggggctgnctgcgaccctgtcagtgggcagtgtcact gtgtggatggctacatggggcccacgtgccgggaaggtgggcccctccggctccccgaga acccgtccttagcccagggctcagcgggcacactgcccgcctccagcagacccacatccc ggagcggtggaccagcgaggcactagtagaggcagtcccgtggagcccgcctctccagtc ccagccagaggggacccctggcctttggtgaccactgagaaggacacttcacgggcccaga gctcctggtactgcccttcctttgagggccgtggagggctgtggacagcccagcaacctg tcgctcttggaggctggtgtggccttgaggagggaagcctcgcatggccgctggaagaga ggcgcctcctggcctggctctgcagaacccaggggcacgctctgggcctgggctgaggaa gtcccgctctccccgcggctctgagttggactgaggacaggtgtgggcgccagtgtgggt gcaggcgcaggtgcaggcacagggccactgtcctccaggcaggctttttggtgctaggcc ctgggactggaagtcgcccagcccgtatttatgtaaaggtatttatgggccactgcacat gcccgctgcagccctgggatcagctggaagctgcctgtcatctcctgcccaatccccaga aaccctgattcaggtctgcaggctcctgcgggctcaccaggctgctggctccggtaccat gtaaacctaggaaggtaaaggagcaggcaacctcaaaannnnnnnnnnnnannnngtgtt

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214051_at	gb|BF677486	Consensus includes gb:BF677486 /FEA=EST /DB_XREF=gi:11951381 /DB_XREF=est:602085745F1 /CLONE=IMAGE:4249834 /UG=Hs.56145 thymosin, beta, identified in neuroblastoma cells tgggcgggaaggctaacctggtgcgnngncagcctgggtctcagccccgcgtnacggcct ttcacgagtcttcaagccttcaggntttcttctagtcaagatgagtgataaanccagact tgtcggaagtggagaagtttgacaggtcaaaactgaagaaaactaatactgaagaaaaaa atactcttccctcaaaggaaactatccagcaggagaaagagtgtgttcaaacatcataaa atggggatctcctccaaagagcagatttcagcattgcctgacagtcttggttttaggctt gttttttgtaaacctgtgtgtttgtagagatttcagacatcttctgatttcttctcacc tatattccctggttaagaggtcaggggtagtgaatgtttccttaagttccttttttaaact tcccattggtatgtaaattccaaatggcagatgctgtcaataaccttgccatggatgacc tttgtgtaggtagtccttgcacctcatgcaggataagccaattttaactttctacaatgg gtgcctcaatagtttcataatcttcatgaagttgcatcctttggcagcttcttacagttt attttcacttccaatgtagcaataaaataataaatataannnnnnnnnnnnnnaaaaaaaa aagtt
214109_at	gb|AI659561	Consensus includes gb:AI659561 /FEA=EST /DB_XREF=gi:4763131 /DB_XREF=est:tu12d08.x1 /CLONE=IMAGE:2250831 /UG=Hs.62354 cell division cycle 4-like tataatgactaaaatcagtatccagtgtttccttgggtcatcactaattatgaatcagaa gaactggatcctaccttgcccaccaacttcagagatttgtccaagccaataggagctctg aacccaaaaagagcagcattcttcgctgagcgttatgaatcatgggaagatgttcaagtt ccaaagtttcactatggtactcattactcaactgcaagttttgttcttgcatggctgcta agaatagagccccatcctcccagaggttctgccatgcaagtgagtccattgatgttcaca gacaaagcccagcaggatgttatcatggtcctcaagtttccctccaactcccctgttact cacgtggcagccaacacccagcctggtttggcaactcccgctgtgatcacagtcactgct aacaggttatttgcggtgaacaaatggcacaaccttcctgctcatcaaggtgctgtacaa gaccagccataccagctgccagtggaaatcgatcctctcatagccagcaatacaggaatg cacaggaggcaaatcactgacctttagaccaaagtattcaagtgcattcccagtgcttt gtcatcacttcagacaaccgctatattctcgtctgtggcttctgggataaaagtttcaga gtctattctacagacacaggaagattgatccaagtggtgtttggccattgggatgtcgtc acttgccttgctcgttctgagtcatatattgggggaaattgctacattctctcagggtca cgtgatgcaactcttttgctgtggtattggaatggaaaatgcagtgggattggagataac ccaggcagtgagactgctgctcctcgggccattttgaccggccatgactatgaggtcaca tgtgctacggtgtgtgcggagctaggcctggtgttgagtggttcacaagaaggaccatgt ctcatacattccatgaatggagacttgttgaggaccttggagggtcctgaaaactgcctg aaaccaaaactcattcaggcttcaagagagggtcattgtgtcatattctatgaaaacggc

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225326_at	gb|AB037732.1	Consensus includes gb:AB037732.1 /DEF=Homo sapiens mRNA for KIAA1311 protein, partial cds. /FEA=mRNA /GEN=KIAA1311 /PROD=KIAA1311 protein /DB_XREF=gi:7242976 /UG=Hs.61441 KIAA1311 proteingtaagagtcgaggcctgagtcgcagtagaagccgaagtaggggcgcagcaaagaccgggatccaaataggaatgttgagcacagggaaagatcgaagtttaaga gtgaaaggaatgacctggagagttcctatgtgcctgtgtctgcaccacctccaaactcttctgagcagtattcctctggggcacagtctattcccagcactgttactgtgatcgcacctgct caccactctgaaaacacaactgagagttggtctaattactataacaatcatagctcntccaattctttggtcgaaacctaccaccaaagaggcgatgcagagattatgatgaaagag gattttgtgtacttggtgacctttgtcagtttgatcatggaaatgatcccctagttgttgatgaagttgctctgccaagtatgattcctttcccaccccctcctcctgggcttcctcctccaccacct cctggaatgttaatgcctccaatgccaggtccaggcccaggcccgggcccaggtccaggcccaggcccgggcccaggtccaggtcctggccatagtatgagacttcctgttcccca aggacatggtcagcctccaccatccgttgtgcttcccataccaagaccacctataacacaatcaagcttgataaacagccgtgaccagcctgggacaagtgcagtgcccaatcttgc atcagtgggaacaagactacctcctccttttaccccagaacctcctttacacagtatcagaacgacagcccatgtactctcgtgaacatggtgctgctgcatctgagcgacttcagttgg ggacaccgcctcctctgttggcagctcgtttggtgccacctcgaaacctcatgggatcctccattggataccatacctcagtctccagccctacccctctggttccagatacatatgaacc agatggttacaacccagaagctcctagtattactagttctggtagatctcagtacagacagttcttttcaagaactcagacacagcgtcccaatctgattggcctaacatctggagatatg gatgtaaatccaagagctgctaacattgtgatccagactgaaccaccagttcctgtttcgattaatagcaacataaccagagtagttcttgaaccagatagtcgaaaaagagctatga gtggtttggaagggccactcacaaagaaaccttggctgggaaagcaaggaaataacaatcaaaataaaccagggttcttacgaaagaatcagtatacaaacaccaaattagaa gtcaagaaaatccctcaggaattgaacaacattaccaagctcaatgaacacttcagcaaatttggaactattgttaatatccaggttgcttttaagggtgacccagaagcagccctaat ccantatcttaccaatgaggaggccaggaaagccatttctagcacagaagcagttctaaacaaccgattcattcgagtcttgtggcatagggaaaataatgagcaaccgacactac agtcctcagcacagctgctcctgcaacaacagcaaacacttagtcacctctcacagcagcaccatcacctgccacagcatctacatcagcagcaggtgctagtggcccagtctgct ccttcaacagtgcacggaggtatccagaagatgatgagcaaaccacagacatcaggtgcatatgttcttaacaaagttcctgttaaacatcgtcttggacatgcaggtggtaaccag agtgatgcatcacatttgttgaatcagtctggtggtgctggagaagattgccagatattttcaactccaggccatccaaaaatgatttacagctcctcaaacttaaagacaccttcaaag ctctgttcagggtctaaatctcatgatgttcaagaagtgcttaaaaaaaaacaggaagcaatgaagttacnacaagatatgaggaaaaaaagacnggaagtgttagaaaagcaa

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		Consensus includes gb:AL354950 /DEF=Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF) /FEA=mRNA_2 /DB_XREF=gi:9908994 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor
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241754_at	gb|AA829836	Consensus includes gb:AA829836 /FEA=EST /DB_XREF=gi:2902935 /DB_XREF=est:od40c07.s1 /CLONE=IMAGE:1370412 /UG=Hs.59504 ESTsccttcatcccggggatctcnatcctttcaccaggaagccactgttcatcatngtggattngtntaatagtgntgcgtataagaatttcacaaacttgtttggacagccactagtctg cttgctttctcctacagcatatccaaaagctttacaagatcaatctcagcgaggtagcctcttcactctcttttgaacaatcctctaatggccttcctatttgtctctggattgtcaagcatgcg cagaggcctatgggaaaagtgtcaagaatatcttcgaaaaatcaaccgtgatattgcccagctactgactcattcacgttcaatagatcaggcatttctccagttttttggagatgaatttc ttcgcttgctcctcacaagatttatctttgttcagccaccatgaggatgcacaagatttttcgggaaacacgaaattatccagaatcatatccacaactgccaagggatgaaacagtgg agaatcctcatctccagaagcacattttggaattagcatccattctggatgttcgaaacgtgttctttgagaataccattgatgactattaaaacaaaaaccctgttgtcgaaacaagttttc antttccacaaattttaaatggtgcagttttctaacgtgataagacacatagtggtgttacttagttttttatttttaatttngggccaccattttacaaaaaaaa
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241975_at	gb|N29850	Consensus includes gb:N29850 /FEA=EST /DB_XREF=gi:1148370 /DB_XREF=est:yw94a12.s1 /CLONE=IMAGE:259870 /UG=Hs.44098 ESTstgggaggatcgttgagccctaggaagtcaaggctgcagtgagtcatgattgctccgctccactgcactctggccttgatgatagagtgagaaccagtctcnaaaaaaaaaa aggtcattttctaagcatttgttgattcaatactgcccactatgtacactgacaattagacataatttaatttcagctcatggtatgaatggagacaaaatgaaatcattttaatgcacnatta aggcaatatagtgcccttaaataaaaagttgaagttcataagggaccatcattaagatttaactttgtaacaaatattttgttttgtttgttttattttagatttgcataataaaacattcatattct taaaa
241985_at	gb|AI814405	Consensus includes gb:AI814405 /FEA=EST /DB_XREF=gi:5425620 /DB_XREF=est:wj72g03.x1 /CLONE=IMAGE:2408404 /UG=Hs.224569 ESTsacccactactggcataacagaagaaaaatatcattcaagattggttctgattcttttggaaaatgacagtttaagcacttggttcctcagttggataacattagatccaaagtnca ttggttcagtggtgtgaagaaaggaagcacaattggcaggttatcactttccagtcgttccaatagatgatggttaacatgaattttacatgtgcaatgttcctgactgcaatgaagaaaa ggccttctggagatttctgttttttaagcacattctccttccatccacatatttacatccttgtaatggccagttaagctagggcttgctntaagttggaagaacactgggttgacagagatcta ctgtgagctgtattgggactgctttgagaaccatctttcaatgcactgaaaagtcatctgaaaaaatagcttcttncatatcagcttatattaaatactgtgacactctgagaaagtttatcat catgatagctgtaagtcaggcattaaaatcaaatggaaatacaaaaaaaaa
242065_x_at	gb|BG477984	Consensus includes gb:BG477984 /FEA=EST /DB_XREF=gi:13410263 /DB_XREF=est:602522982F1 /CLONE=IMAGE:4641356 /UG=Hs.147801 ESTsgccggcttccgcccgcagcccgaggggtctgggcgcgctgaagacccccttcggctgctgggccaacgcccccaccctttggtcacctactcctgccgccgagcggttcgcg ggaggtggcctcgggggtcgtagctactcaccggcggggcgctccgagtccatctgccccgtagcccggcagccggggcgggagggctgcgagcccggggcgcggtccgcct gaggcctgagacccggggccgcctgcgctcagggccgcggtgccggccgcgcgggagcctggcggggacggcgcggtcagtgttcggctcctccgcagtgactcaccagcgt cctgaagcttttgatcaccattggctgggaaggaaaaacagaatcagctgttccctgcgaaaggtatcatatgtttcttacaaagtggaggtttgtggcagccctgcatggagcaagtct gtcagcaccatctttctaacagtatgtgctcacttcatgtctctctcacattttggtaattcttggaatgtttccgttattaaatcagttatagtgancngtgattagtgatctttgatcattacctgtc atacttgccttgggggggcaccatgaaccacccctа
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242363_at	gb|BF592008	Consensus includes gb:BF592008 /FEA=EST /DB_XREF=gi:11684332 /DB_XREF=est:7o35e09.x1 /CLONE=IMAGE:3576280 /UG=Hs.87372 ESTscagcattgtctacaagtccgaaagtacggtgacaaatatctaagaatcagtattgaaatcagtnaatttcaggaatngaggaaaggactatgatcagatcttgattttatctactt taaattgtctatttatttgatcccaacctttgtactntctgaagtgtaactgtctttattcaacagaacatgaactaggaagagagattagaaaacagaatgtgaacatttttcttttaataatt gtaacaaagatttgttgggagagaaatttccaaataatgagtagtgtatagtgtaaggaataattgacctggaattattggccccaaactctgattcttgctgaagcatctatgagaagtg tgattttagccaagtctgtgccgcattctttatatgtaggaanttaagttttgatttaatgatttctgaattttctttcagctctactcaattnaggggtatcagtatgtgaaatggaatatagaaaa gtaggcaattctttacttttctntattcagtttcataanattnataccccataattgcccattatataccaaagacaatatctcaagttatctcattgtagcagtgtctgtgagtcaaaacttcaat tttnagtagagtcacactttctntnnnnanannnattcatgtactcactactcatgtagttactgtatctttaccttcagtttgtaaaaatgactaaaagtagggaaaacaangtgttaaaac ataanggataagaaaaggttggaaatcatatggcaaatcacatgttcctcagcctcaaggtgtgtttagttgtgaaagaaagaataaaattgtttaaatatttcaaaaaaaaa
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WO 03/039443

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Claims

1. A method of determining whether a patient sample contains leukemia cells or other cells comprising the steps of
a) determining the the expression profile of a group of markers in a patient sample and
b) concluding from expression profile whether the patient sample contains leukemia cells or other cells
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 3 to 6, tables 15 to 20, tables 29, 30, 41, or 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42.

2. The method according to claim 1
characterized in that
the number of markers in the group is between two and the total number of markers listed in the tables tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42.

3. The method according to claim 1 or 2
characterized in
that the group of markers consists of all markers listed in one or more tables, whereby the tables are selected from the tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42.

4. A method of determining whether a patient sample contains leukemia cells or other cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, comprising the steps of
a) determining the expression profile of a group of markers in a patient sample and
b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present,
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 16 to 20 or table 29 or 30 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 16 to 20 or table 29 or 30.

5. The method according to claim 4
characterized in that
the number of markers in the group is between two and the total number of markers listed in the tables 16 to 20 or table 29 or 30.

6. The method according to claim 4 or 5
characterized in
that the group of markers consists of all markers listed in one or more tables, whereby the tables are selected from the tables 16 to 20 or table 29 or 30.

7. The method according to any of claims 4 to 6
characterized in
that it is differentiated between four types of leukemia cells in the patient sample and that the other cells are normal cells.

8. The method according to any of claims 1 to 7
characterized in that at least one marker is selected from the group consisting of
- *ADCY3,*
- adenosine deaminase (*ADA*),

- *ARGHGAP4,*
- B-cell, a specific coactivator of octamer binding transcription factors,
- *CAPN3,* a member of the papain superfamily,
- *CBFß-MYH11,*
- *CD24,*
- *CD27,*
- *CD74,*
- connective tissue growth factor (*CTGF*),
- *CTGF,*
- *CTSW,*
- *MYH11*
- glucocorticoid receptor beta
- *CBFA2T1* (formerly *ETO*)
- *HLA-DMB*
- *HOXA9*
- *HOXB5*
- *IRF4*, an immune system-restricted interferon regulatory factor
- *KIAA1013*
- *LCN2,* a modulator of inflammation
- *LEF-1*
- *MBNL*
- *MSF* translocation partner of the mixed-lineage leukemia gene (MLL) in AML
- *NCOA1,*
- *OS-9*
- Phospholipidscramblase 1 (*PLSCR1*)
- *POU2AF1*
- *POU2F2*
- *POU4F1*
- *SCYA3*
- *DEFA3, SGP28, CAMP, CLC*

- *SOCS-2 and*
- *TRB and CD3D*

9. A method of differentiating between two types of leukemia cells or one type of leukemia cells and normal cells or non-leukemia in a patient sample comprising the steps of
a) determining the expression profile of a group of markers in the patient sample and
b) concluding from the expression profile which type of leukemia cells the patient sample contains or whether it contains normal cells or non-leukemia characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 3 to 6 or tables 7 to 12 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 3 to 6 or tables 7 to 12.

10. The method according to claim 9
characterized in that
the number of markers in the group is between two and the total number of markers listed in one or more of the tables 3 to 6 or tables 7 to 12.

11. The method according to claim 9 or 10
characterized in
that the group of markers consists of all markers listed in one or more of the tables 3 to 6 or tables 7 to 12.

12. A method of differentiating between the subtypes of AML cells or the subtypes of AML cells and normal cells in a patient sample comprising the steps of
a) determining the expression profile of a group of markers in the patient sample and
b) concluding from the expression profile which subtypes of AML cells the patient

sample contains or whether it contains normal cells
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36and whereby the number of markers in the group is between one and the total number of markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.

13. The method according to claim 12
characterized in that
the number of markers in the group is between two and the total number of markers listed in the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.

14. The method according to claim 12 or 13
characterized in
that the group of markers consists of all markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.

15. The method according to any of claims 12 to 14
characterized in
that three, four or more subtypes of AML cells are determined.

16. A method of assessing the efficacy of a test compound for inhibiting leukemia, the method comprising comparing the expression profile of a group of markers in a first sample obtained from the patient and maintained in the presence of the test compound and the expression profile of a group of markers in a second sample obtained from the patient and maintained in the absence of the test compound, wherein a significantly altered expression profile of the group of markers in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting leukemia in the patient
characterized in
that the group of markers consists of markers selected independently from the

markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

17. A method of assessing the efficacy of a therapy for inhibiting leukemia in a patient, the method comprising comparing the expression profile of a group of markers in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient and the expression profile of a group of markers in a second sample obtained from the patient following provision of the portion of the therapy, wherein a significantly altered expression profile of the marker(s) in the second sample, relative to the first sample, is an indication that the therapy is efficacious for inhibiting leukemia in the patient
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

18. A method of selecting a composition for inhibiting leukemia in a patient, the method comprising:
a) separately maintaining aliquots of cells of a patient sample in the presence of a plurality of test compositions;
c) comparing the expression profile of a group of markers in each of the aliquots, and
d) selecting one of the test compositions which induces an altered expression profile of the group of markers in the aliquot containing that test composition, relative to other test compositions
characterized in
that the group of markers consists of markers selected independently from the

markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

19. A method of determining new subtypes of leukemia cells, the method comprising:
a) determining the expression profile of a group of markers of leukemia cells of unknown subtype
b) comparing the expression profile of said leukemia cells of ??? subtype to the expression profile of a group of markers of leukemia cells of known subtype(s), thereby concluding that a new subtype is determined when the expression profile is different to all known subtypes,
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

20. A method for guiding the therapy of leukemia in a patient depending on the leukemia subtype and/or the risk of relapse of disease, the method comprising:
a) determining the expression profile of a group of markers in the patient sample, and
b) deciding about the therapy strategy depending on the leukemia subtype and/or the risk of relapse of disease
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25

or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

21. A method for monitoring the progression of leukemia in a patient, the method comprising:

a) determining the expression profile of a group of markers in a patient sample at a first point in time, and

b) repeating step a) at a subsequent point in time; and

c) comparing the expression profile detected in steps a) and b) , and therefrom monitoring the progression of leukemia in the patient,

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

22. The method of claim 21, wherein between the first point in time and the subsequent point in time, the patient has undergone chemotherapy.

23. The method according to any of the claims 1 to 22, wherein a transcribed polynucleotide or portion thereof is the marker or at least one of the markers.

24. The method of claim 23, wherein the transcribed polynucleotide is a mRNA.

25. The method of claim 23, wherein the transcribed polynucleotide is a cDNA.

26. The method according to any of claims 23 to 25, wherein the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.

27. The method according to any of the claims 23 to 26, wherein the expression profile of the group of transcribed polynucleotides is determined by annealing the

transcribed polynucleotides with a complementary polynucleotide or a portion thereof under stringent hybridization conditions.

28. The method according to any of the claims 1 to 27, wherein the patient sample is blood or bone marrow.

29. The method according to any of the claims 1 to 22, wherein a protein is the marker or at least one of the markers.

30. The method of claim 29, wherein the expression profile of the proteins is detected using a reagent which specifically binds to one of the proteins.

31. The method of claim 30, wherein the reagent is selected from the group consisting of an antibody, an antibody derivative, and an antibody fragment.

32. The method according to any of claims 16 to 31
characterized in that
the number of markers in the group is between two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

33. The method according to any of claims 16 to 32
characterized in
that the group of markers consists of all markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

34. A kit for assessing the suitability of each of a plurality of compounds for inhibiting leukemia in a patient, the kit comprising:
a) (optionally) a plurality of compounds; and
b) a reagent for assessing the expression profile of a group of markers

characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

35. A kit for assessing whether a patient is afflicted with leukemia, the kit comprising reagents for assessing the expression profile of a group of markers
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

36. A kit for assessing the presence of human leukemia cells, the kit comprising an antibody, wherein the antibody specifically binds with a protein corresponding to a marker
characterized in
that the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

37. A kit for assessing the leukemia cell carcinogenic potential of a test compound, the kit comprising leukemia cells and a reagent for assessing expression of a marker, wherein the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

38. A protein or mRNA, cDNA or cRNA corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 for the treatment of leukemia.

39. A method for the preparation of a pharmaceutical composition for the treatment of leukemia
characterized in
that a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.

40. A method for the preparation of a pharmaceutical composition for the treatment of leukemia
characterized in
that a vector comprising a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.

41. A method for the preparation of a pharmaceutical composition for the treatment of leukemia
characterized in
that an antisense oligonucleotide complementary to a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.

42. Use of a marker or a group of markers selected individually from one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 for the determination of leukemia cells, the type or subtype of leukemia cells.

43. Use of a marker or a group of markers selected individually from one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 or 36for the determination of the subtype of AML cells.

44. A composition comprising a group of markers and substances chemically different to the markers
characterized in
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

45. The composition according to claim 44
characterized in
that the group of markers consists of all markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

46. The composition according to claim 45
characterized in
that the group of markers consists of all markers listed in one or more of the tables 14 or tables 16 to 20 or table 29 or 30.

47. The composition according to claim 46
characterized in
that the group of markers consists of all markers listed in the tables 16 to 20 or table 29 or 30.

48. The composition according to claim 44 to 47
characterized in
that the markers are polynucleotides or oligonucleotides and are bound to a solid phase in the form of an array.

49. A method of determining the subtypes of ALL cells in a patient sample comprising the steps of

a) determining the level of expression of a group of markers in the patient sample and

b) concluding from the differences in the level of expression which subtypes of ALL cells the patient sample contains

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 18, 32 or 33 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 18, 32 or 33.

50. The method according to claim 49

characterized in

that the group of markers consists of all markers listed in one or more of the tables 18, 32 or 33.

51. A method of determining the subtypes of CLL cells in a patient sample comprising the steps of

a) determining the level of expression of a group of markers in the patient sample and

b) concluding from the differences in the level of expression which subtypes of CLL cells the patient sample contains

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 38 or 39 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 38 or 39.

52. The method according to claim 51

characterized in

that the group of markers consists of all markers listed in one or more of the tables

38 or 39.

53. A method of determining whether a patient sample contains leukemia cells or other cells and at the same time determining the type and subtype of leukemia cells, comprising

a) providing a patient sample,

b) isolating RNA from the patient sample, transcribing the RNA into cDNA and transcribing the cDNA into cRNA while simultaneously labelling the cRNA

c) hybridising the cRNA to a microarray having attached thereto a group of markers selected from the group listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38,. 39, 41, 42 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38,. 39, 41, 42, and

d) determining the level of expression of a marker or a group of markers.

54. Use of a marker or a group of markers selected from the group of members contained in the appended tables for determining whether a patient sample contains leukemia cells or other cells.

55. Use of claim 54 wherein said determination comprises the simultaneous determination of the type and subtype of leukemia cells.

Figure 1a Principal Component Analysis

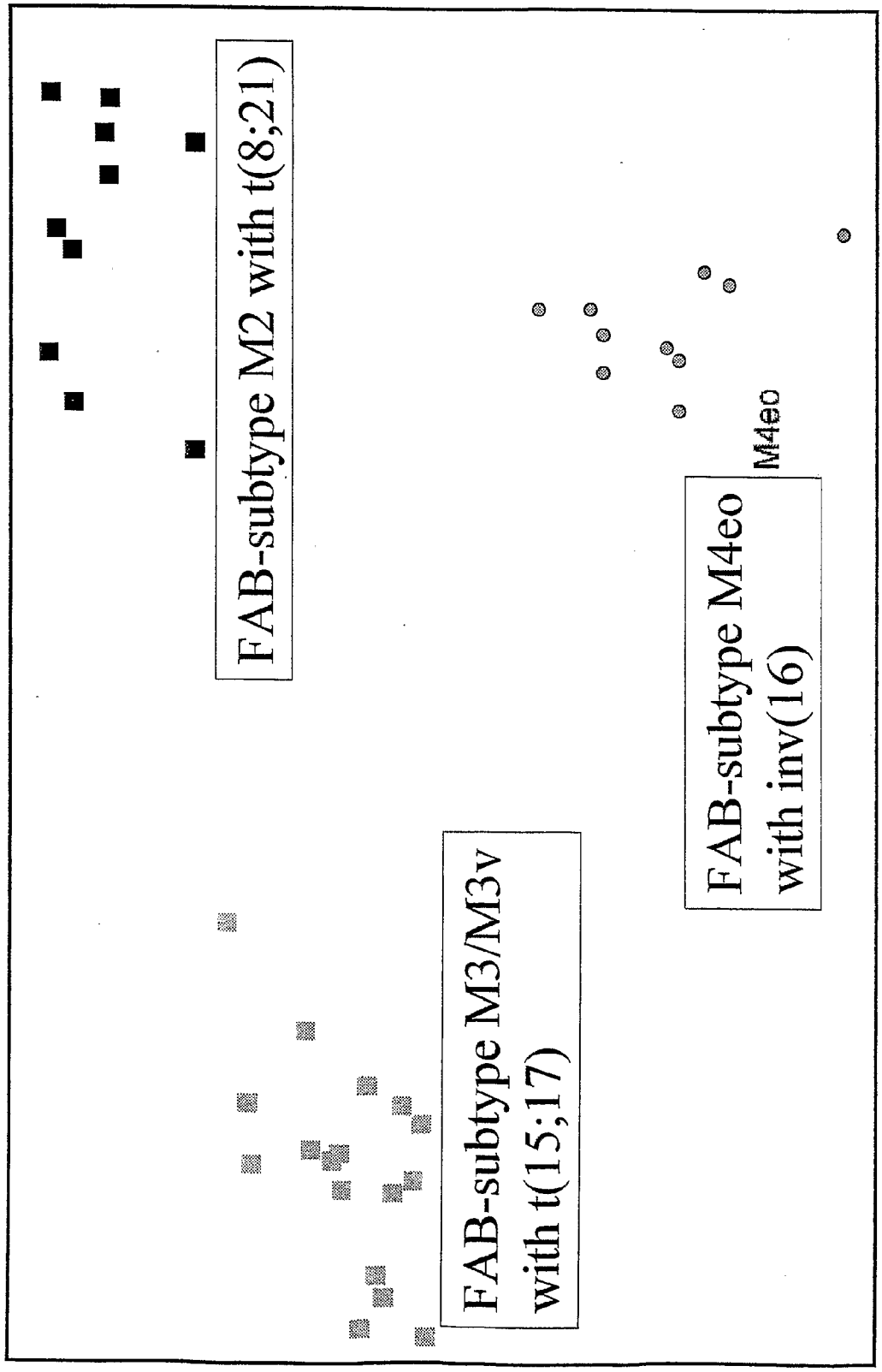


Figure 1b Hierarchical Cluster Analysis

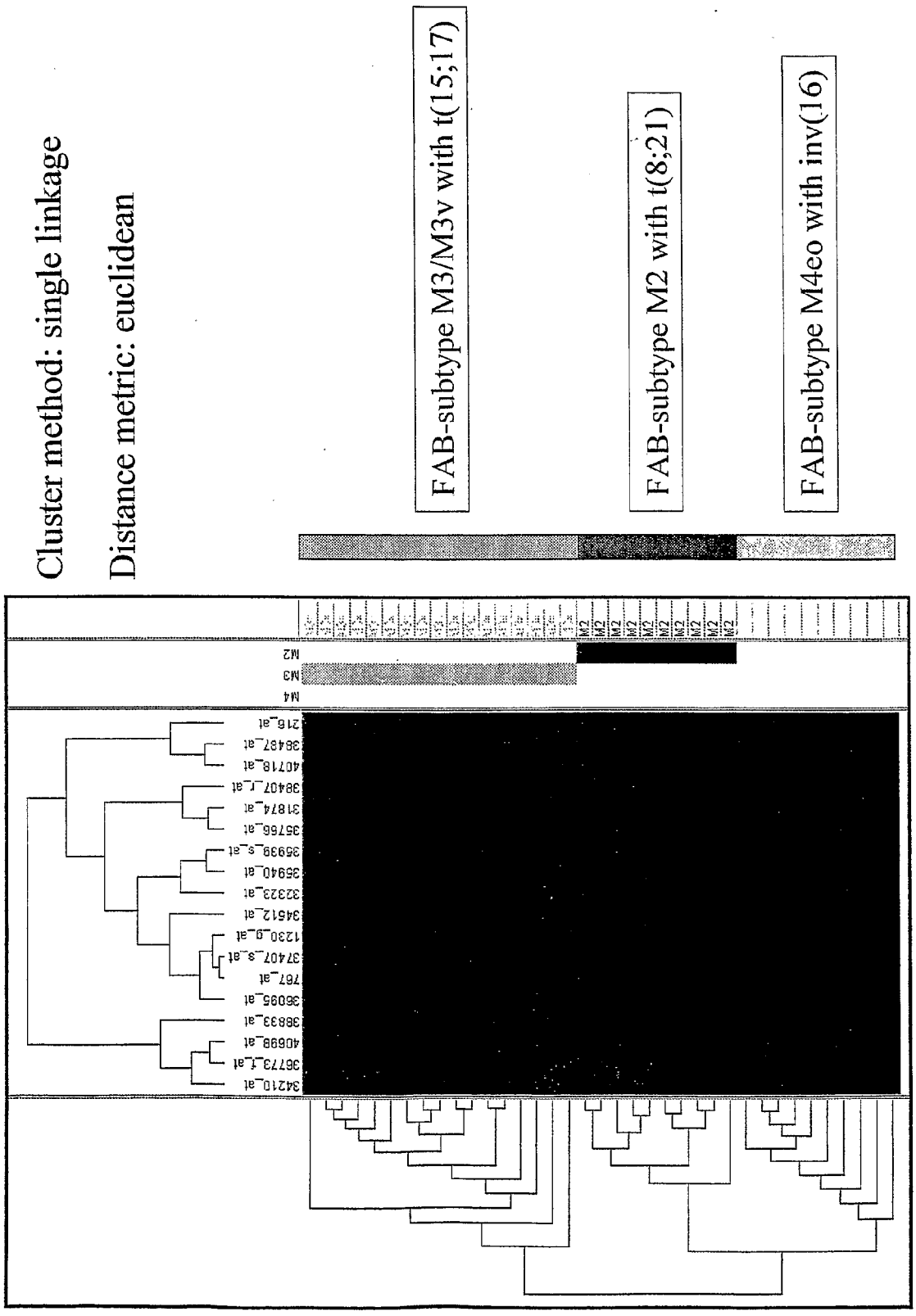


Figure 2 **Classification Accuracy**

accuracy	t(15;17) - t(8;21)	t(15;17) - inv(16)	inv(16) - t(8;21)	t(8;21) - R	t(15;17) - R	inv(16) - R
U78556						1.00
M98539					1.00	
Y07846				1.00		
M63582				1.00		
N90866		1.00				
J03853			1.00	1.00		
M26326	1.00			1.00		
L20433			1.00	1.00		
X64624	1.00		1.00	1.00		
N99340			1.00			1.00
M81141	1.00				1.00	
AF013570			1.00			1.00
AI207842		1.00			1.00	1.00
D87433	1.00			1.00		
X00457	1.00					
X96719		1.00			1.00	
AF013611	1.00			1.00		
AF001548			1.00			1.00

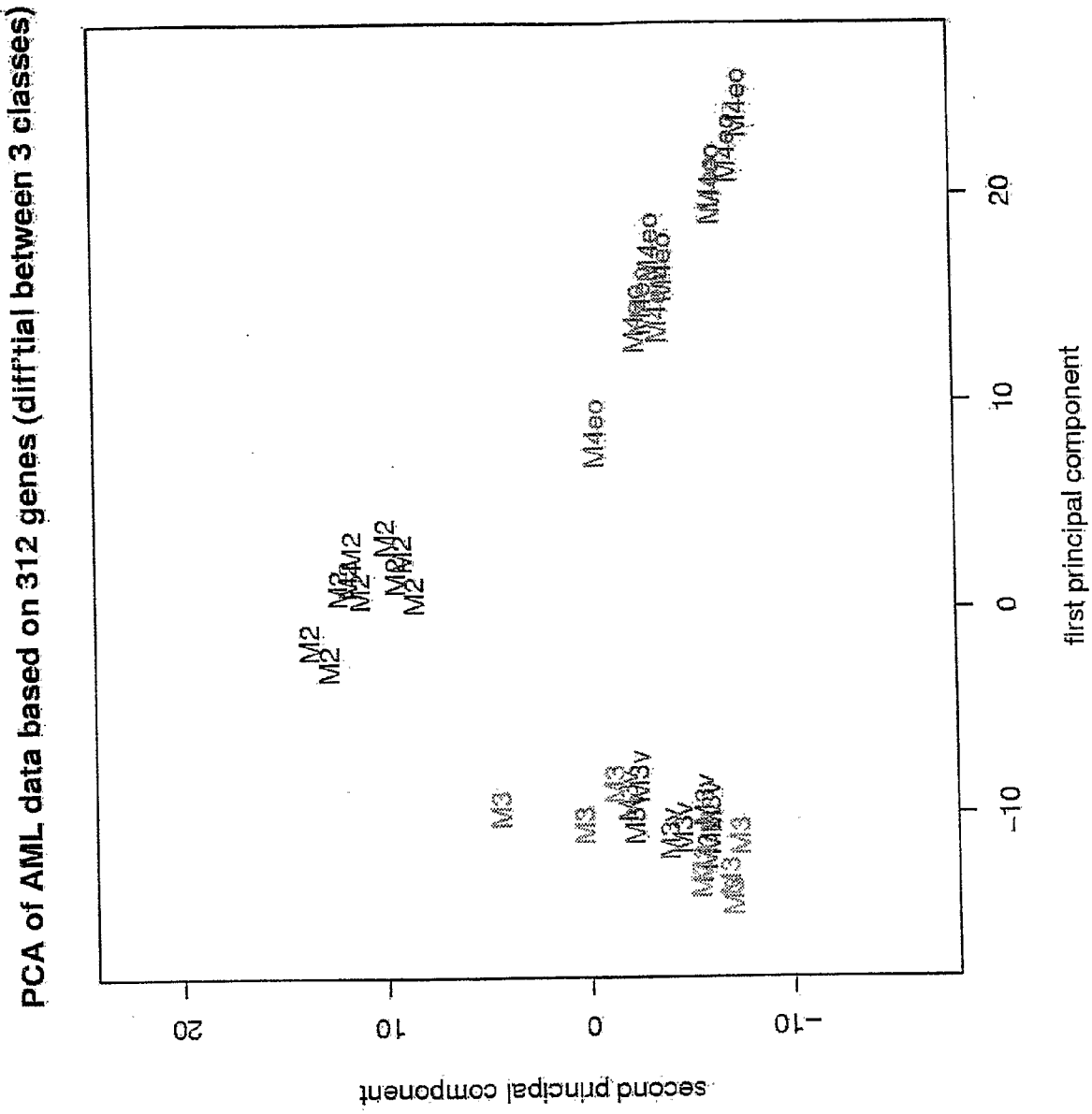

PCA of AML data based on 312 genes (diff'tial between 3 classes)
second principal component
first principal component
20
10
0
−10
−10
0
10
20
M2
M3
M4eo
M3v

Figure 3a

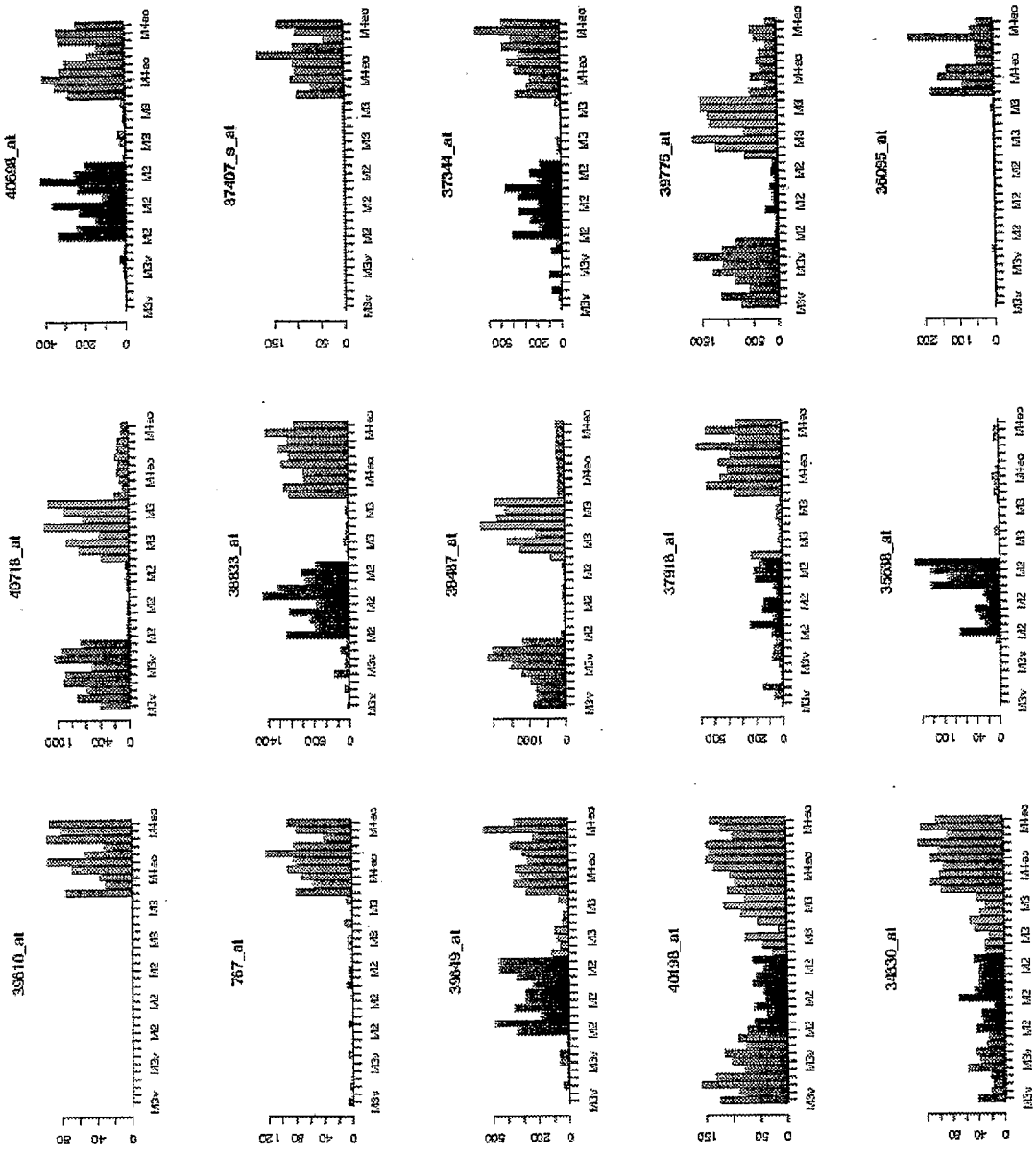

40699_at
37407_s_at
37344_at
39775_at
36695_at
40718_at
38833_at
38487_at
37918_at
35638_at
39610_at
767_at
39049_at
40198_at
38330_at

Figure 3b1

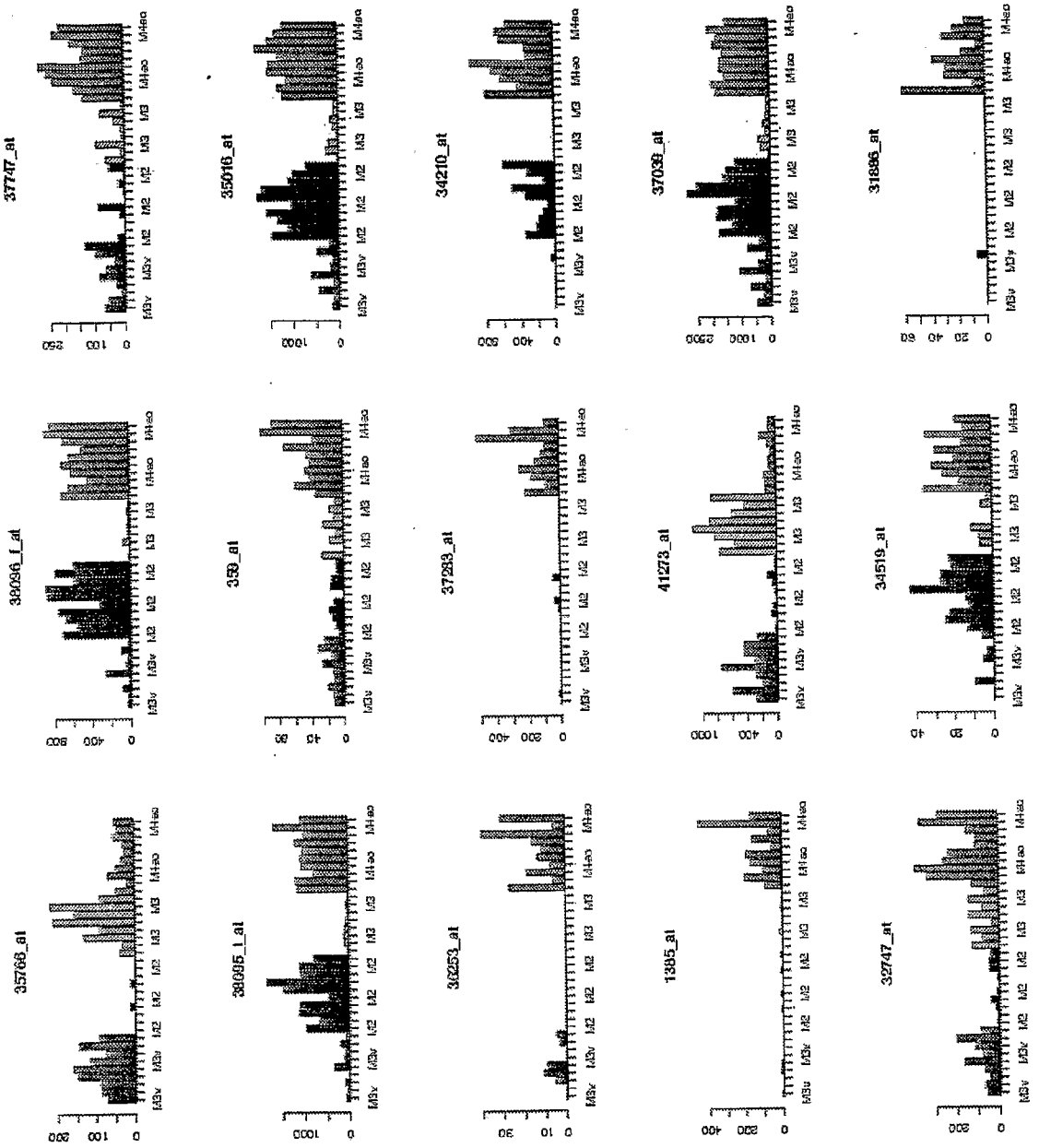

37747_at
35016_at
34210_at
37038_at
31886_at
38096_f_at
359_at
37283_at
41273_at
34519_at
35766_at
38095_i_at
36253_at
1385_at
32747_at

Figure 3b2

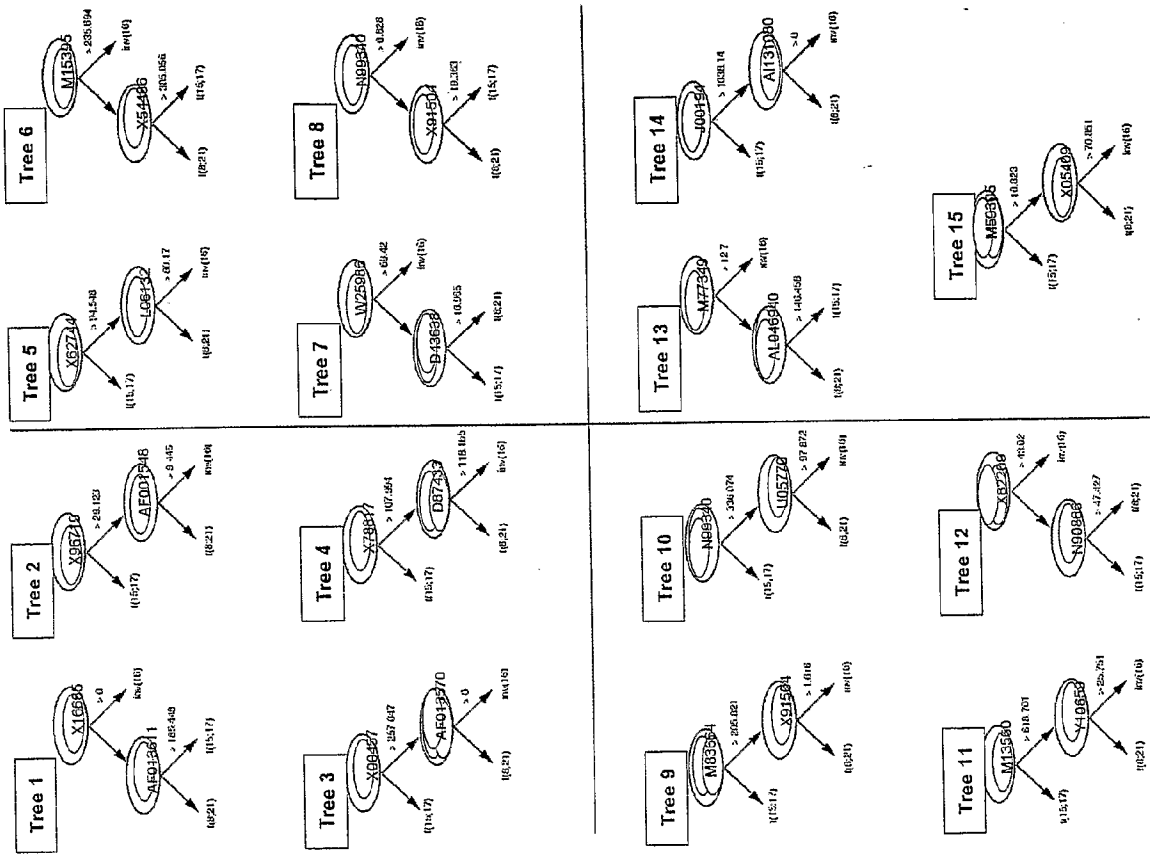
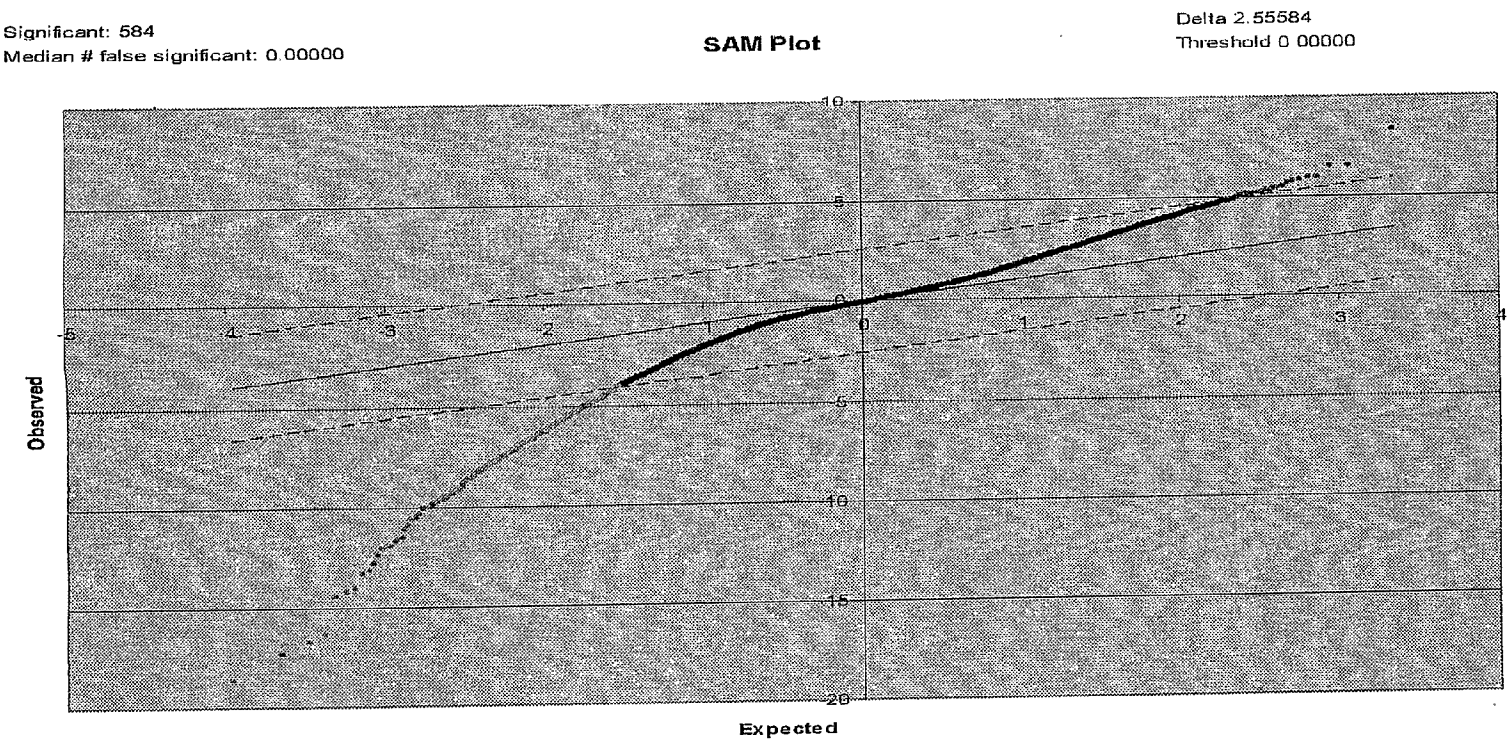


Figure 4

Decision trees according to IE

5a) Pairwise Comparison of Normal BM and AML

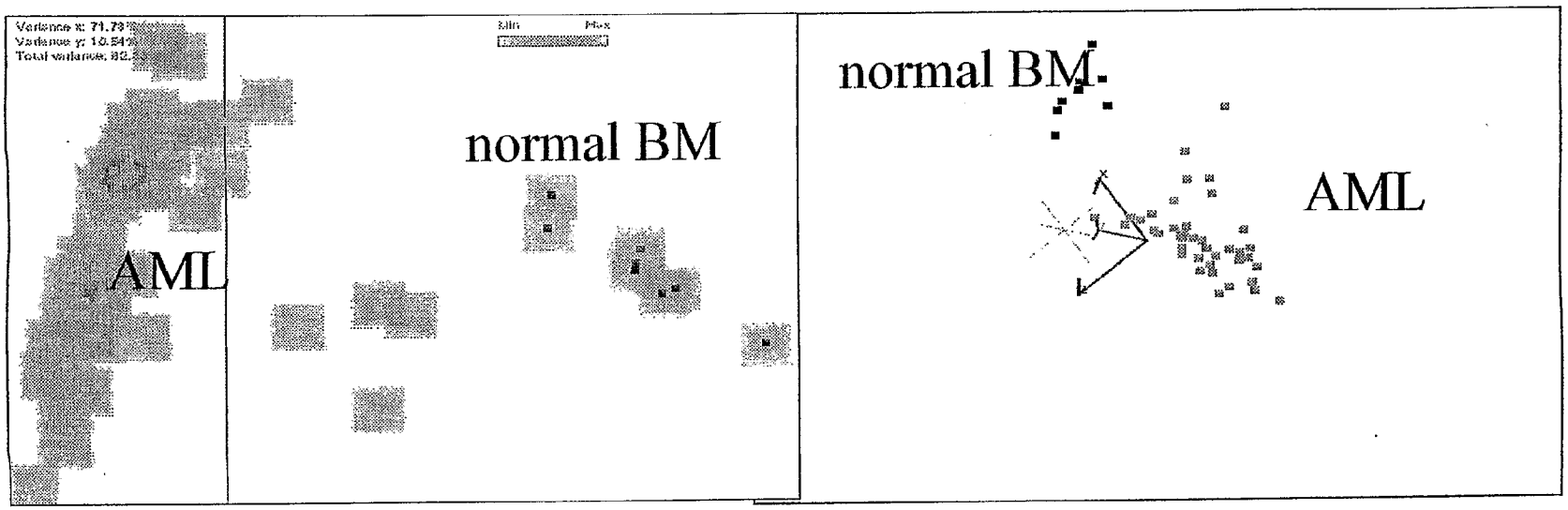
Significance Analysis of Microarrays:
Selection of 127 differentially expressed genes based on a permutation test (K-Nearest Neighbour Imputer)



5b) Principal Component Analysis

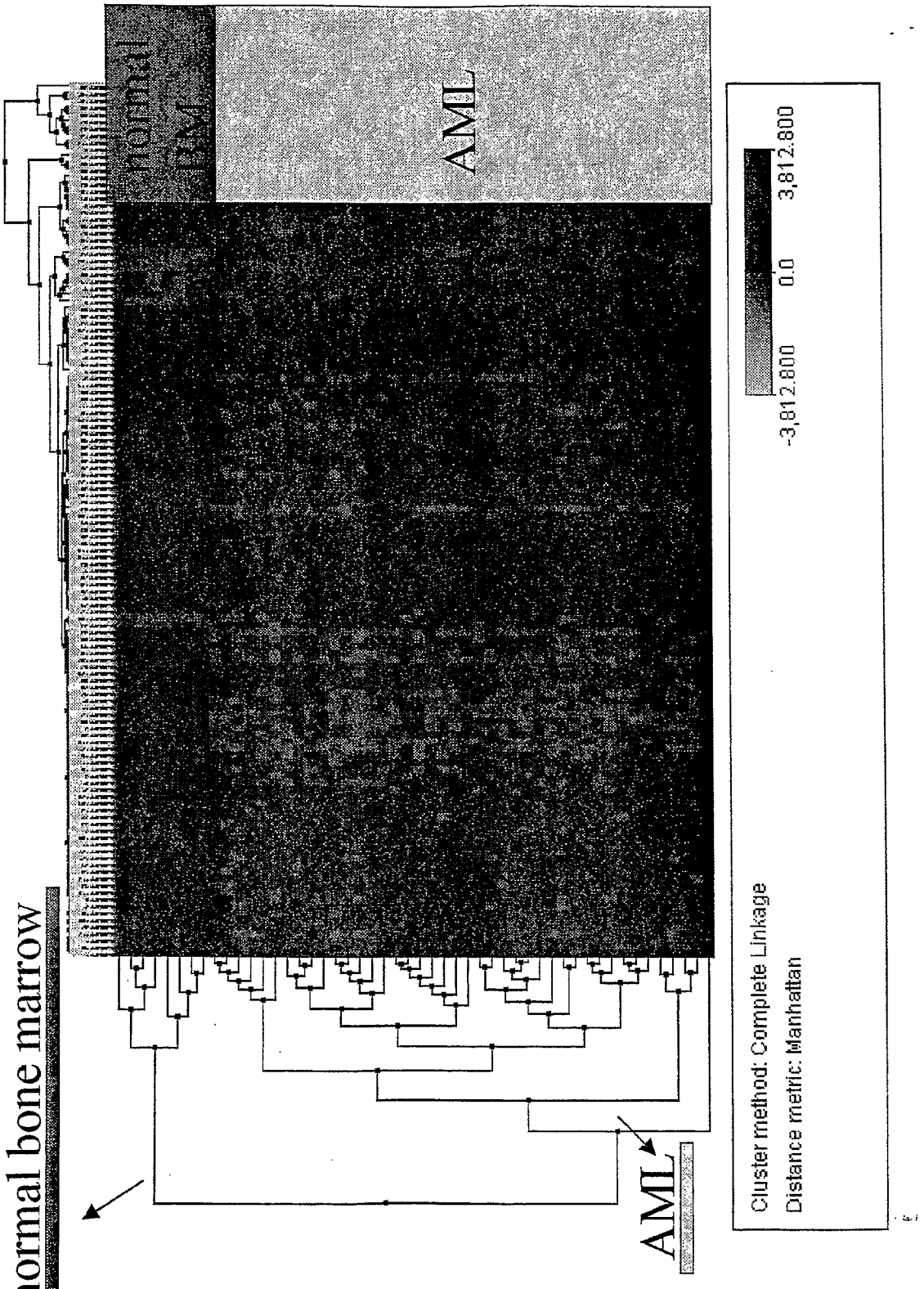
based on 127 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

2-dimensional *3-dimensional*



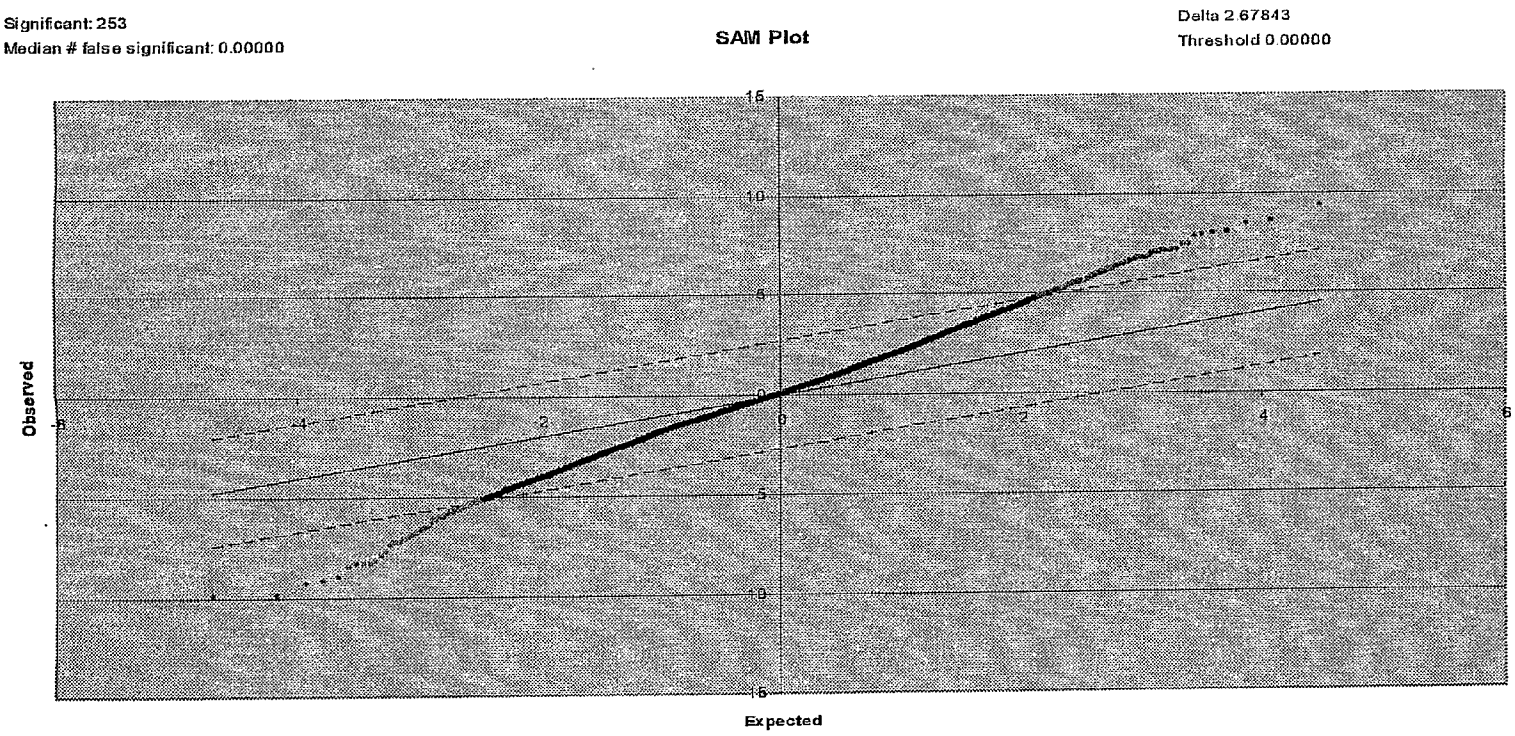
AML	=	acute myeloid leukemia, n = 48
normal BM	=	bone marrow from healthy volunteers, n = 8

5c) Hierarchical Cluster Analysis



6a) Pairwise Comparison of Normal BM and ALL

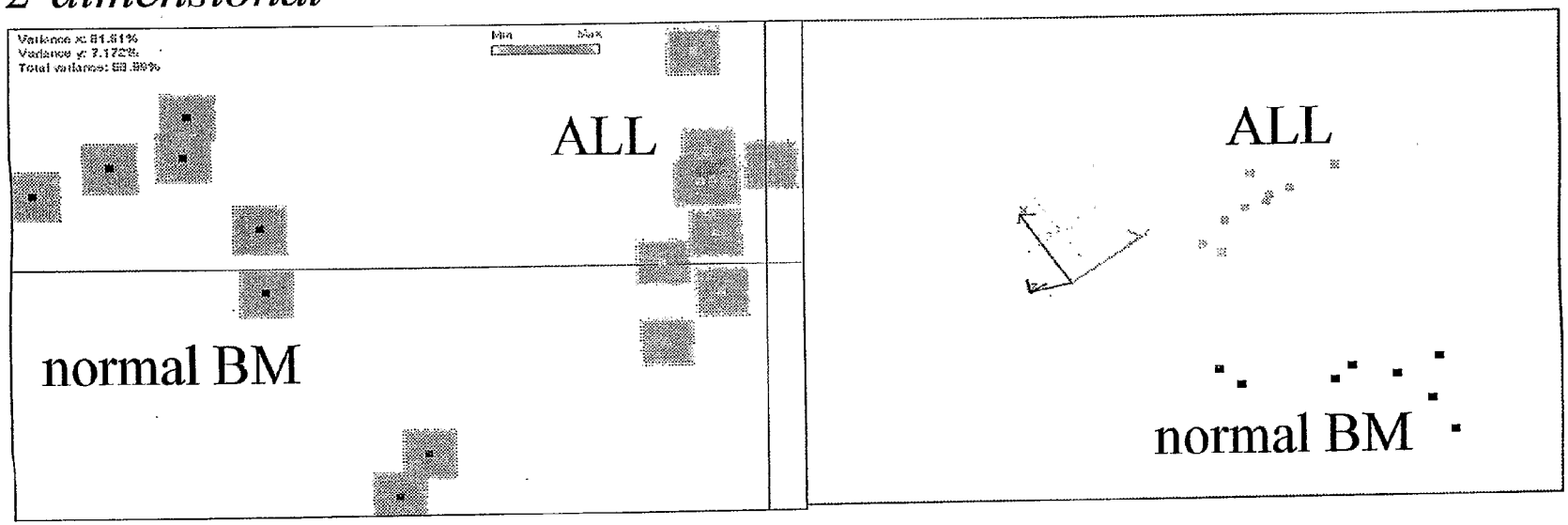
Significance Analysis of Microarrays:
Selection of 186 differentially expressed genes based on a *permutation test* (K-Nearest Neighbour Imputer)



6b) Principal Component Analysis

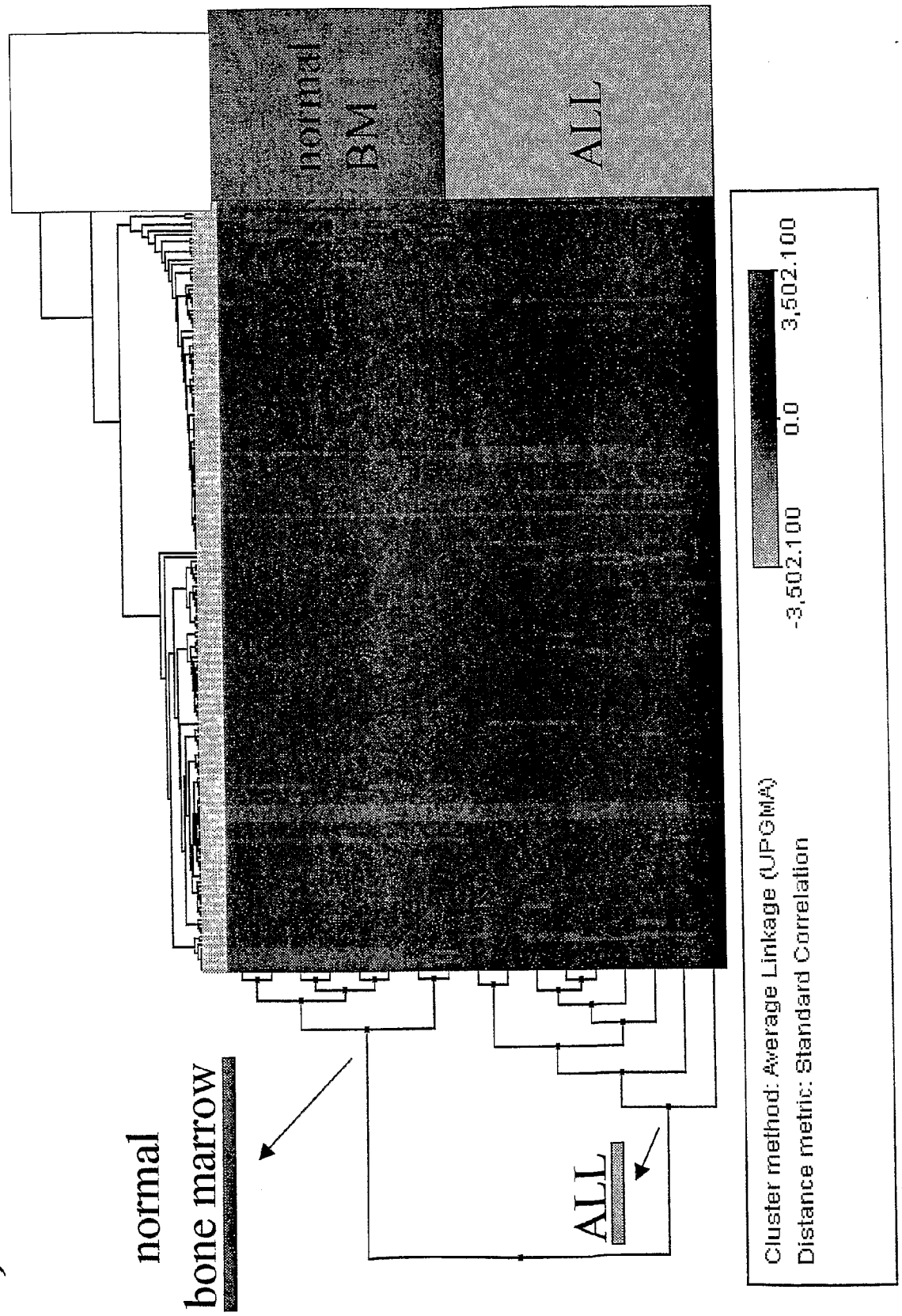
based on 186 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

2-dimensional *3-dimensional*



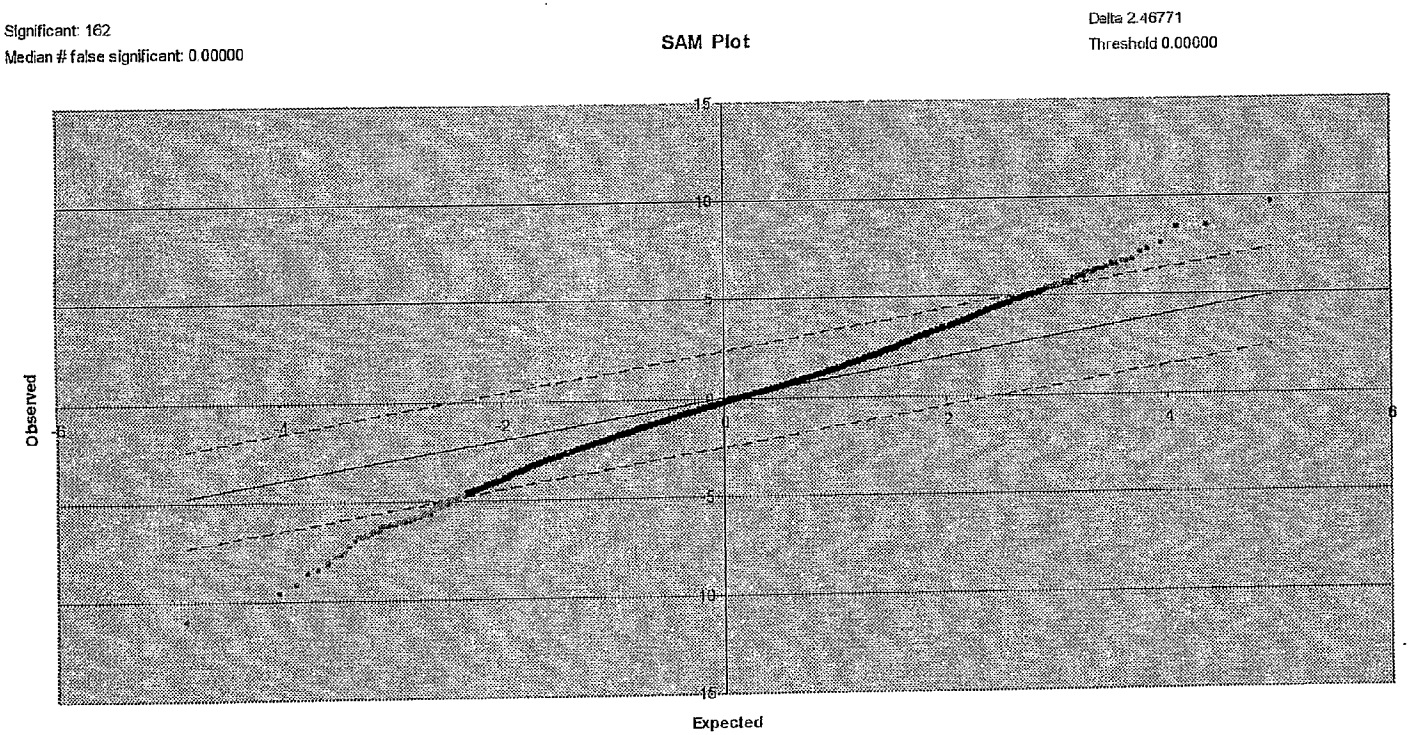
ALL	=	akute lymphoblastic leukemia, n = 9
normal BM	=	bone marrow from healthy volunteers, n =8

6c) Hierarchical Cluster Analysis



7a) Pairwise Comparison of Normal BM and CML

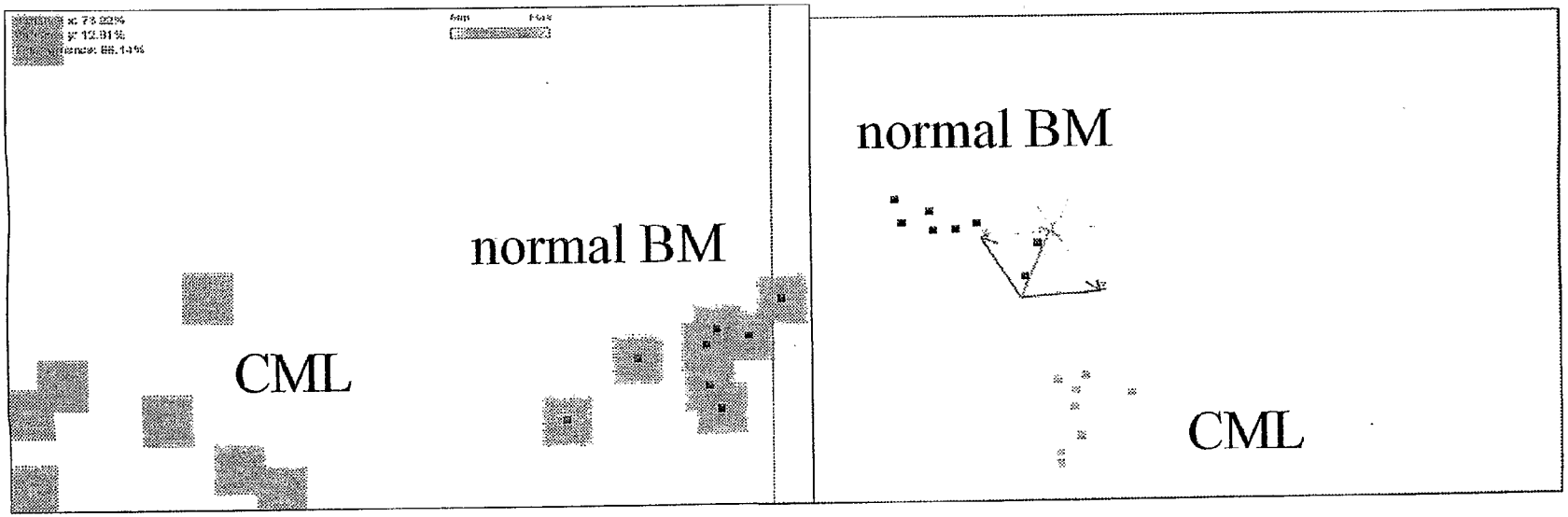
Significance Analysis of Microarrays:
Selection of 162 differentially expressed genes based on a permutation test (K-Nearest Neighbour Imputer)



7b) Principal Component Analysis

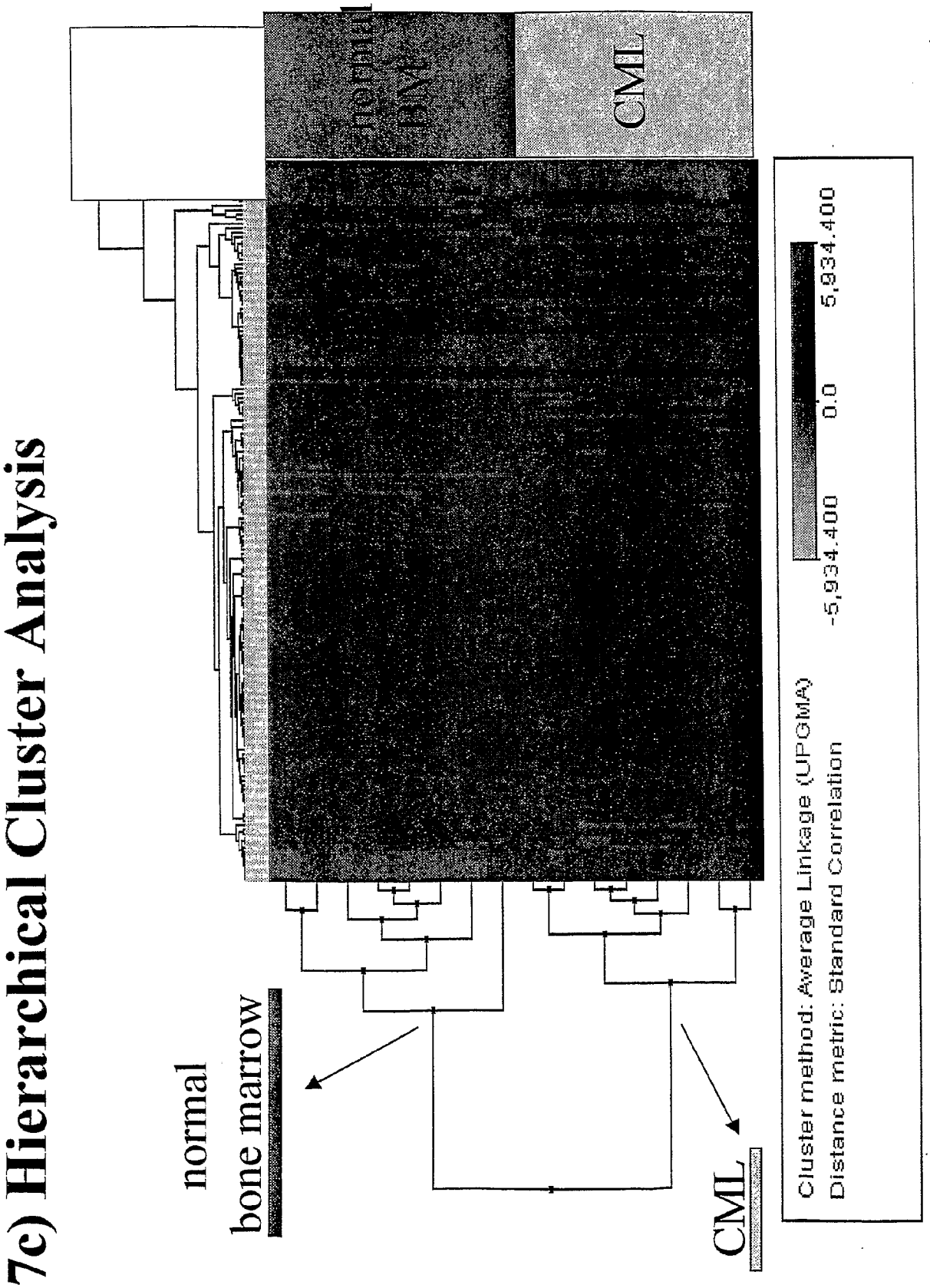
based on 200 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

2-dimensional *3-dimensional*



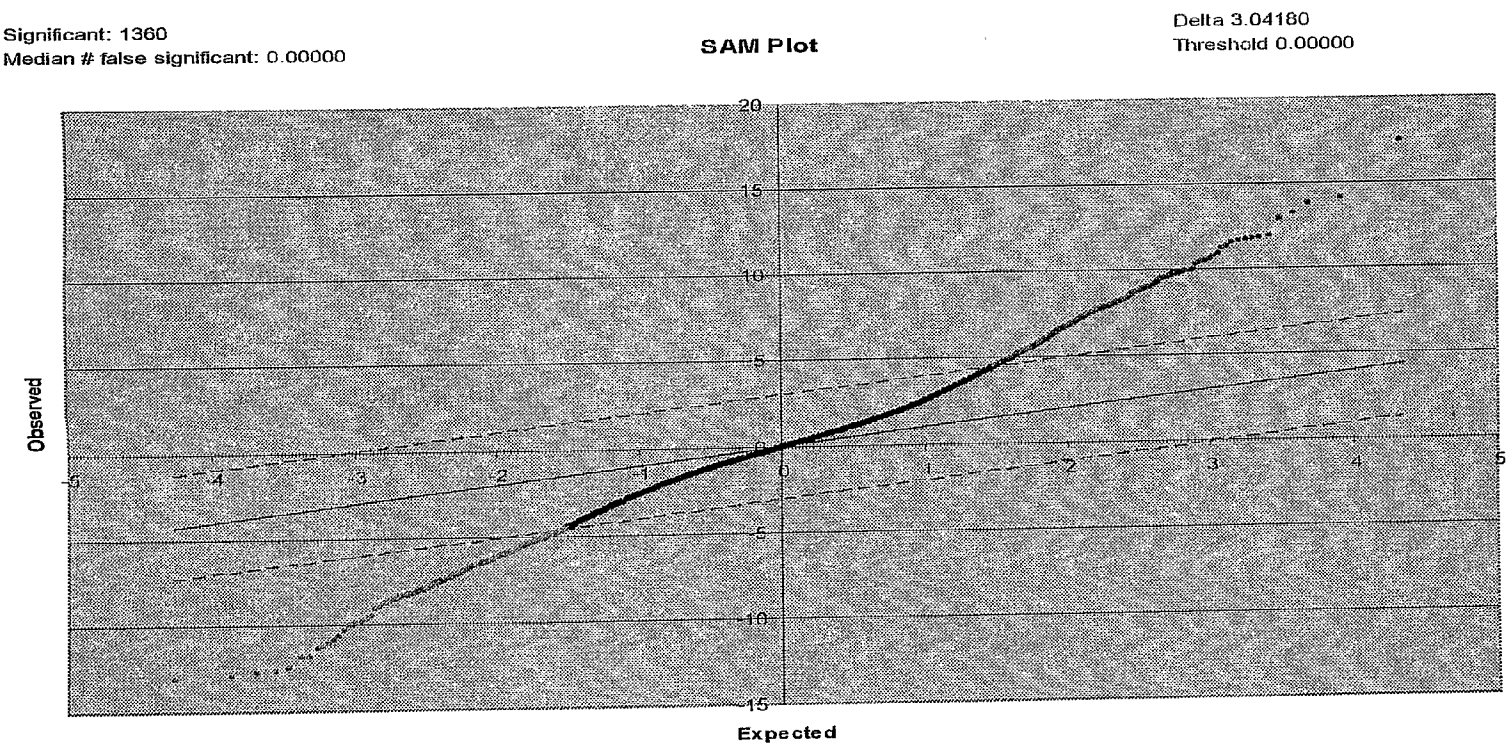
CML	=	chronic myeloid leukemia, n = 8
normal BM	=	bone marrow from healthy volunteers, n =8

7c) Hierarchical Cluster Analysis



8a) Pairwise Comparison of Normal BM and CLL

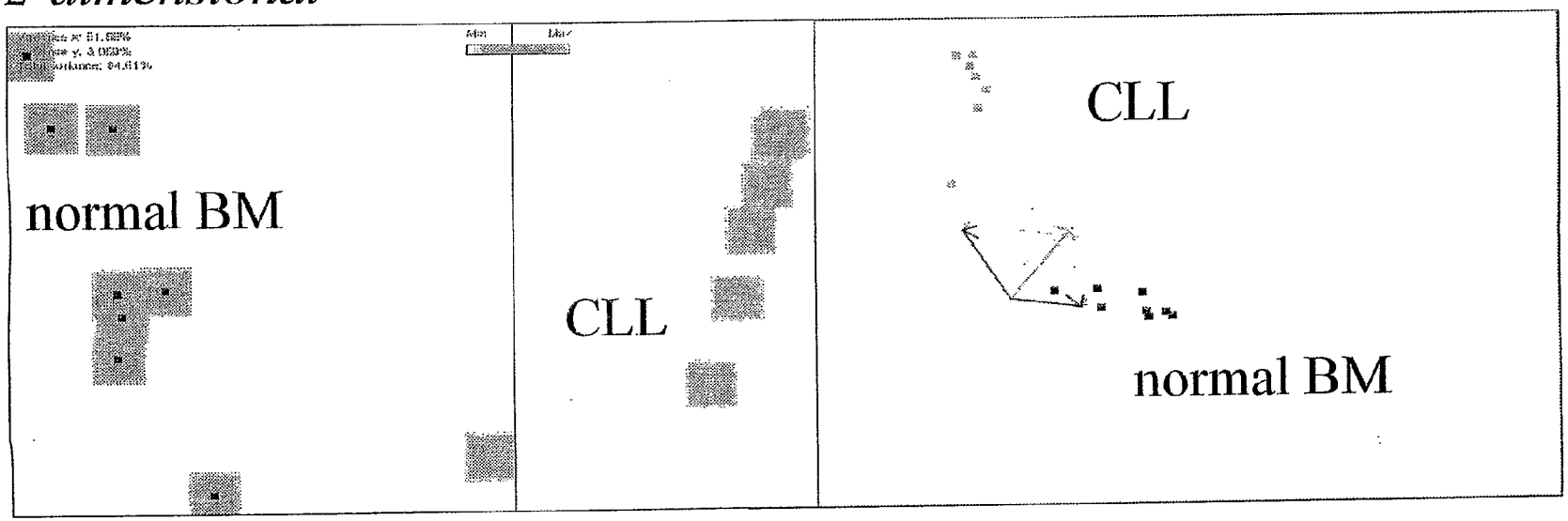
Significance Analysis of Microarrays:
Selection of 200 differentially expressed genes based on a permutation test (K-Nearest Neighbor Imputer)



8b) Principal Component Analysis

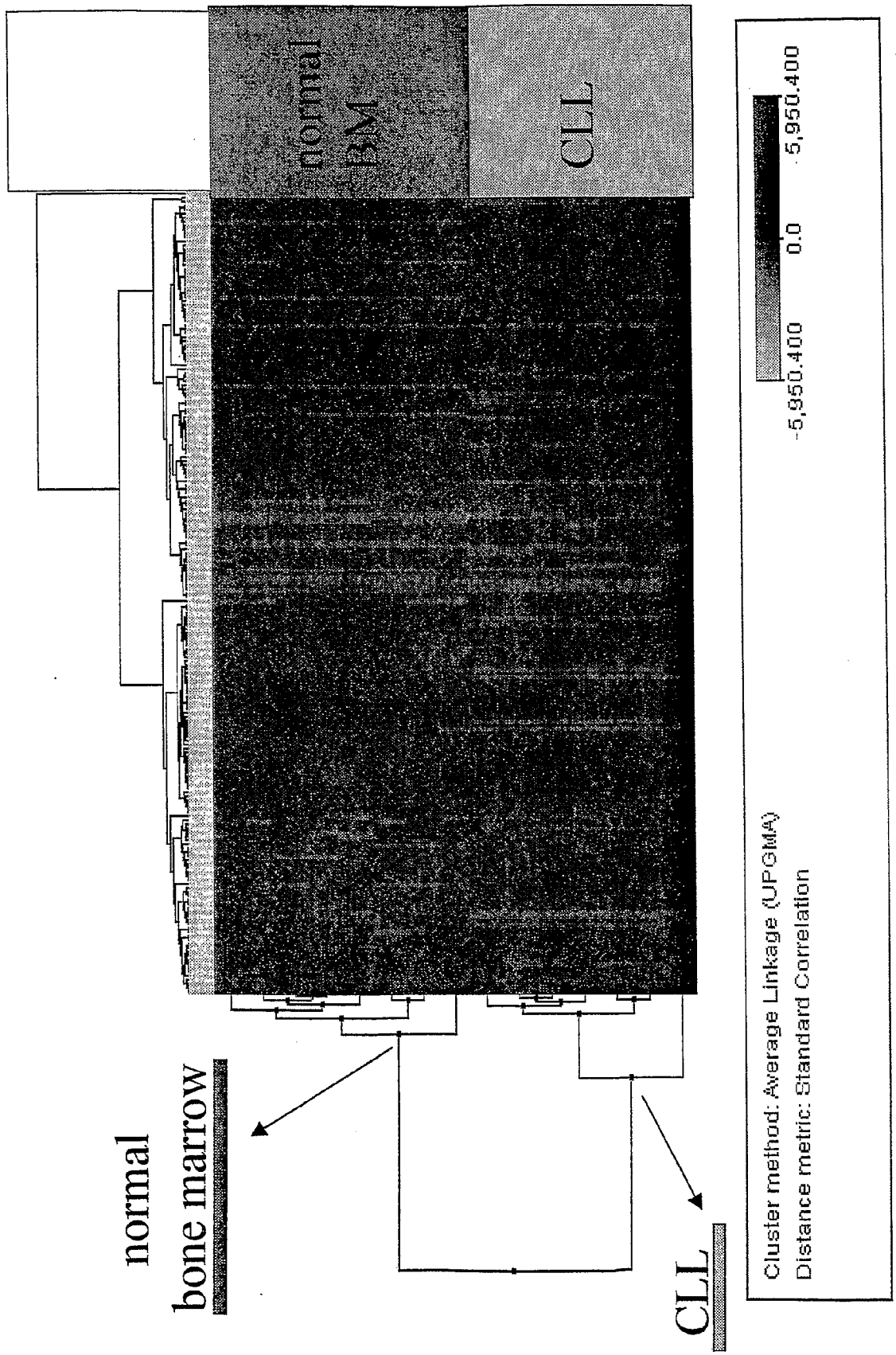
based on 200 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

2-dimensional *3-dimensional*



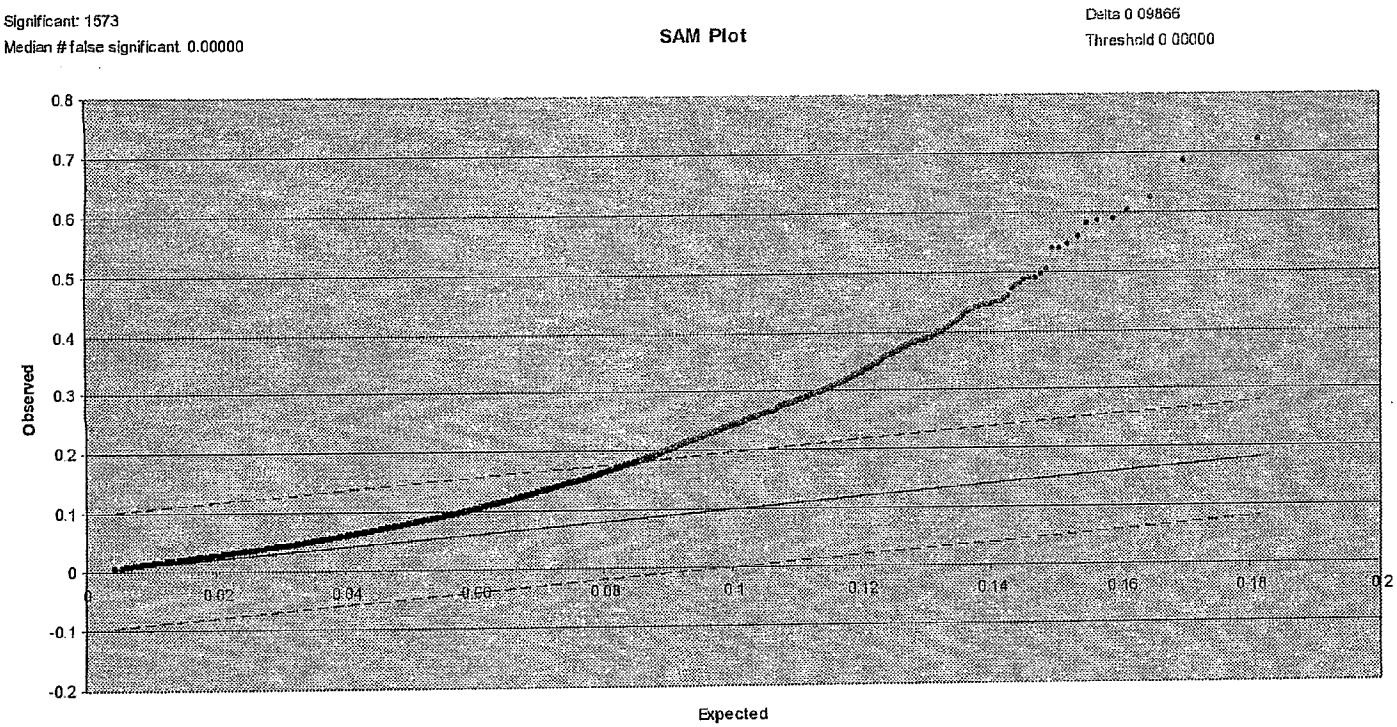
CLL	=	chronic lymphatic leukemia, n = 7
normal BM	=	bone marrow from healthy volunteers, n =8

8c) Hierachical Cluster Analysis



9a) AML-WHO Classification

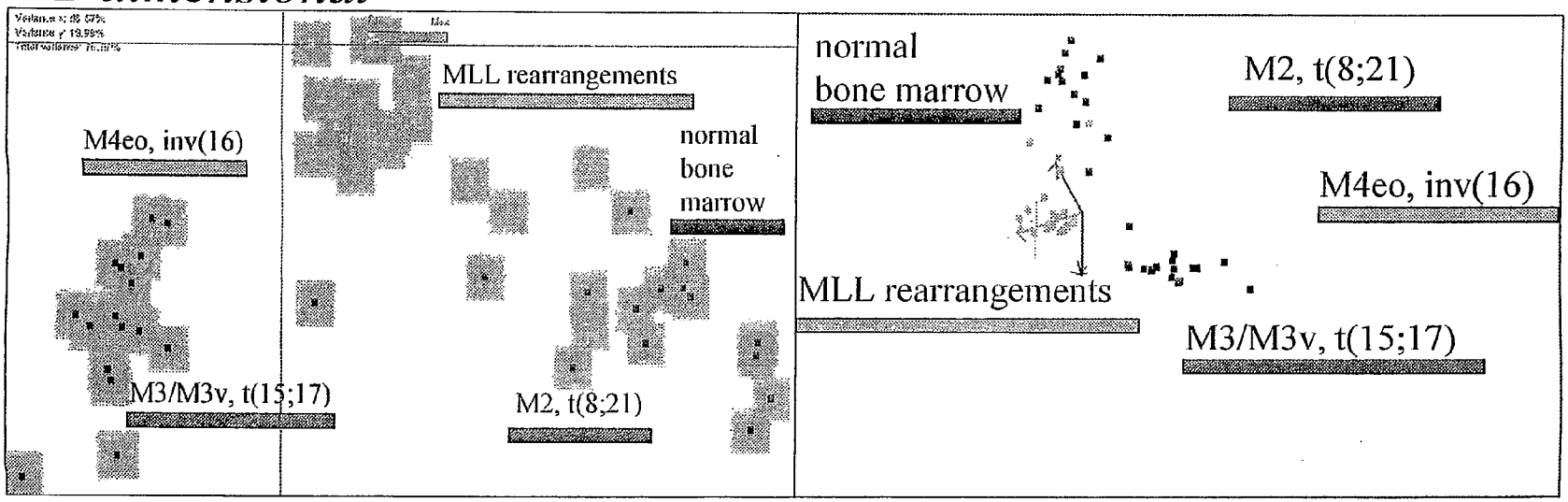
Significance Analysis of Microarrays:
Selection of 124 differentially expressed genes based on a permutation test (K-Nearest Neighbor Imputer)



9b) Principal Component Analysis

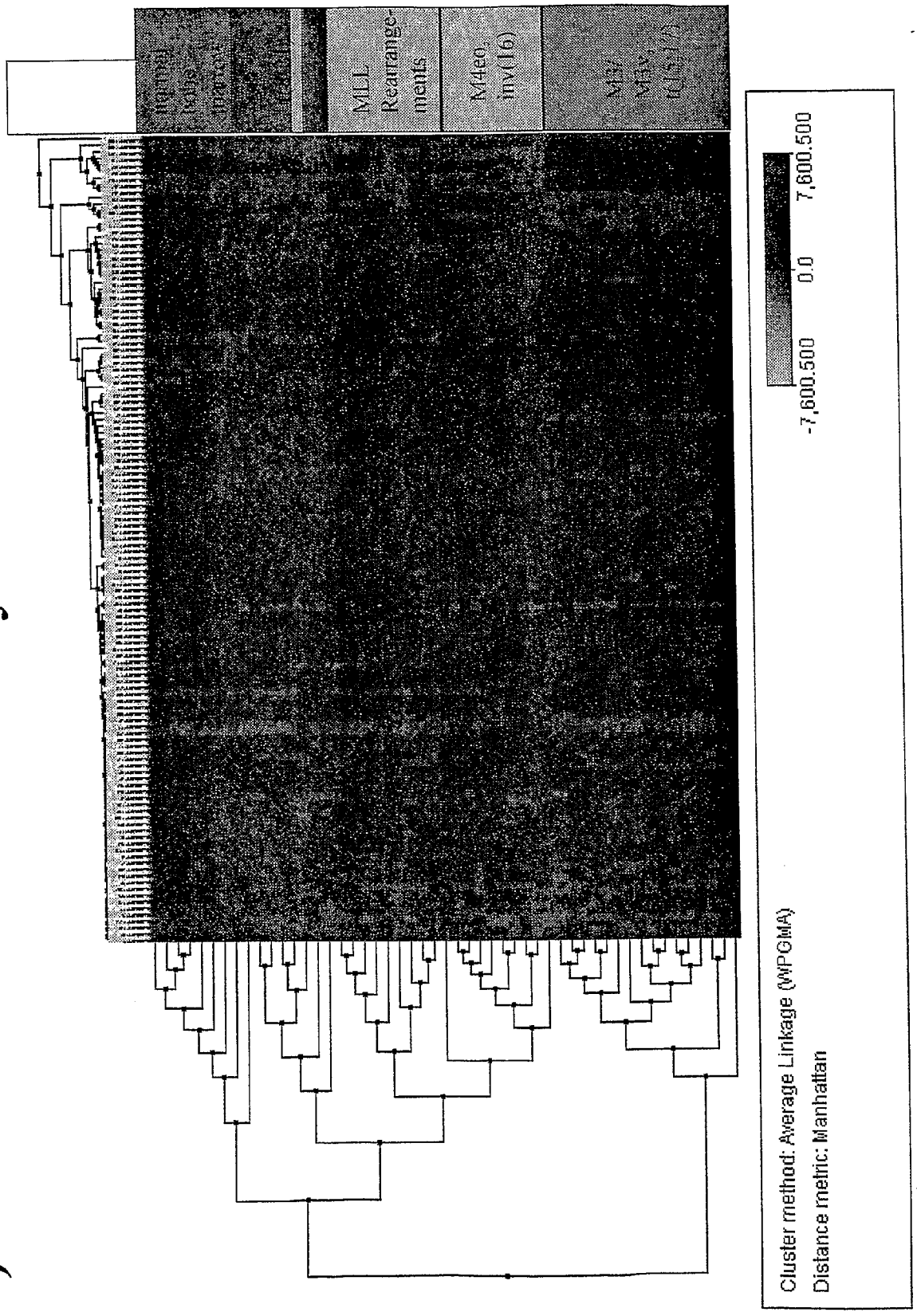
based on 124 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

2-dimensional *3-dimensional*



AML = 4 distinct cytogenetic subgroups, n = 48
normal BM = bone marrow from healthy volunteers, n =8

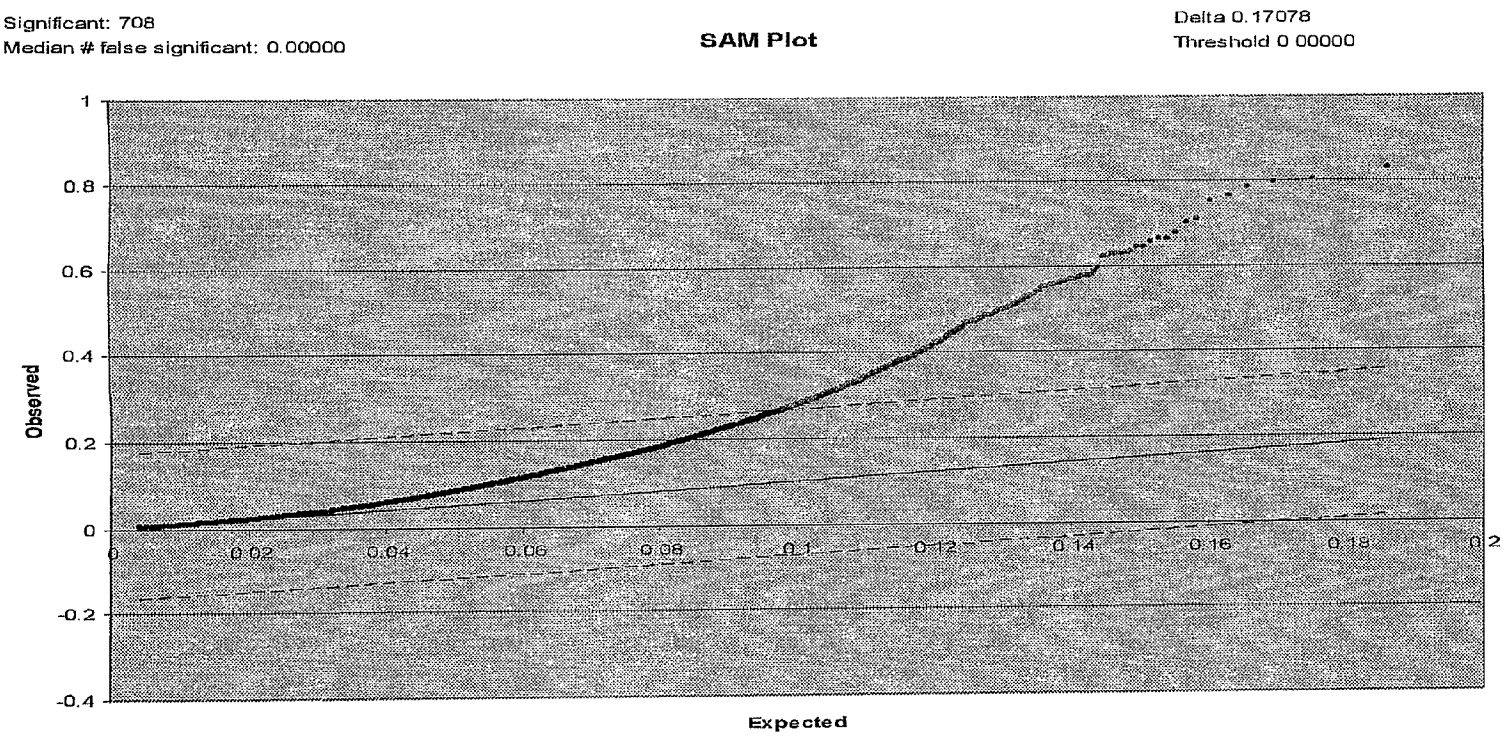
9c) Hierachical Cluster Analysis



10a) Comparison of Normal BM versus Leukemia

Significance Analysis of Microarrays:

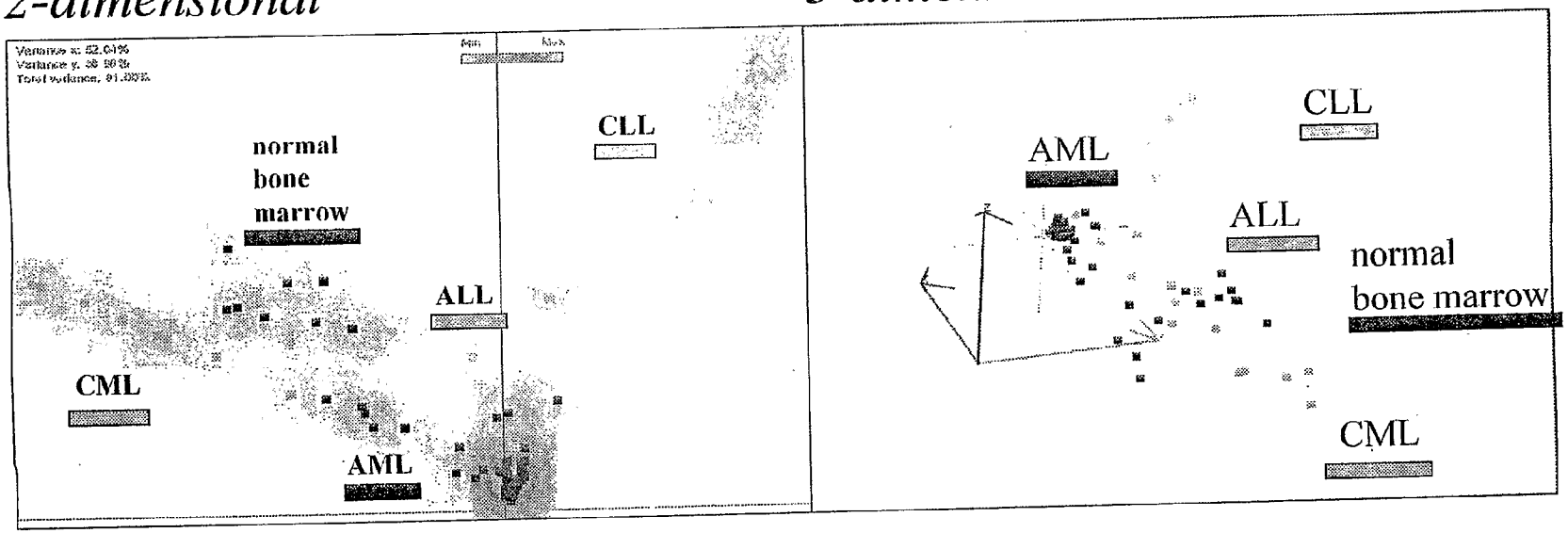
Selection of Top100 differentially expressed genes based on a permutation test (K-Nearest Neighbour Imputer)



10b) Principal Component Analysis

based on 100 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

2-dimensional *3-dimensional*



leukemia = 4 entities: AML, ALL, CML, CLL, n = 72

normal BM = bone marrow from healthy volunteers, n =8

10c) Hierachical Cluster Analysis

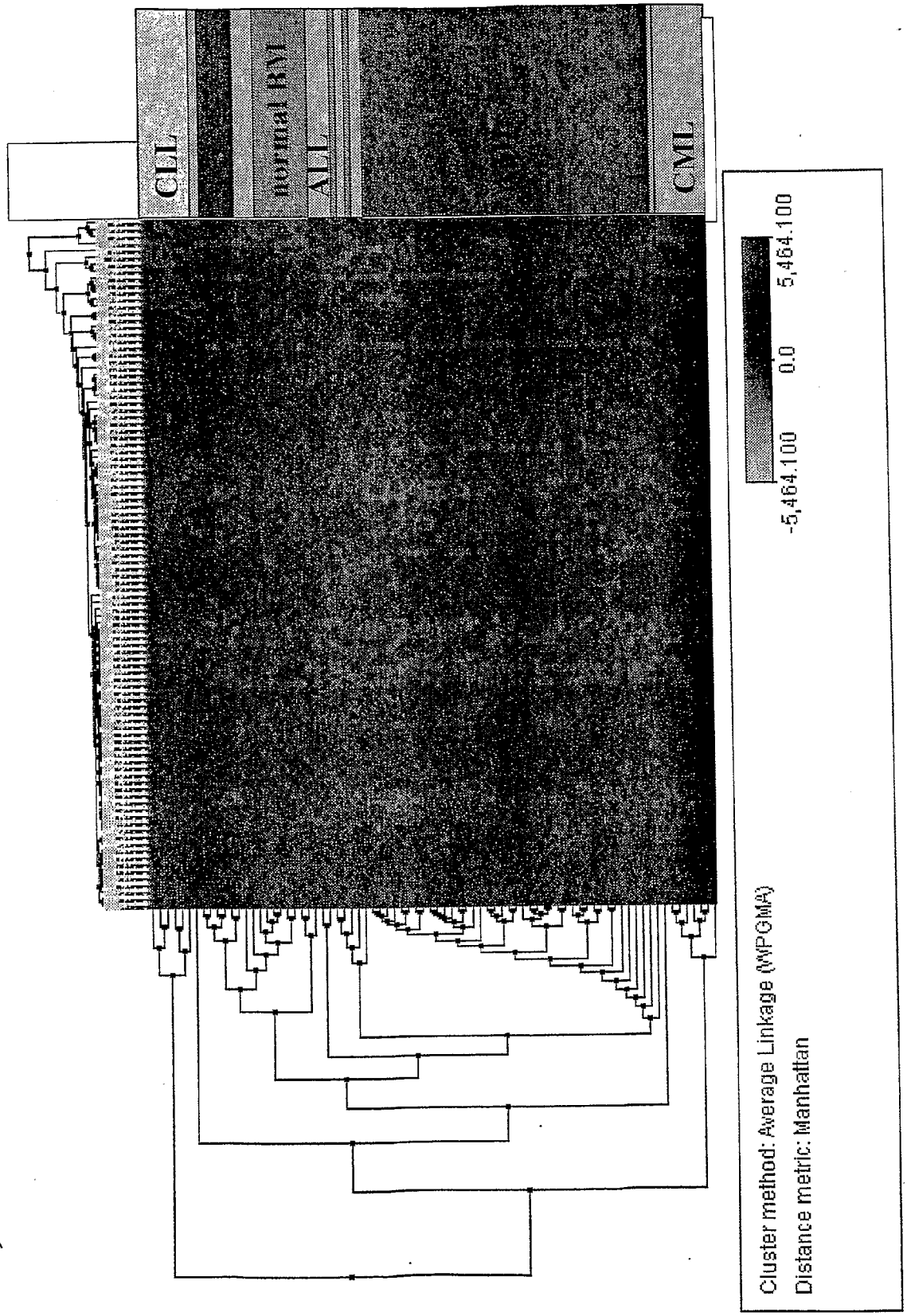
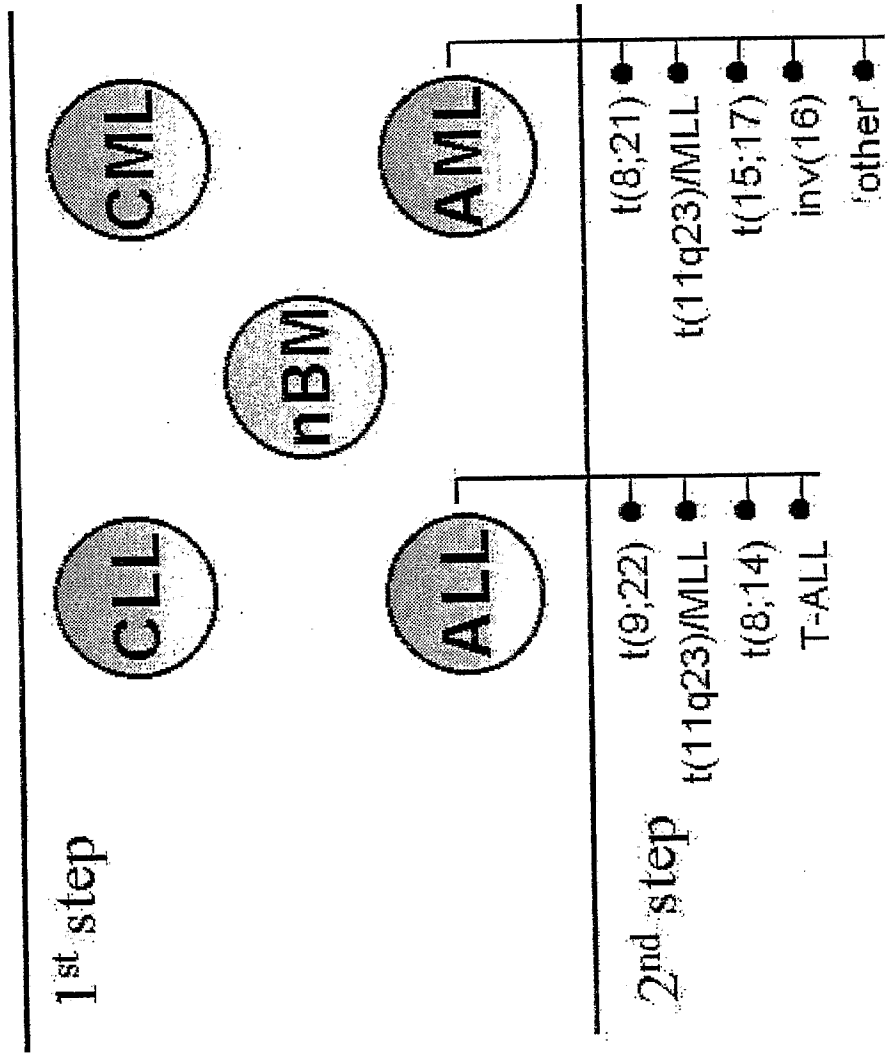


Figure 11a


1st step
CML
CLL
nBM
AML
ALL
2nd step
t(9;22)
t(11q23)/MLL
t(8;14)
T-ALL
t(8;21)
t(11q23)/MLL
t(15;17)
inv(16)
'other'

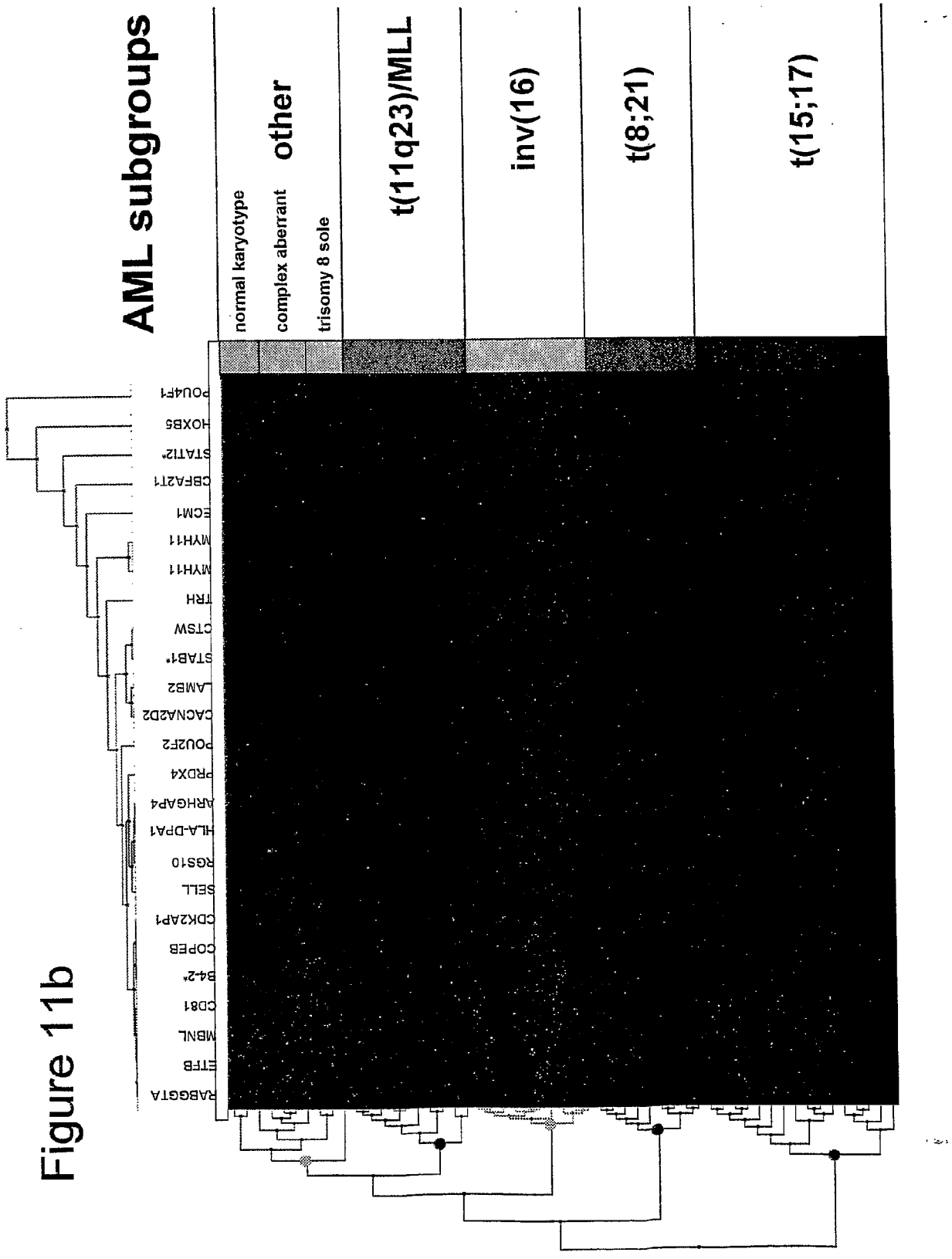

AML subgroups
normal karyotype
complex aberrant
other
trisomy 8 sole
t(11q23)/MLL
inv(16)
t(8;21)
t(15;17)
POU4F1
HOXB5
STAT12*
CBFA2T1
ECM1
MYH11
MYH11
TRH
CTSW
STAB1*
LAMB2
CACNA2D2
POU2F2
PRDX4
ARHGAP4
HLA-DPA1
RGS10
SELL
CDK2AP1
COPEB
B4-2*
CD81
MBNL
ETFB
RABGGTA

Figure 11b

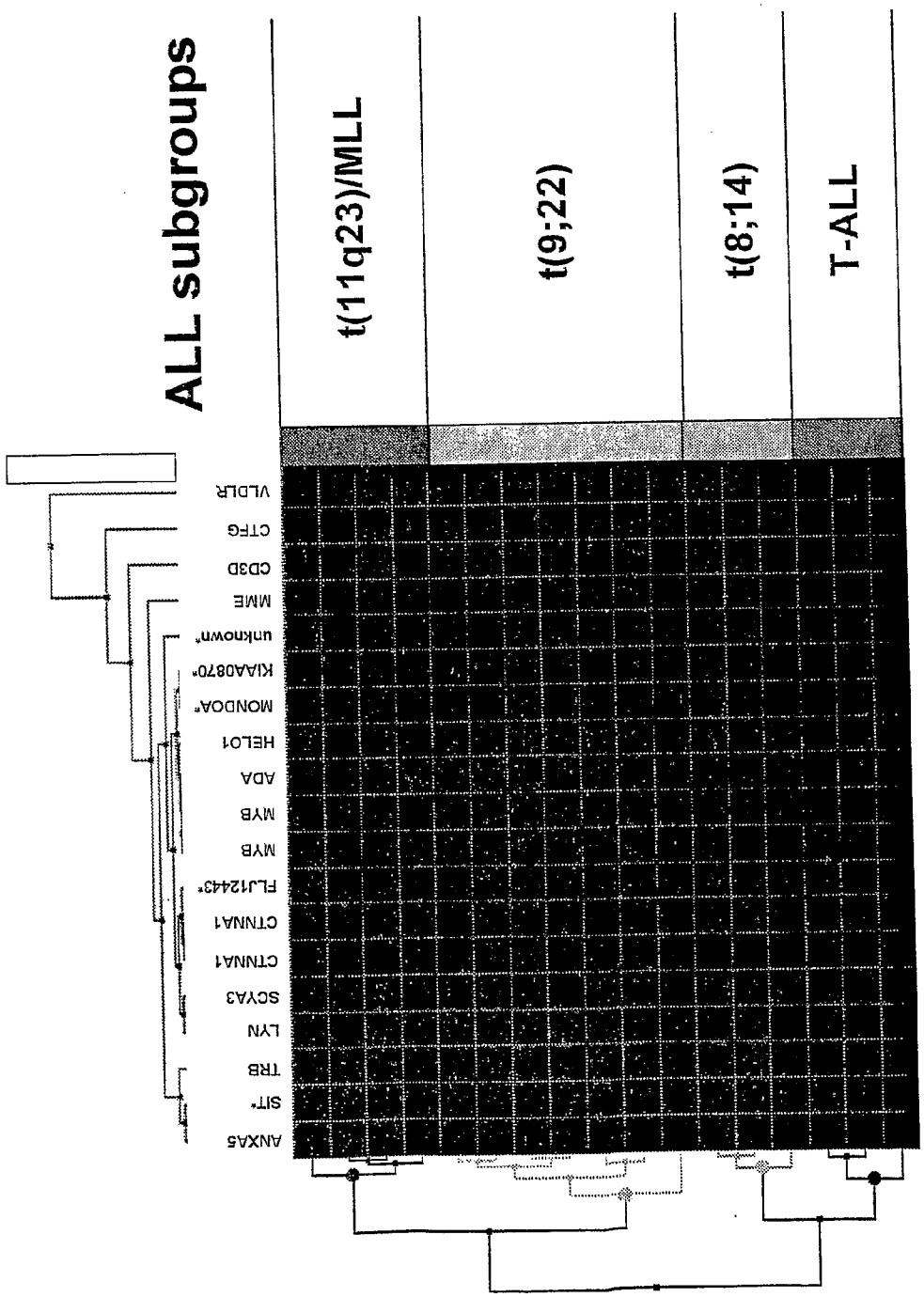

ALL subgroups
t(11q23)/MLL
t(9;22)
t(8;14)
T-ALL
VLDLR
CTFG
CD3D
MME
unknown*
KIAA0870*
MONDOA*
HELO1
ADA
MYB
MYB
FLJ12443*
CTNNA1
CTNNA1
SCYA3
LYN
TRB
SIT*
ANXA5

Figure 11c

Figure 12a

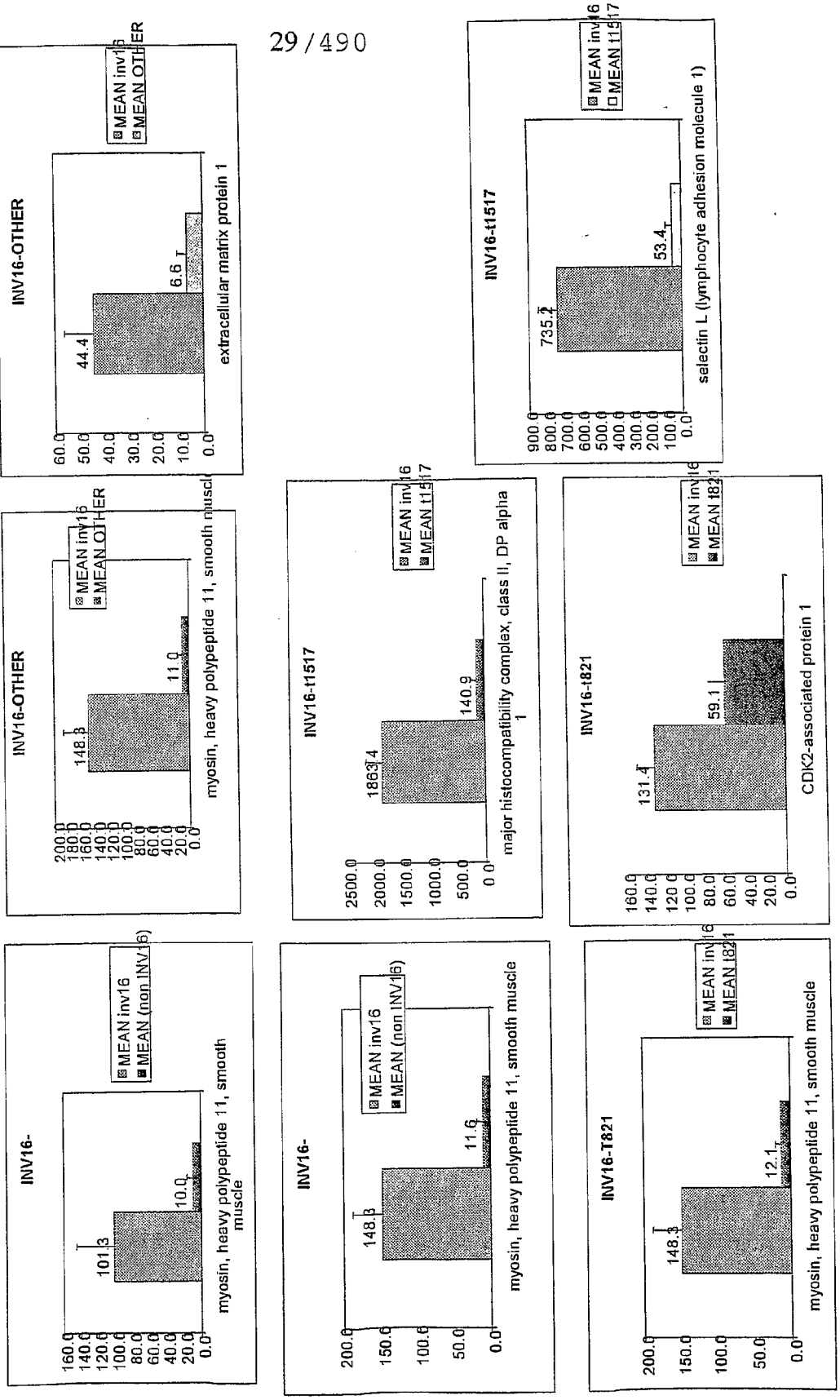

INV16-
MEAN inv16
MEAN (non INV16)
myosin, heavy polypeptide 11, smooth muscle
INV16-OTHER
MEAN inv16
MEAN OTHER
extracellular matrix protein 1
INV16-t1517
MEAN inv16
MEAN t1517
major histocompatibility complex, class II, DP alpha 1
INV16-t821
MEAN inv16
MEAN t821
CDK2-associated protein 1
INV16-T821
selectin L (lymphocyte adhesion molecule 1)

Figure 12b

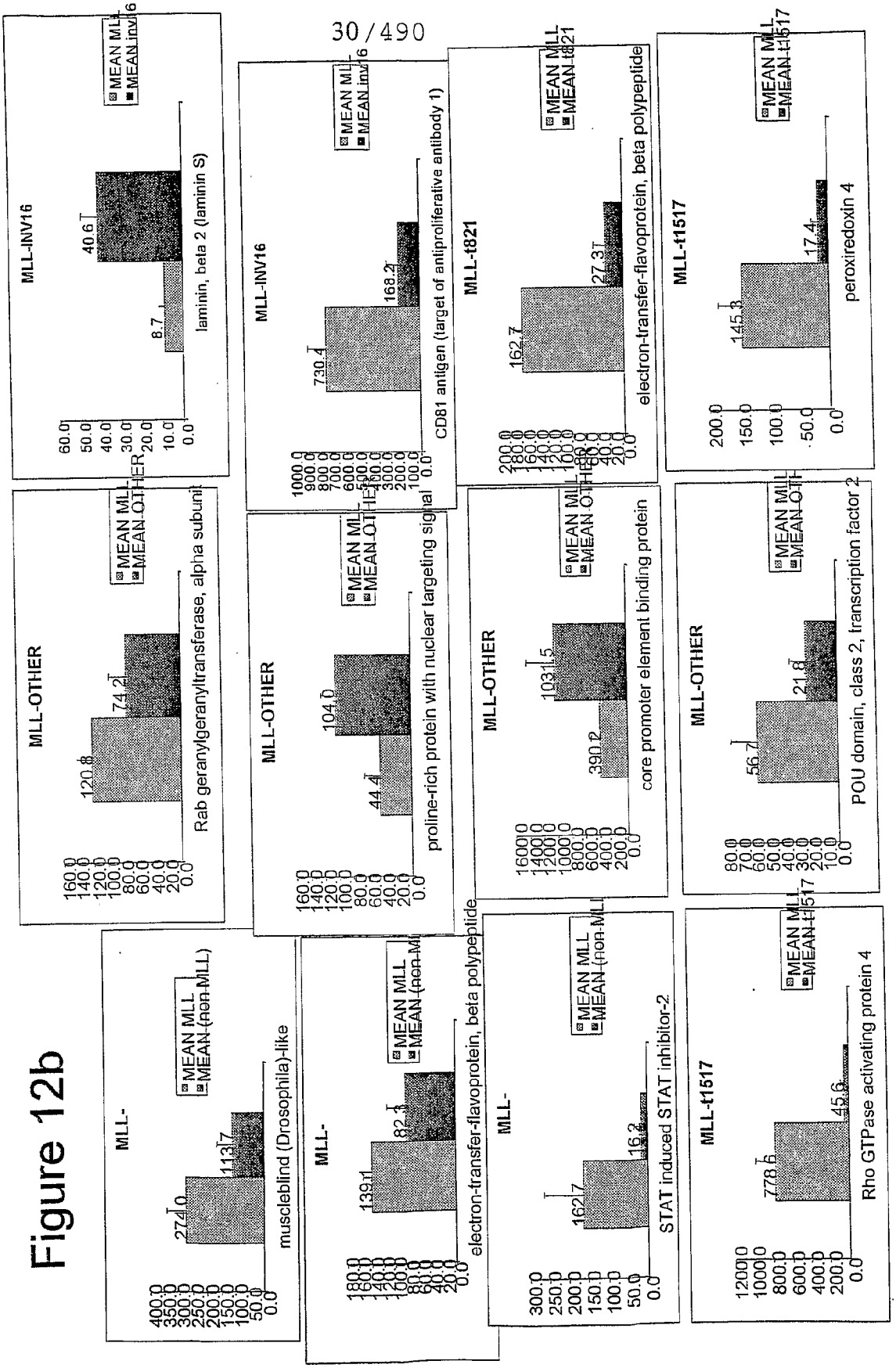

MLL-
MEAN MLL
MEAN (non-MLL)
muscleblind (Drosophila)-like
MLL-OTHER
MEAN MLL
MEAN OTHER
Rab geranylgeranyltransferase, alpha subunit
MLL-INV16
MEAN MLL
MEAN inv16
laminin, beta 2 (laminin S)
MLL-OTHER
MEAN MLL
MEAN OTHER
proline-rich protein with nuclear targeting signal
MLL-INV16
MEAN MLL
MEAN inv16
CD81 antigen (target of antiproliferative antibody 1)
MLL-
MEAN MLL
MEAN (non-MLL)
electron-transfer-flavoprotein, beta polypeptide
MLL-OTHER
MEAN MLL
MEAN OTHER
core promoter element binding protein
MLL-t821
MEAN MLL
MEAN t821
electron-transfer-flavoprotein, beta polypeptide
MLL-
MEAN MLL
MEAN (non-MLL)
STAT induced STAT inhibitor-2
MLL-OTHER
MEAN MLL
MEAN OTHER
POU domain, class 2, transcription factor 2
MLL-t1517
MEAN MLL
MEAN t1517
peroxiredoxin 4
MLL-t1517
MEAN MLL
MEAN t1517
Rho GTPase activating protein 4

Figure 12c

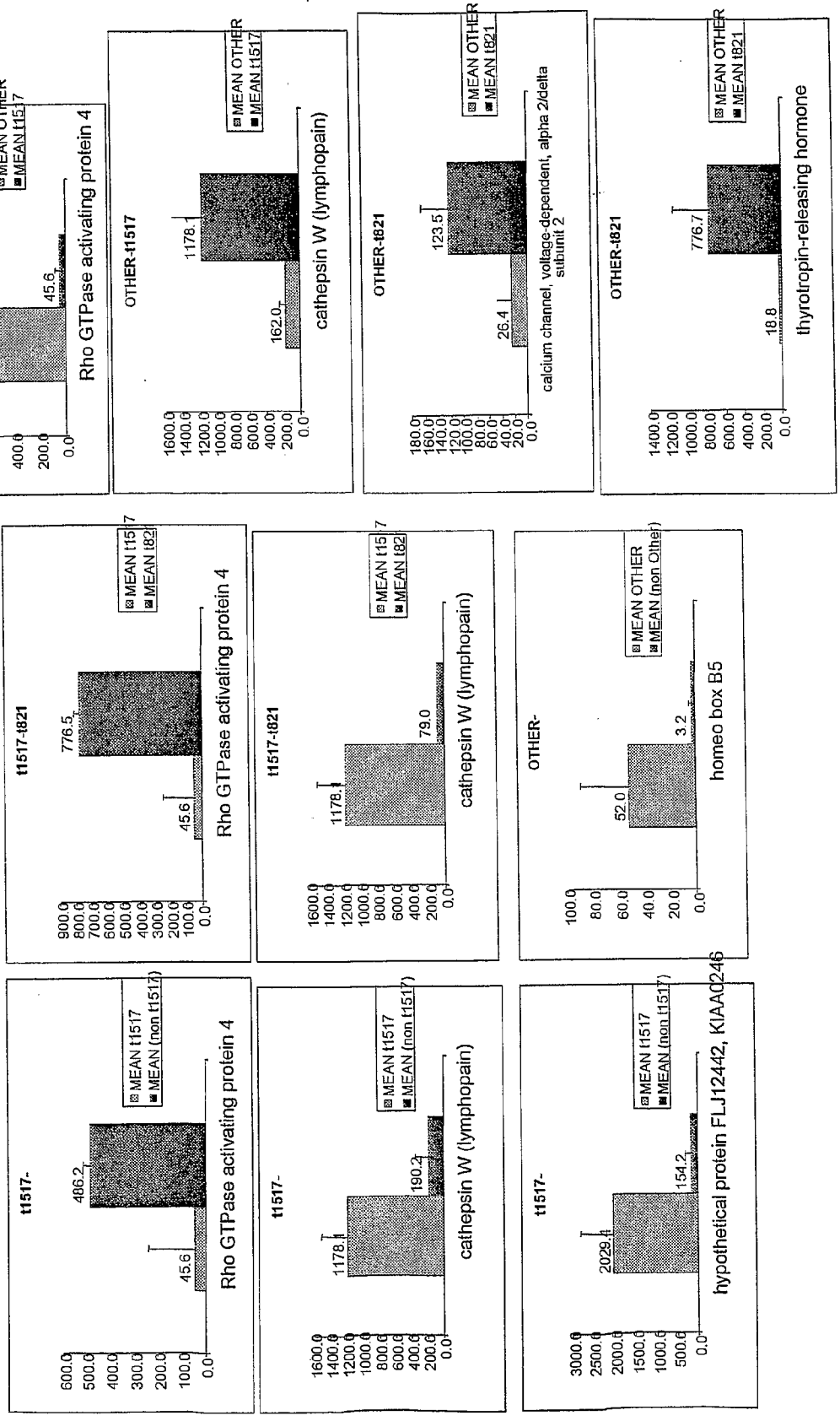

OTHER-t1517
MEAN OTHER
MEAN t1517
716.0
45.6
Rho GTPase activating protein 4
OTHER-t1517
1178.1
162.0
cathepsin W (lymphopain)
OTHER-t821
123.5
26.4
calcium channel, voltage-dependent, alpha 2/delta subunit 2
MEAN t821
776.7
18.8
thyrotropin-releasing hormone
t1517-t821
776.5
45.6
MEAN t1517
MEAN t82
t1517-
486.2
45.6
MEAN t1517
MEAN (non t1517)
OTHER-
52.0
3.2
homeo box B5
2029.4
154.2
hypothetical protein FLJ12442, KIAA0246

Figure 12d

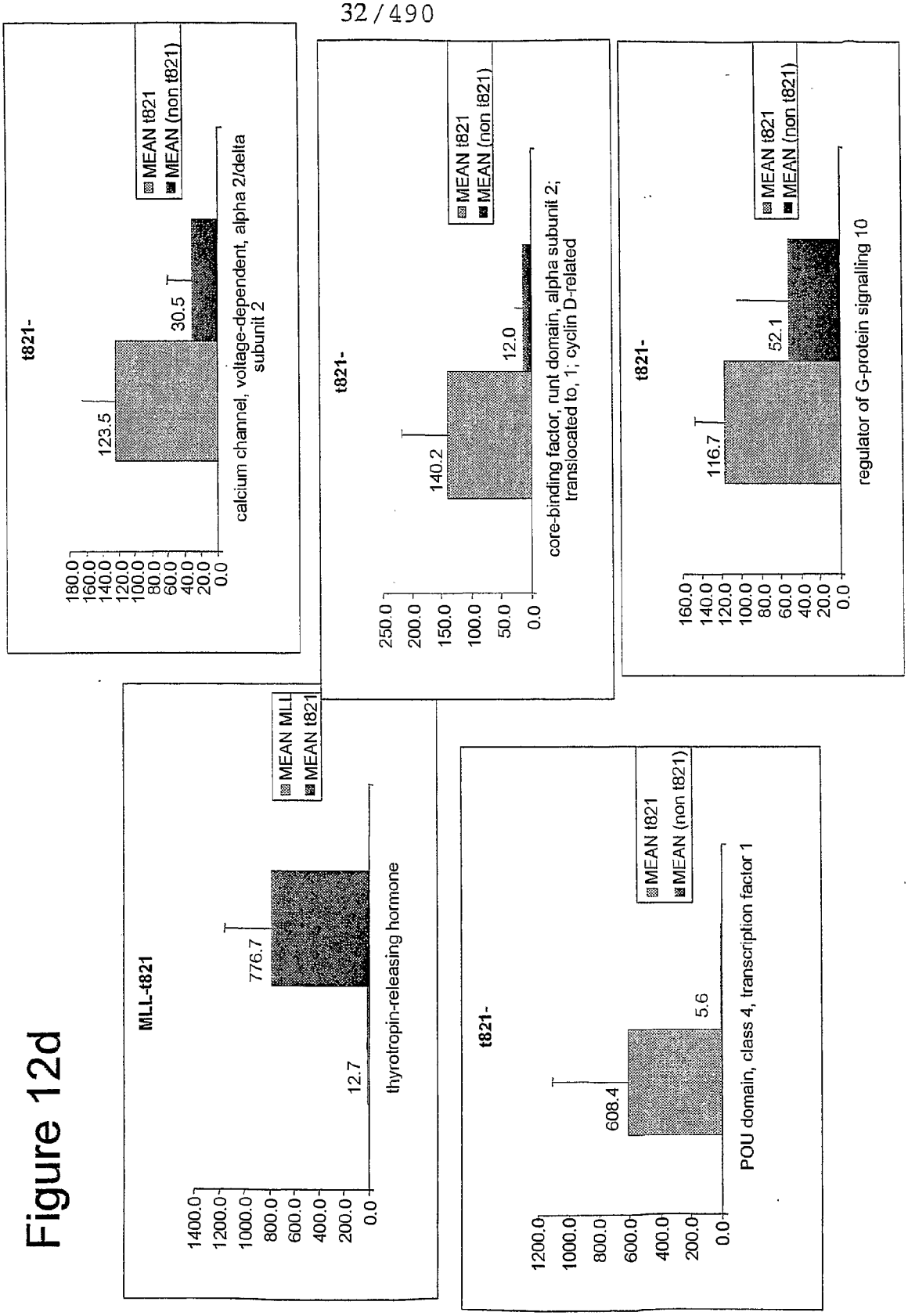

MLL-t821
MEAN MLL
MEAN t821
1400.0
1200.0
1000.0
800.0
600.0
400.0
200.0
0.0
776.7
12.7
thyrotropin-releasing hormone
t821-
MEAN t821
MEAN (non t821)
250.0
200.0
150.0
100.0
50.0
0.0
140.2
12.0
core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related
t821-
MEAN t821
MEAN (non t821)
160.0
140.0
120.0
100.0
80.0
60.0
40.0
20.0
0.0
116.7
52.1
regulator of G-protein signalling 10
t821-
MEAN t821
MEAN (non t821)
180.0
160.0
140.0
120.0
100.0
80.0
60.0
40.0
20.0
0.0
123.5
30.5
calcium channel, voltage-dependent, alpha 2/delta subunit 2
t821-
MEAN t821
MEAN (non t821)
1200.0
1000.0
800.0
600.0
400.0
200.0
0.0
608.4
5.6
POU domain, class 4, transcription factor 1

Figure 12e

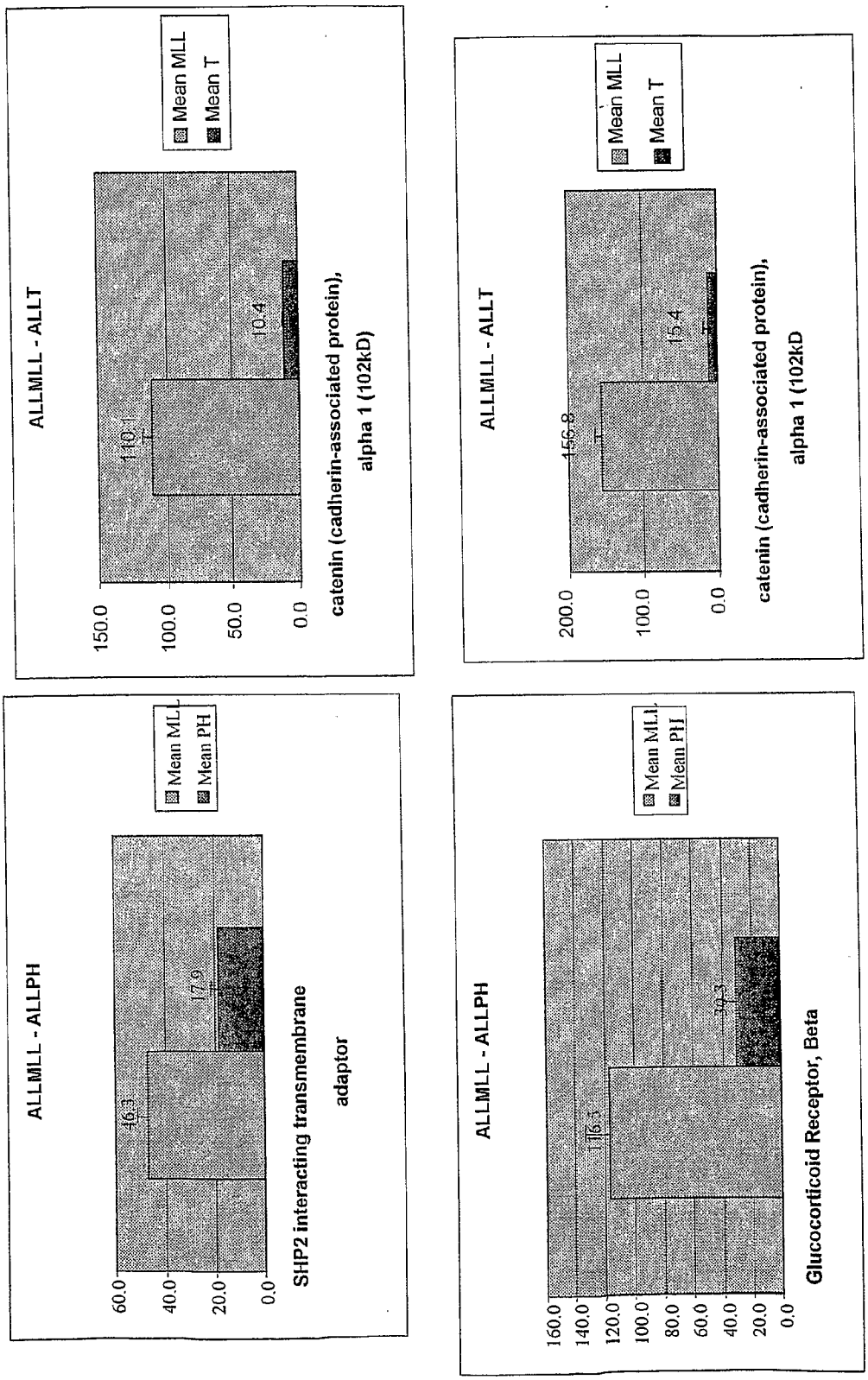

ALLMLL - ALLT
Mean MLL
Mean T
150.0
100.0
50.0
0.0
110.1
10.4
catenin (cadherin-associated protein), alpha 1 (102kD)
ALLMLL - ALLT
Mean MLL
Mean T
200.0
100.0
0.0
156.8
15.4
catenin (cadherin-associated protein), alpha 1 (102kD
ALLMLL - ALLPH
Mean MLL
Mean PH
60.0
40.0
20.0
0.0
16.3
17.9
SHP2 interacting transmembrane adaptor
ALLMLL - ALLPH
Mean MLL
Mean PH
160.0
140.0
120.0
100.0
80.0
60.0
40.0
20.0
0.0
116.5
30.3
Glucocorticoid Receptor, Beta

Figure 12f

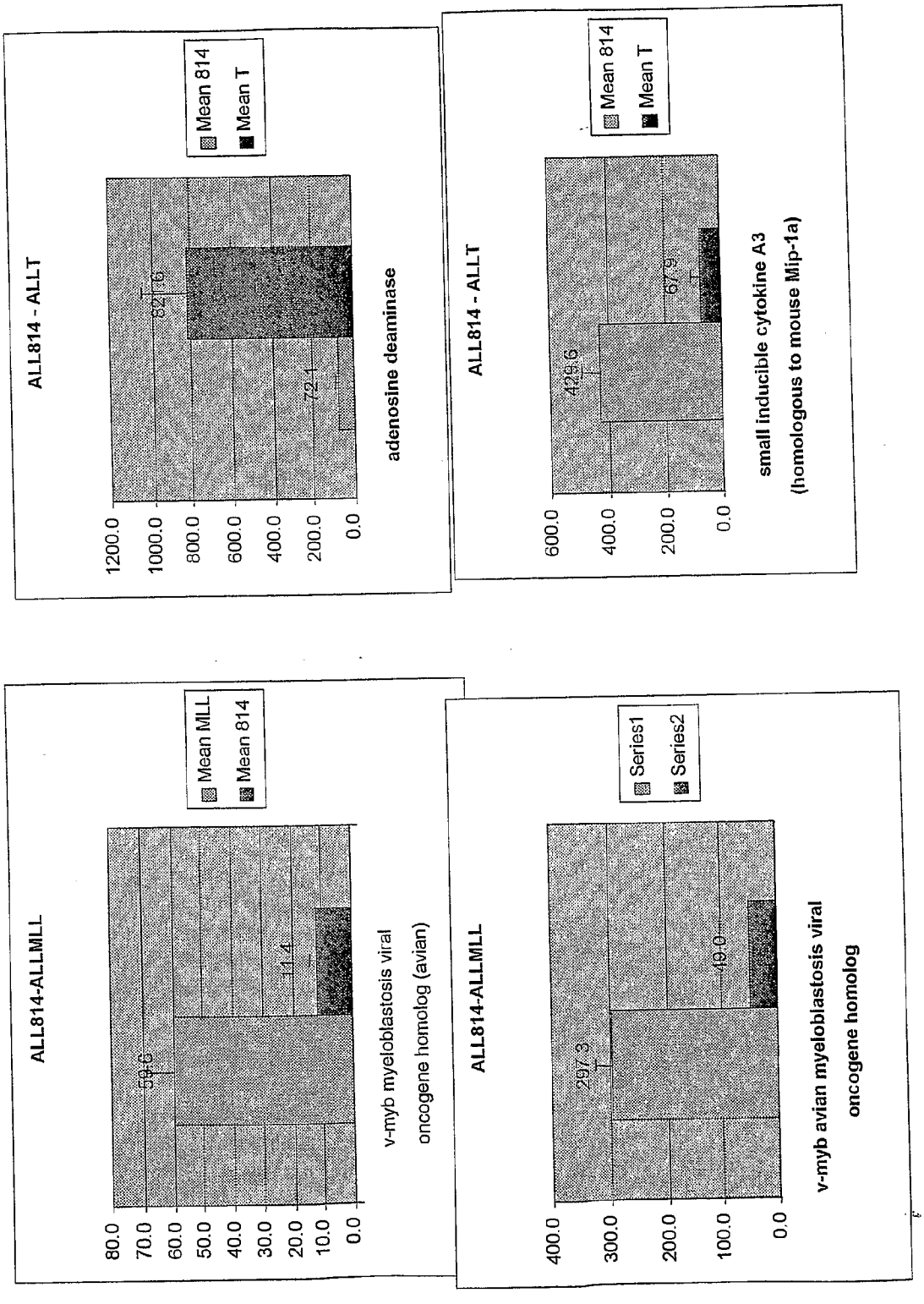

ALL814 - ALLT
Mean 814
Mean T
1200.0
1000.0
800.0
600.0
400.0
200.0
0.0
821.6
721.4
adenosine deaminase
ALL814 - ALLT
Mean 814
Mean T
600.0
400.0
200.0
0.0
429.6
67.9
small inducible cytokine A3
(homologous to mouse Mip-1a)
ALL814-ALLMLL
Mean MLL
Mean 814
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
59.6
11.4
v-myb myeloblastosis viral
oncogene homolog (avian)
ALL814-ALLMLL
Series1
Series2
400.0
300.0
200.0
100.0
0.0
297.3
49.0
v-myb avian myeloblastosis viral
oncogene homolog

Figure 12g

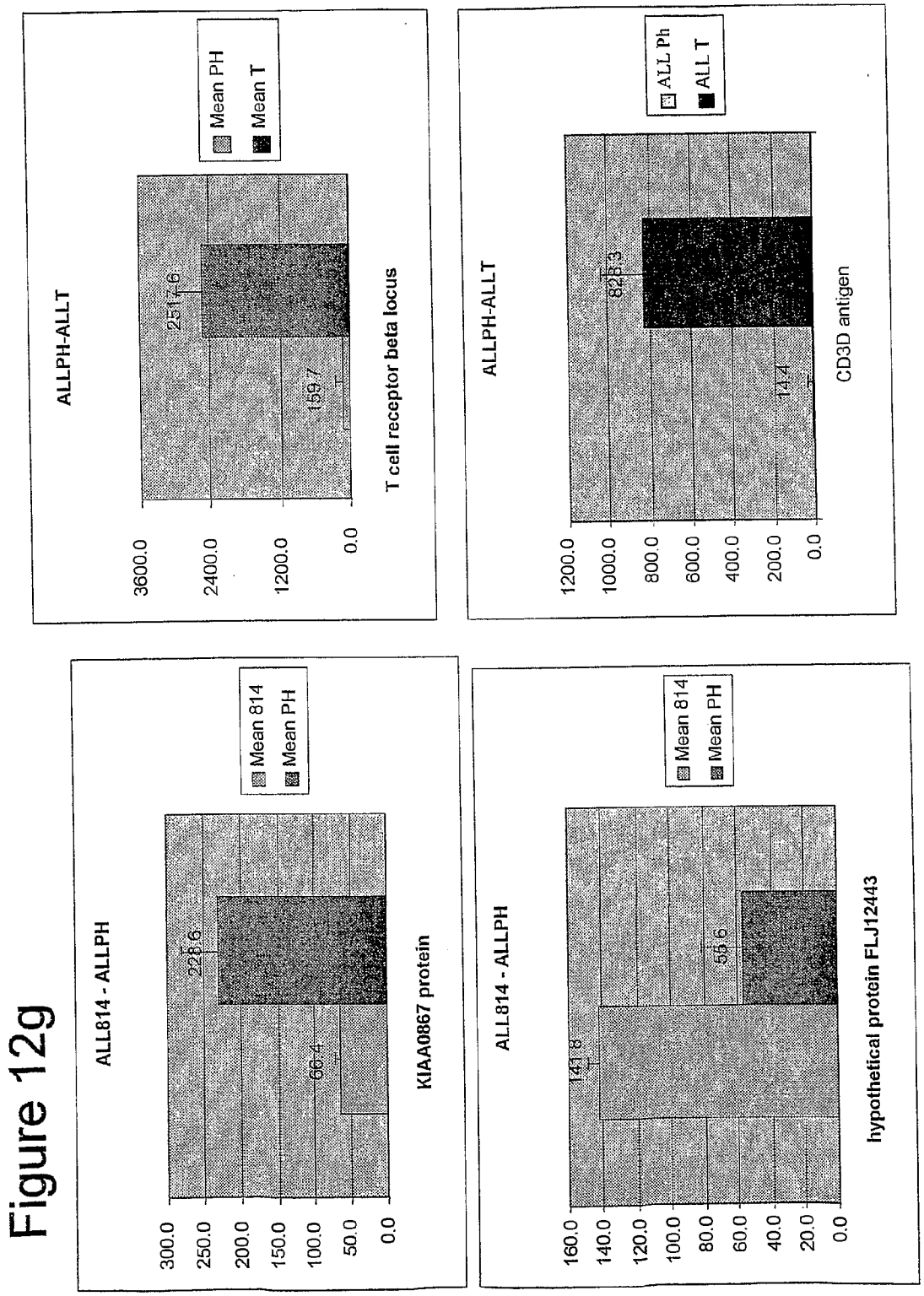

ALLPH-ALLT
Mean PH
Mean T
251.6
159.7
3600.0
2400.0
1200.0
0.0
T cell receptor beta locus
ALLPH-ALLT
ALL Ph
ALL T
828.3
14.4
1200.0
1000.0
800.0
600.0
400.0
200.0
0.0
CD3D antigen
ALL814 - ALLPH
Mean 814
Mean PH
228.6
66.4
300.0
250.0
200.0
150.0
100.0
50.0
0.0
KIAA0867 protein
ALL814 - ALLPH
Mean 814
Mean PH
141.8
55.6
160.0
140.0
120.0
100.0
80.0
60.0
40.0
20.0
0.0
hypothetical protein FLJ12443

Figure 12h

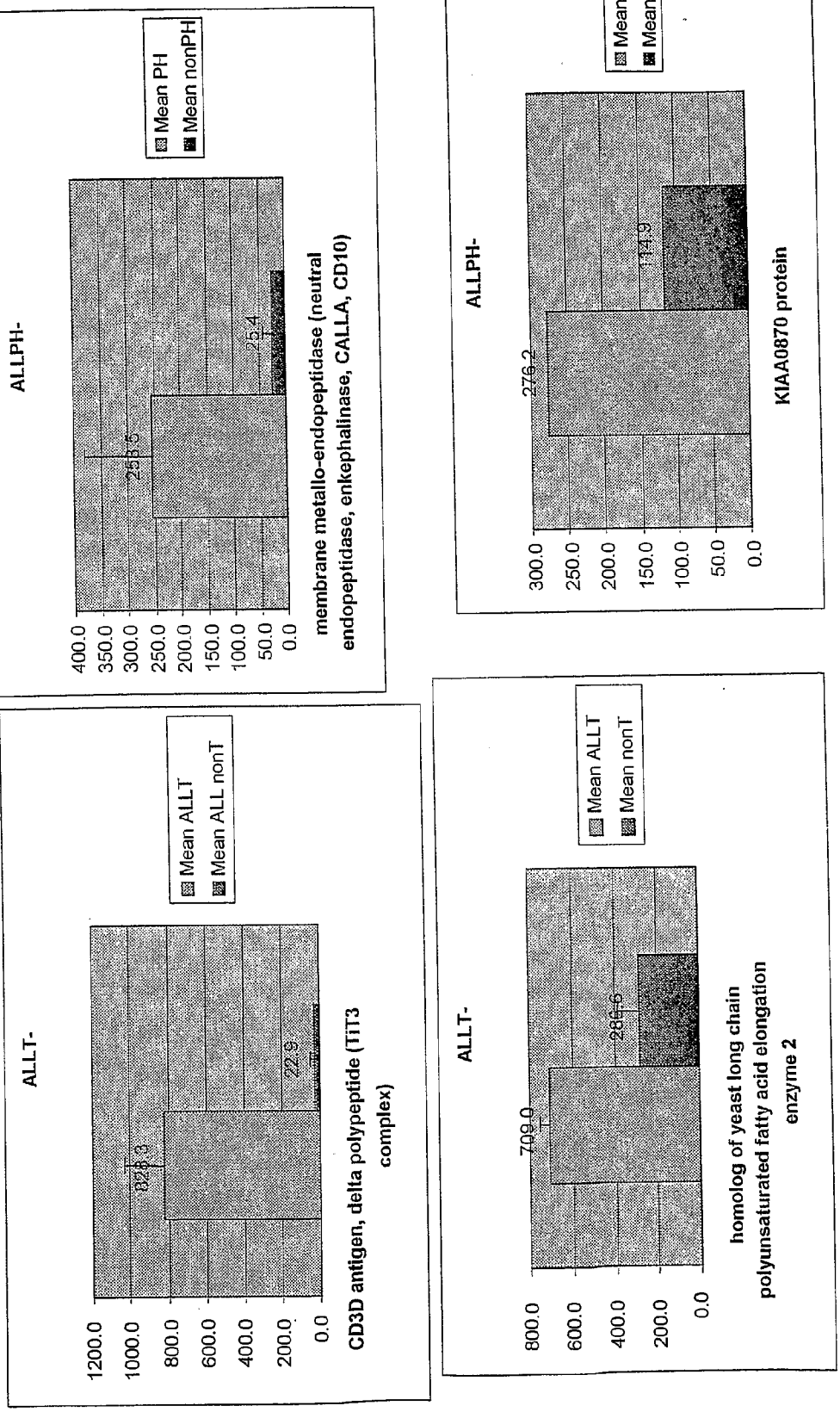
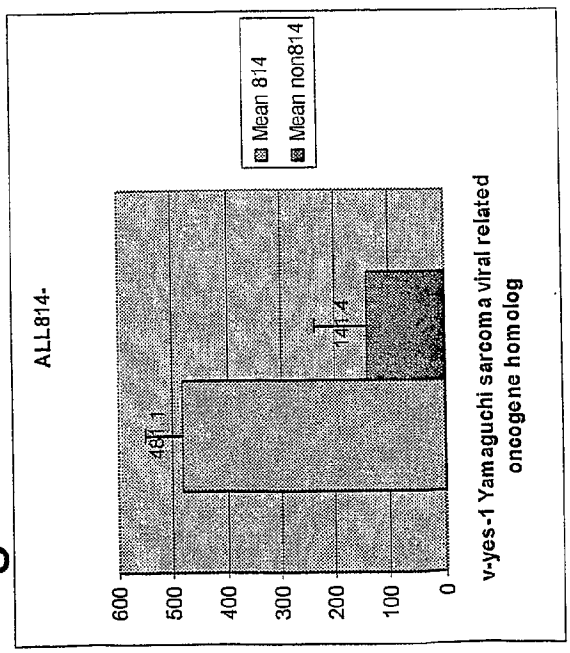
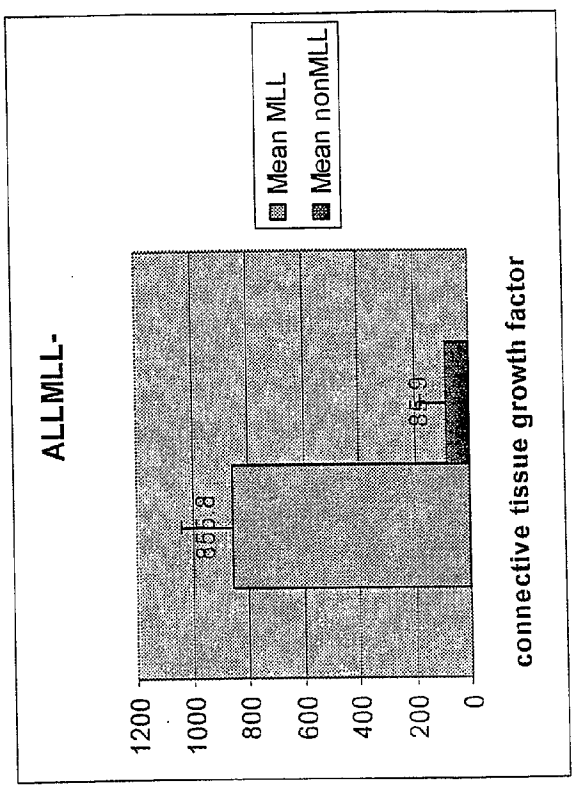
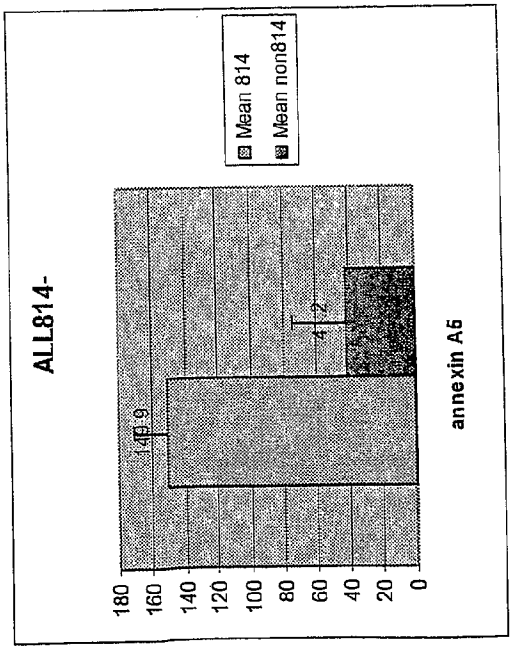

ALLT-
Mean ALLT
Mean ALL nonT
1200.0
1000.0
800.0
600.0
400.0
200.0
0.0
828.3
22.9
CD3D antigen, delta polypeptide (TiT3 complex)
ALLPH-
Mean PH
Mean nonPH
400.0
350.0
300.0
250.0
200.0
150.0
100.0
50.0
0.0
253.5
25.4
membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
ALLPH-
Mean PH
Mean nonPH
300.0
250.0
200.0
150.0
100.0
50.0
0.0
276.2
114.9
KIAA0870 protein
ALLT-
Mean ALLT
Mean nonT
800.0
600.0
400.0
200.0
0.0
709.0
286.6
homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2

Figure 12i


ALL814-
Mean 814
Mean non814
48.1
141.4
600
500
400
300
200
100
0
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog


ALLMLL-
Mean MLL
Mean nonMLL
865.8
85.6
1200
1000
800
600
400
200
0
connective tissue growth factor


ALL814-
Mean 814
Mean non814
145.9
41.2
180
160
140
120
100
80
60
40
20
0
annexin A6

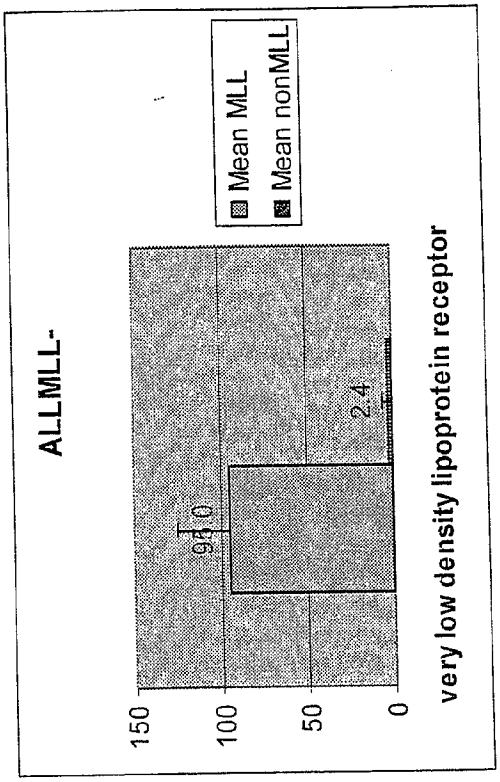
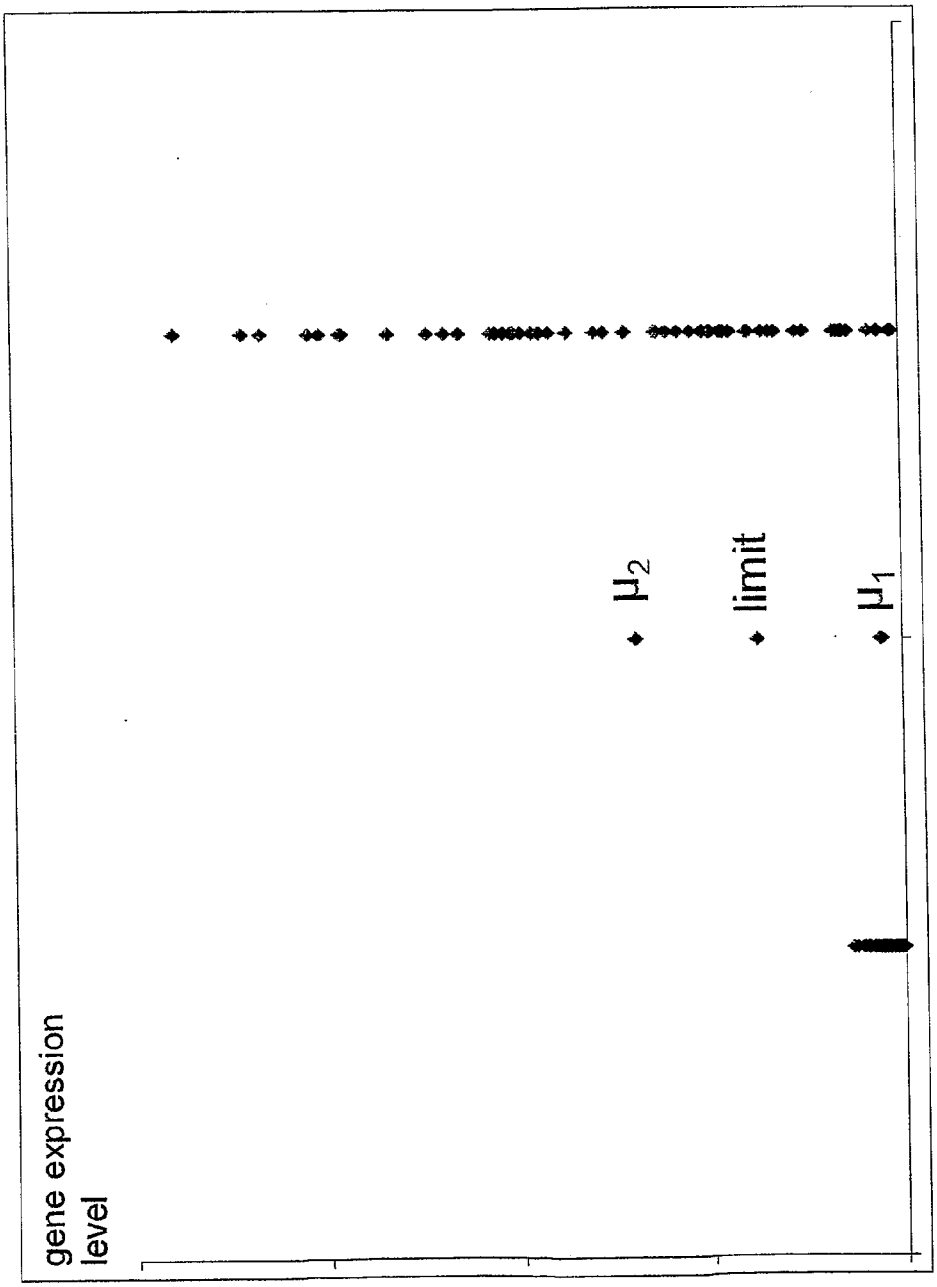

ALLMLL-
Mean MLL
Mean nonMLL
93.0
2.4
150
100
50
0
very low density lipoprotein receptor

Figure 13a



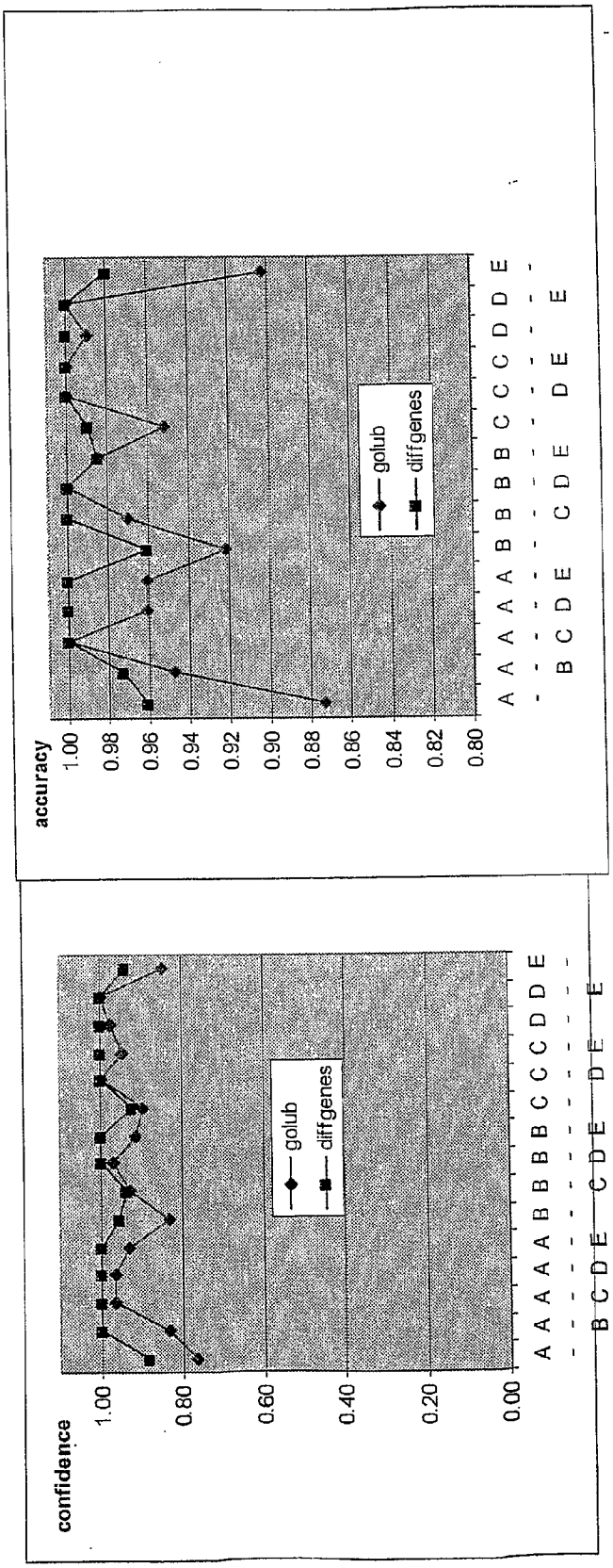

accuracy
1.00
0.98
0.96
0.94
0.92
0.90
0.88
0.86
0.84
0.82
0.80
golub
diffgenes
A A A A B B B B C C C C D D E
- - - - - - - - - - - - - - -
B C D E C D E D E E
confidence
1.00
0.80
0.60
0.40
0.20
0.00
golub
diffgenes
A A A A B B B B C C C C D D E
- - - - - - - - - - - - - - -
B C D E C D E D E E

Figure 13b

Figure 14

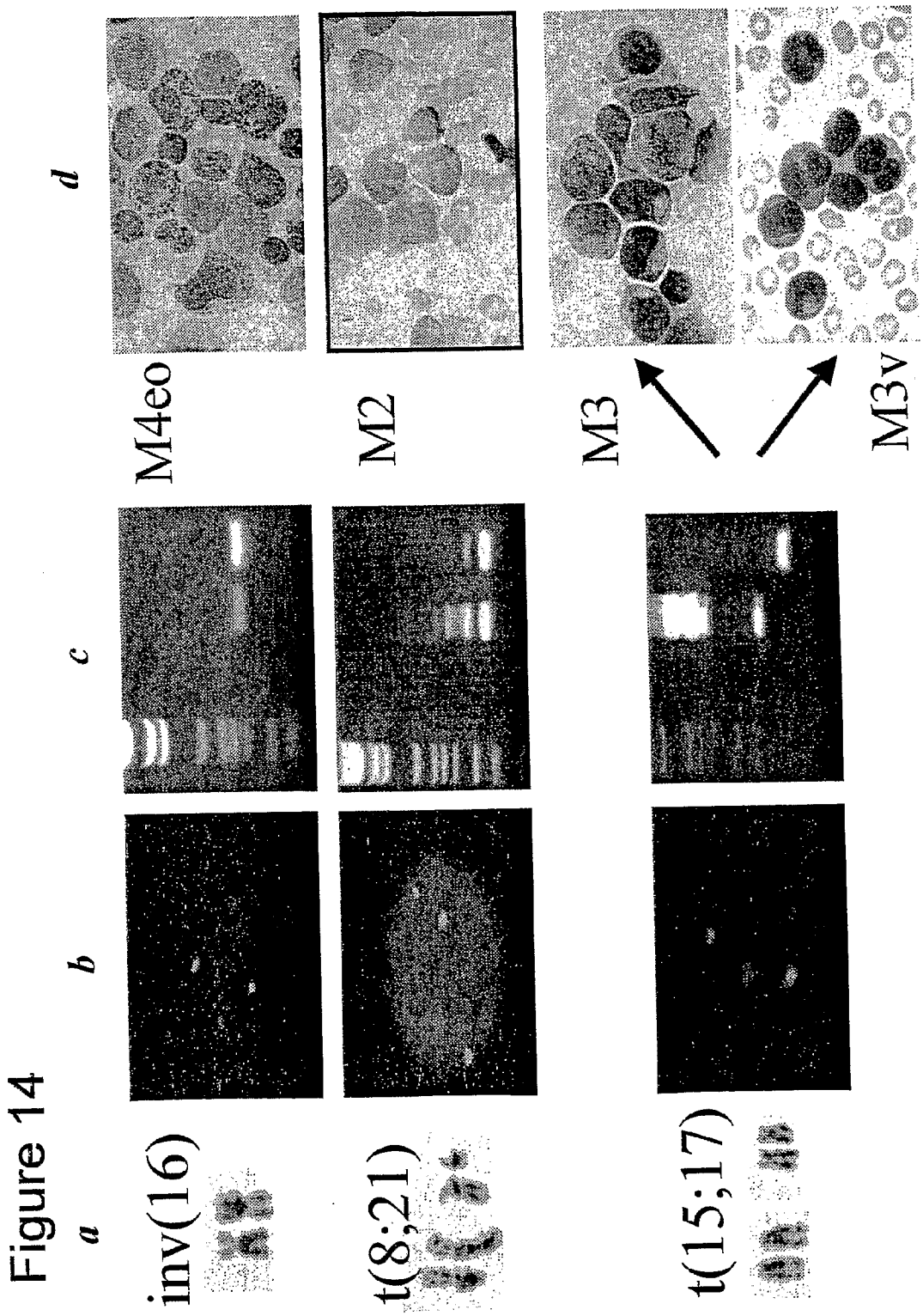
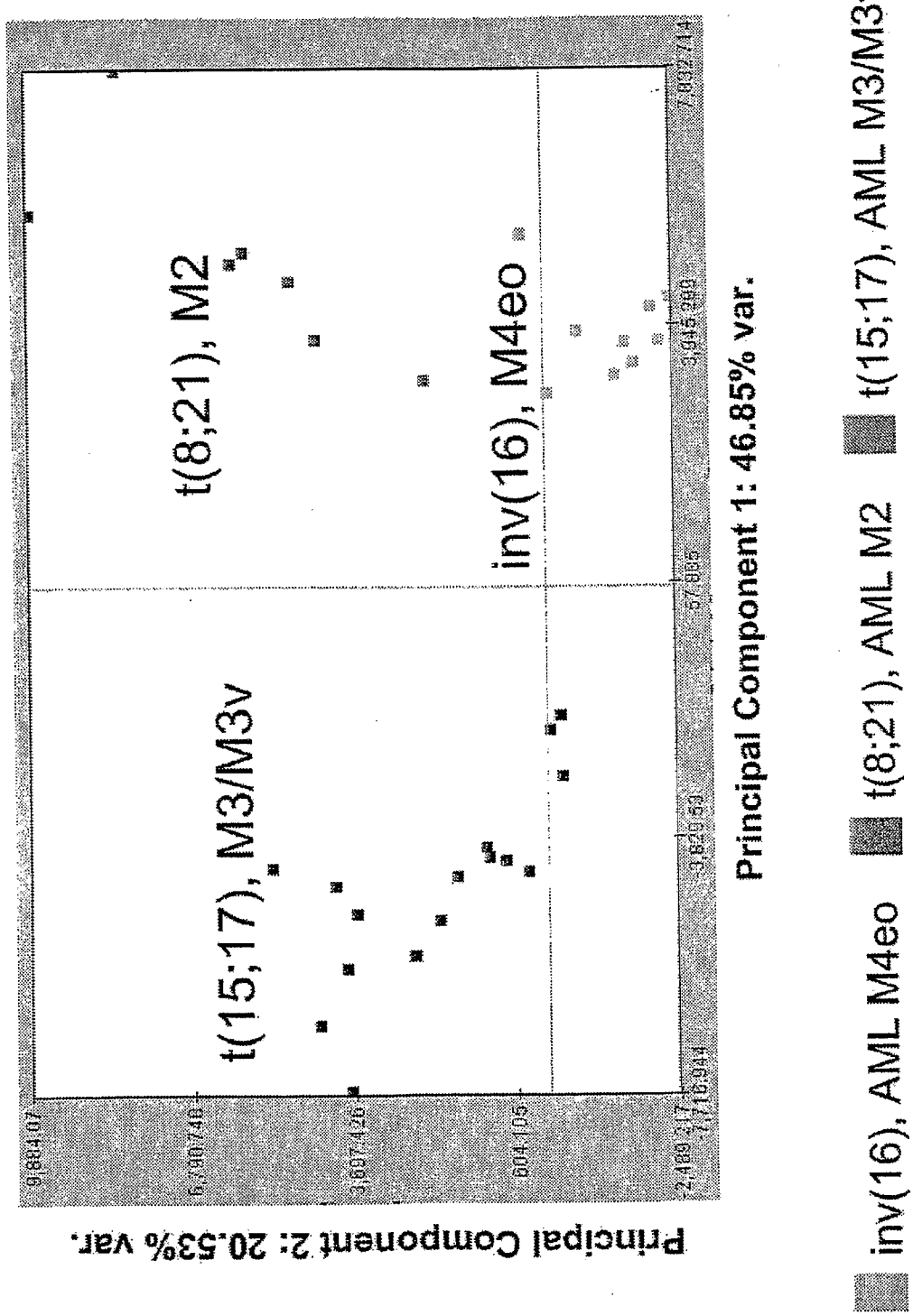


Figure 15


t(15;17), M3/M3v
t(8;21), M2
inv(16), M4eo
Principal Component 2: 20.53% var.
Principal Component 1: 46.85% var.
inv(16), AML M4eo
t(8;21), AML M2
t(15;17), AML M3/M3v

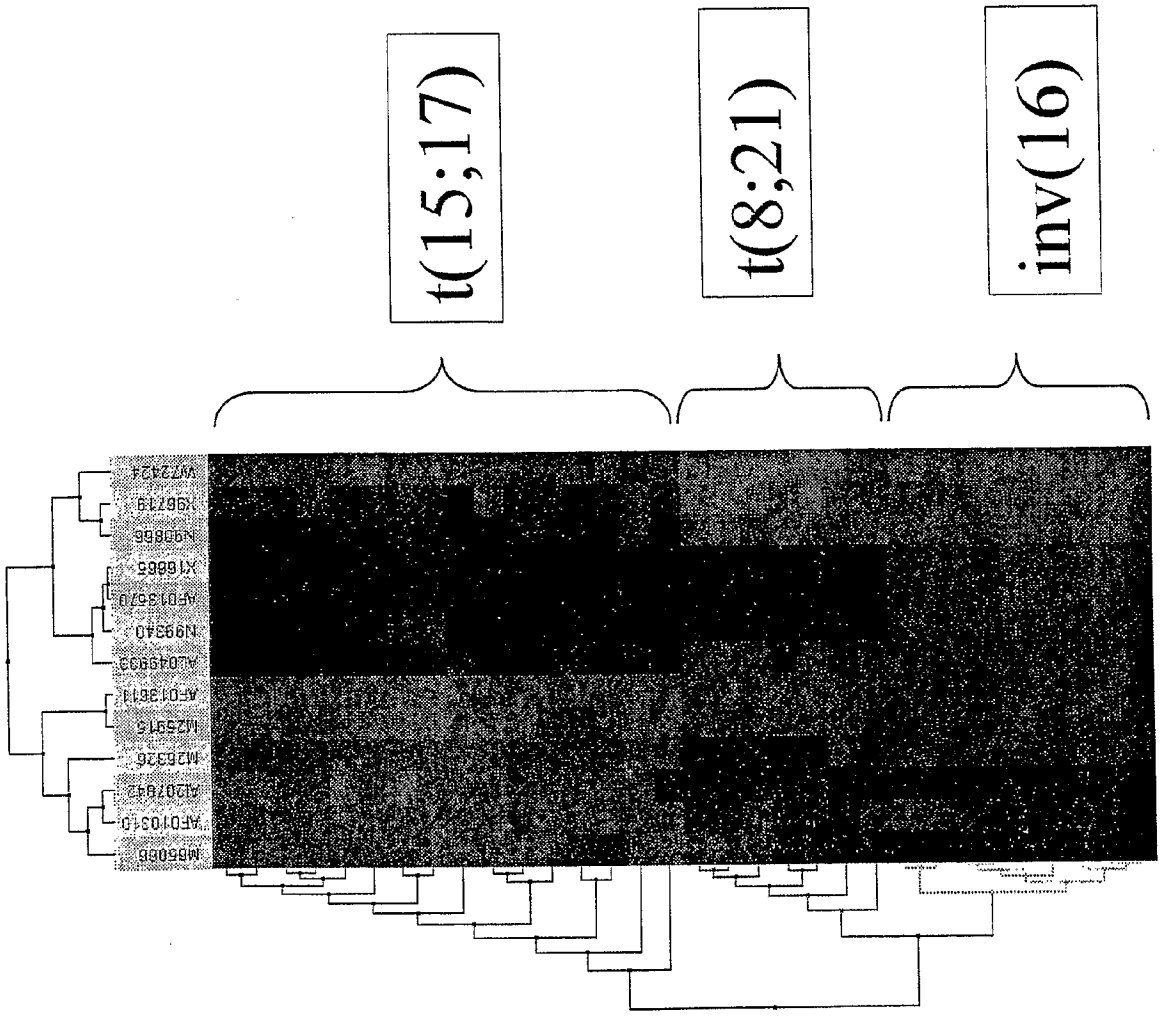

t(15;17)
t(8;21)
inv(16)
M65065
AF010310
AJ207042
M26326
U25015
AF013611
AL049933
N99340
AF013570
X16865
N90866
Z96219
W72424

Figure 16

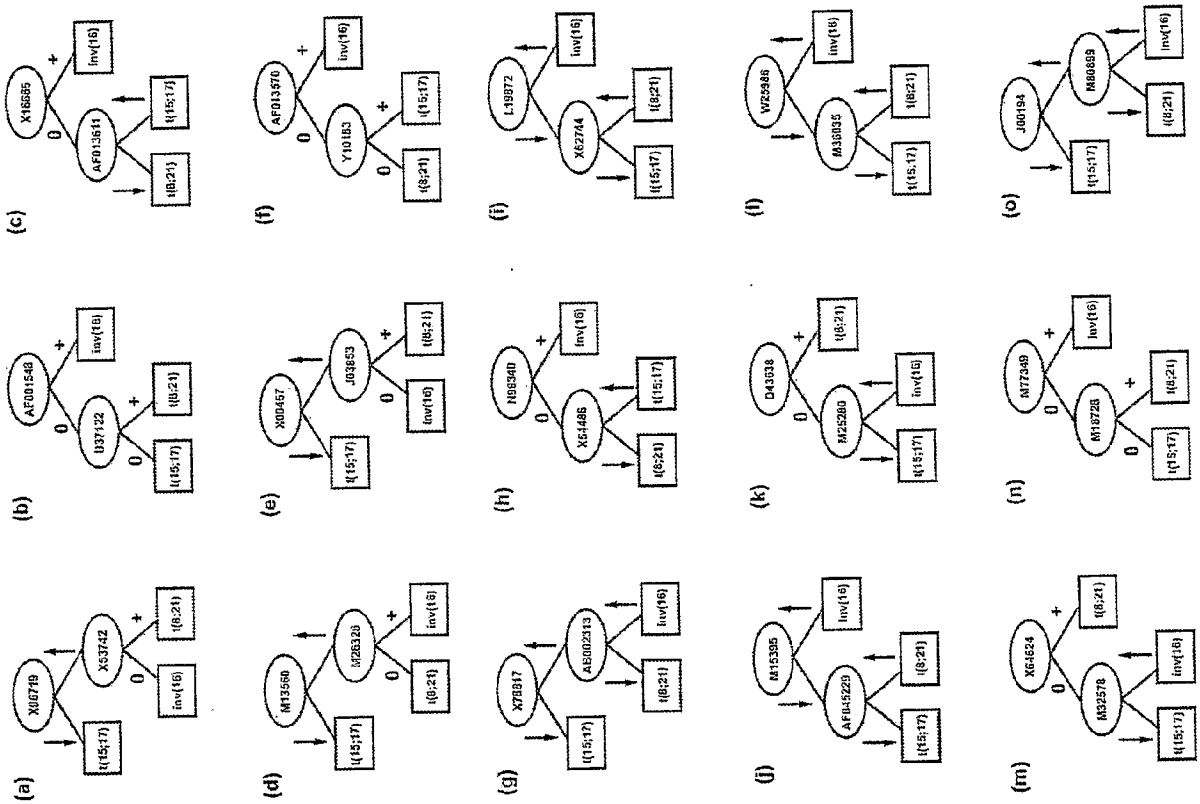

(a)
X06719
X53742
t(15;17)
inv(16)
t(8;21)
(b)
AF001548
U37122
inv(16)
t(8;21)
t(15;17)
(c)
X16385
AF013611
inv(16)
t(15;17)
t(8;21)
(d)
M13560
M26329
t(15;17)
inv(16)
t(8;21)
(e)
X00457
J03853
t(15;17)
t(8;21)
inv(16)
(f)
AF013670
Y10183
inv(16)
t(15;17)
t(8;21)
(g)
X78917
AB002313
t(15;17)
inv(16)
t(8;21)
(h)
N68340
X51486
inv(16)
t(15;17)
t(8;21)
(i)
L19872
X62744
inv(16)
t(8;21)
t(15;17)
(j)
M15395
AF043229
inv(16)
t(8;21)
t(15;17)
(k)
D43638
M25280
t(8;21)
inv(16)
t(15;17)
(l)
V25986
M38035
inv(16)
t(8;21)
t(15;17)
(m)
X64624
M32578
t(8;21)
inv(16)
t(15;17)
(n)
M77349
M18728
inv(16)
t(8;21)
t(15;17)
(o)
J00194
M80669
inv(16)
t(8;21)
t(15;17)

Figure 17

Figure 18

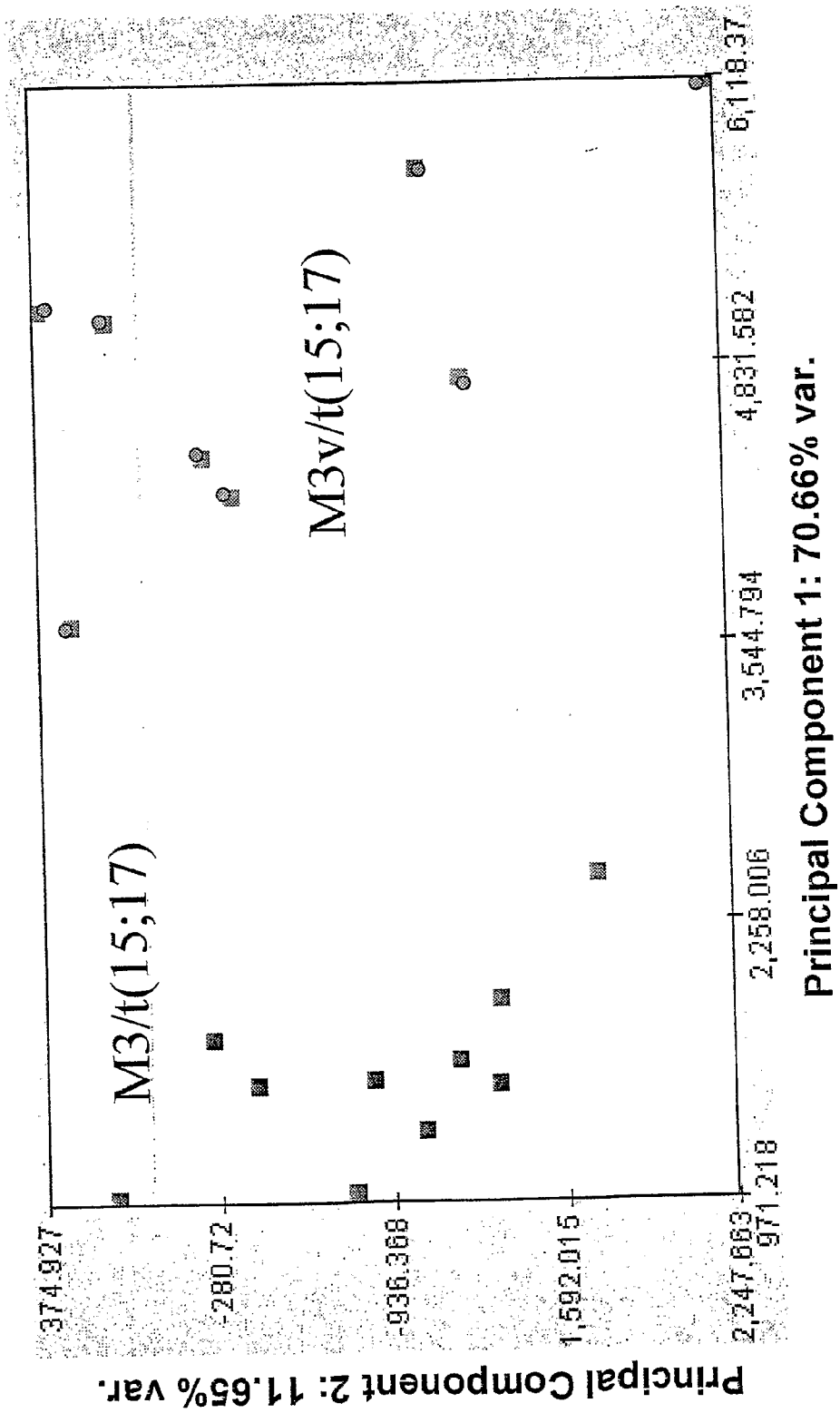

M3/t(15;17)
M3v/t(15;17)
-374.927
-280.72
-936.368
1,592.015
2,247.663
971.218
2,258.006
3,544.794
4,831.582
6,118.37
Principal Component 2: 11.65% var.
Principal Component 1: 70.66% var.

Figure 19

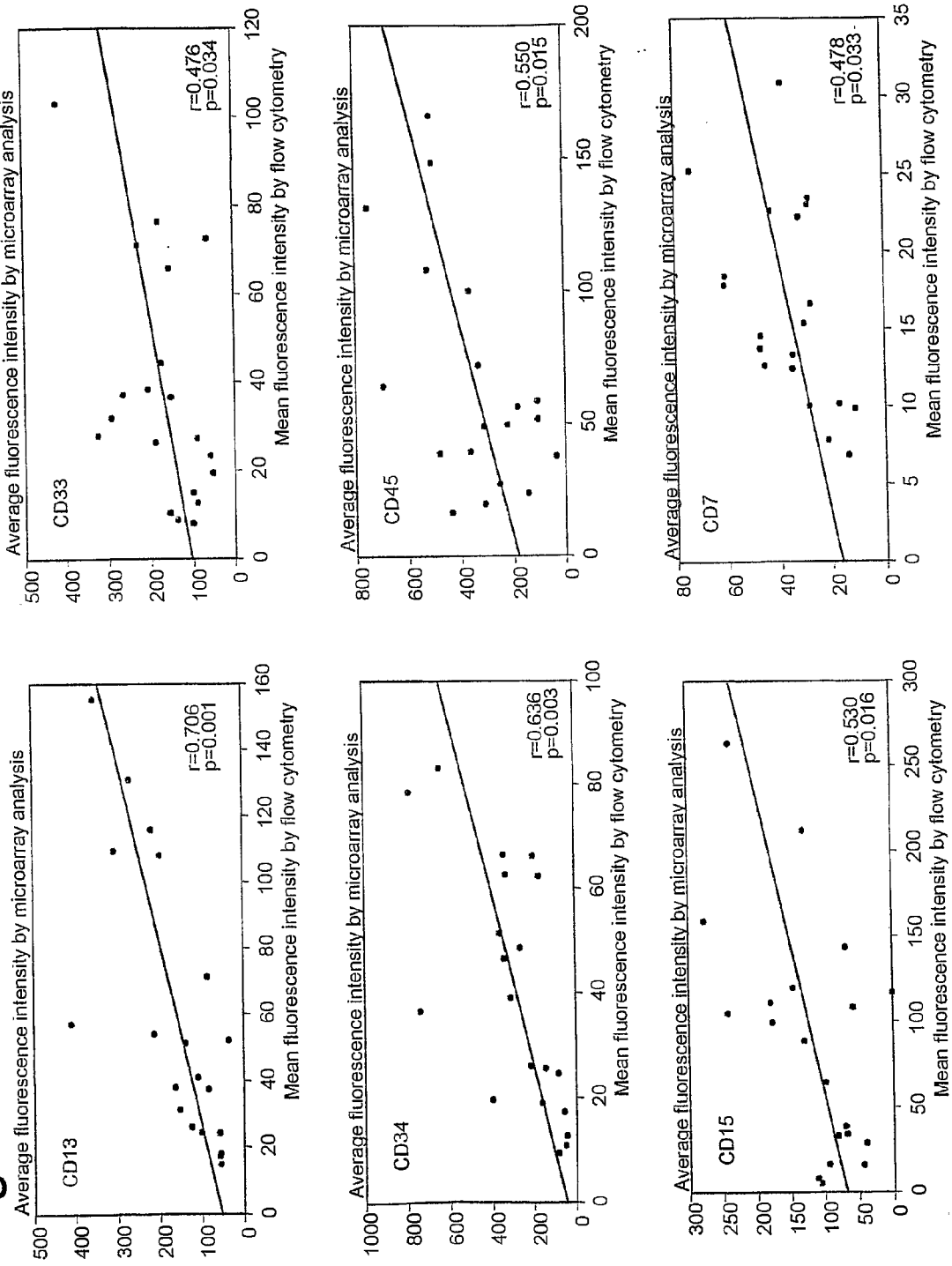
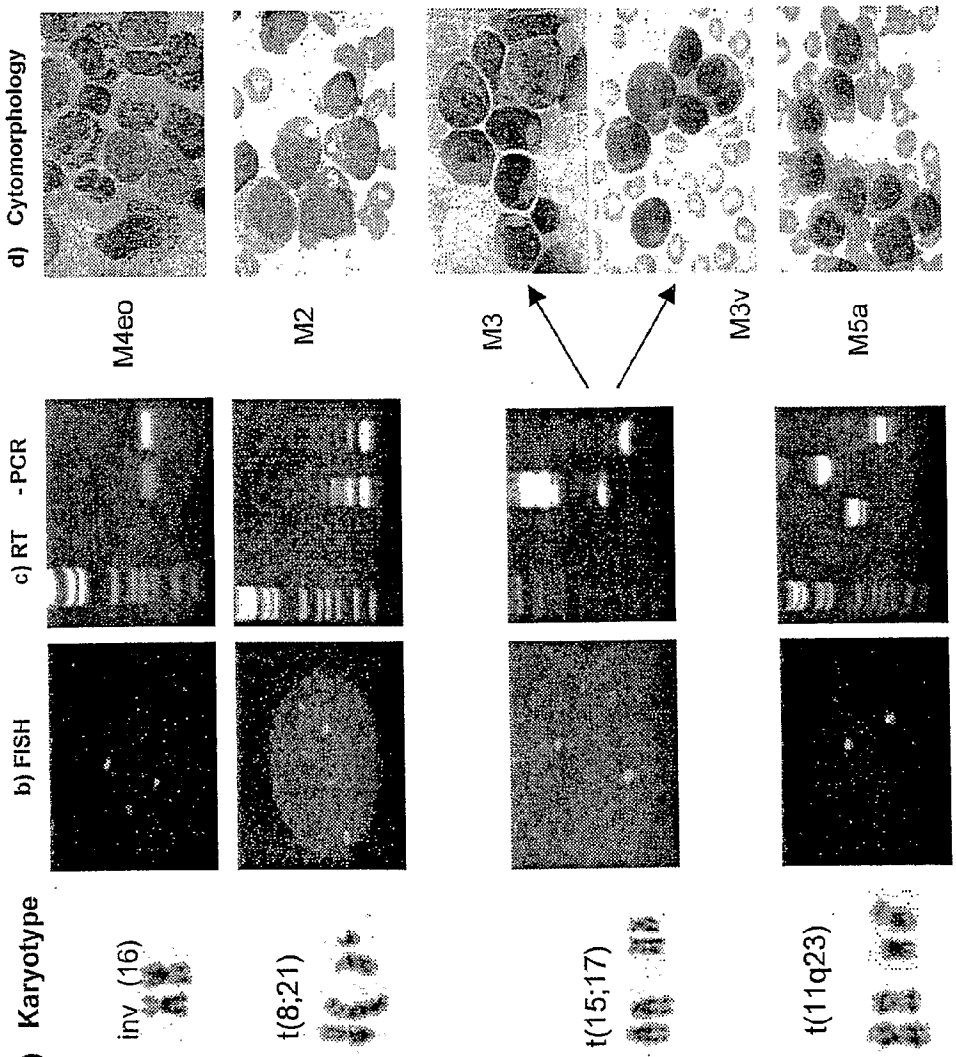

CD13
r=0.706
p=0.001
CD33
r=0.476
p=0.034
CD34
r=0.636
p=0.003
CD45
r=0.550
p=0.015
CD15
r=0.530
p=0.016
CD7
r=0.478
p=0.033
Average fluorescence intensity by microarray analysis
Mean fluorescence intensity by flow cytometry

Figure 20


a) Karyotype
b) FISH
c) RT -PCR
d) Cytomorphology
inv (16)
t(8;21)
t(15;17)
t(11q23)
M4eo
M2
M3
M3v
M5a

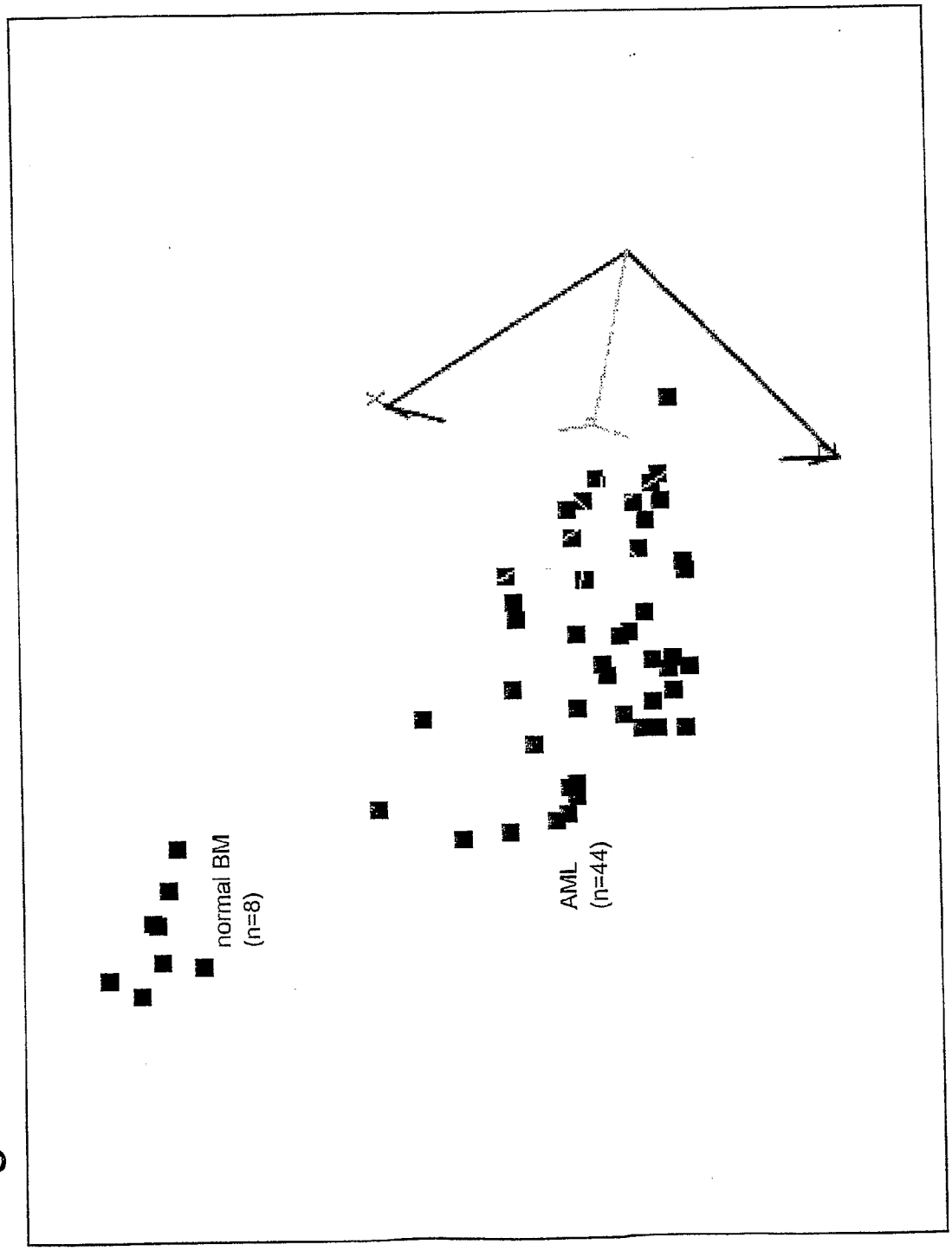


Figure 21

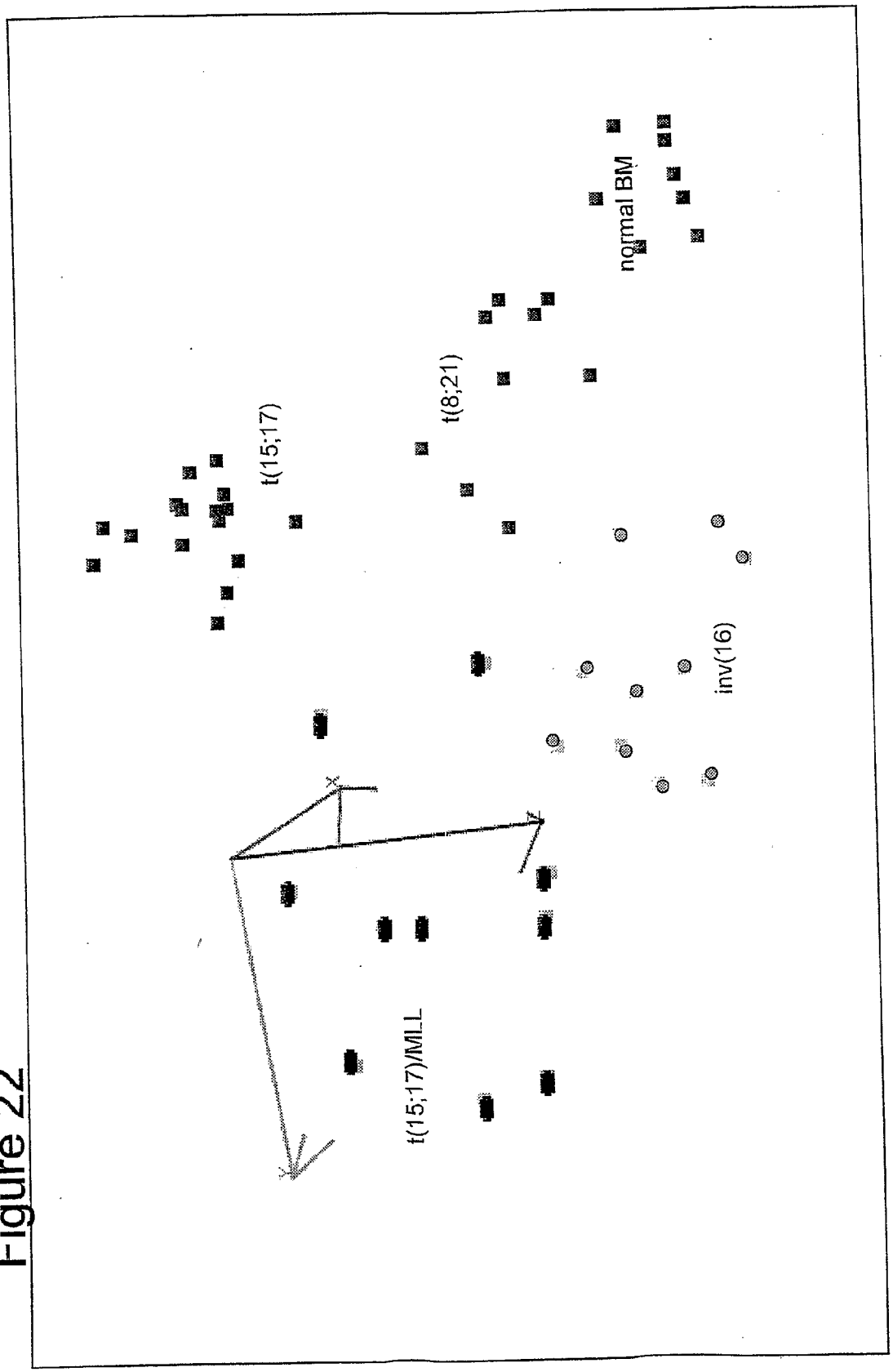


Figure 22

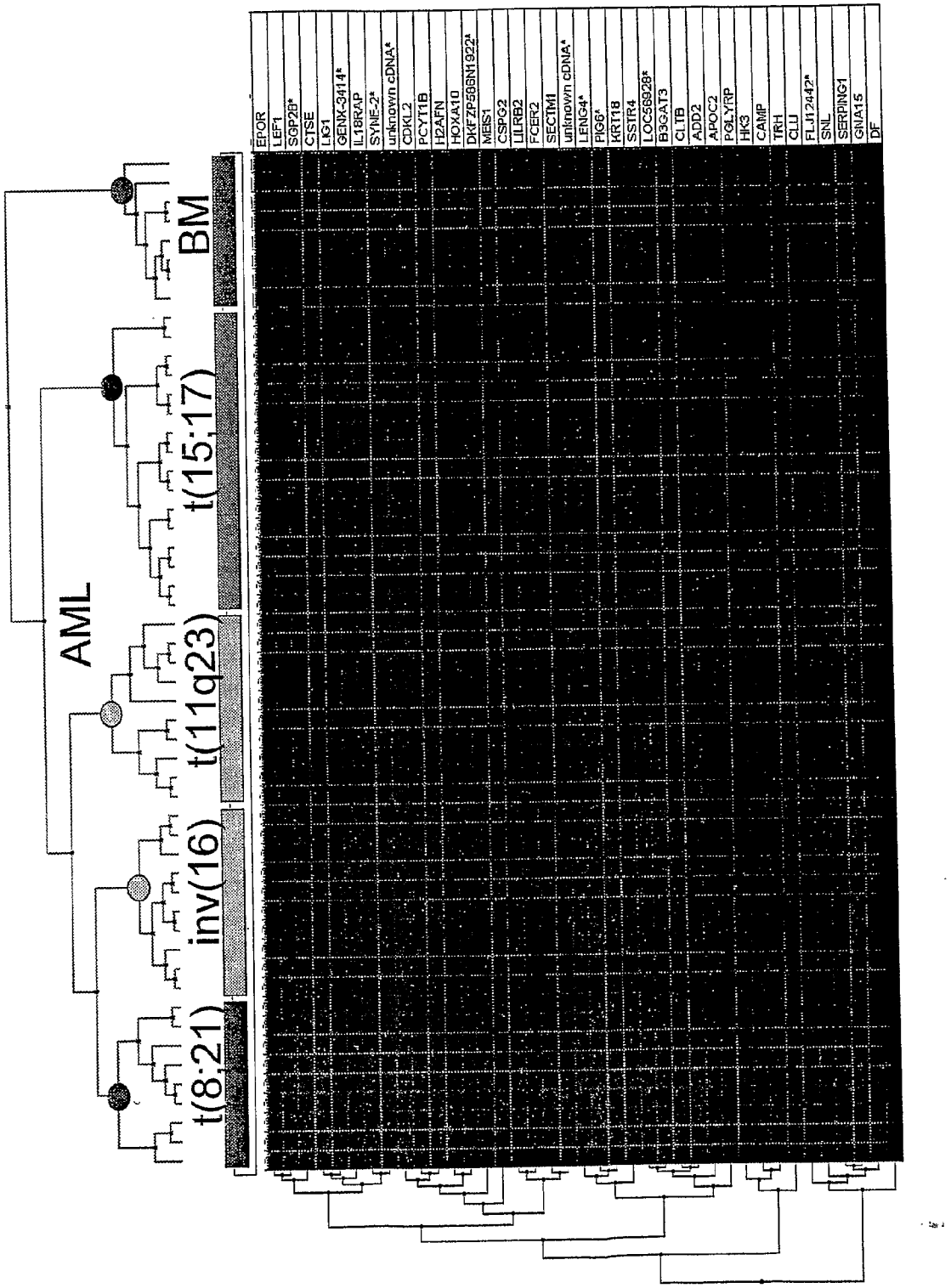

AML
BM
t(8;21)
inv(16)
t(11q23)
t(15;17)
EPOR
LEF1
SGP28*
CTSE
LIG1
GENX-3414*
IL18RAP
SYNE-2*
unknown cDNA*
CDKL2
PCYT1B
H2AFN
HOXA10
DKFZP566N1922*
MEIS1
CSPG2
LILRB2
FCER2
SECTM1
unknown cDNA*
LENG4*
PIG6*
KRT18
SSTR4
LOC56928*
B3GAT3
CLTB
ADD2
APOC2
POLYRP
HK3
CAMP
TRH
CLU
FLI12442*
SNL
SERPING1
GNA15
DF

Figure 23

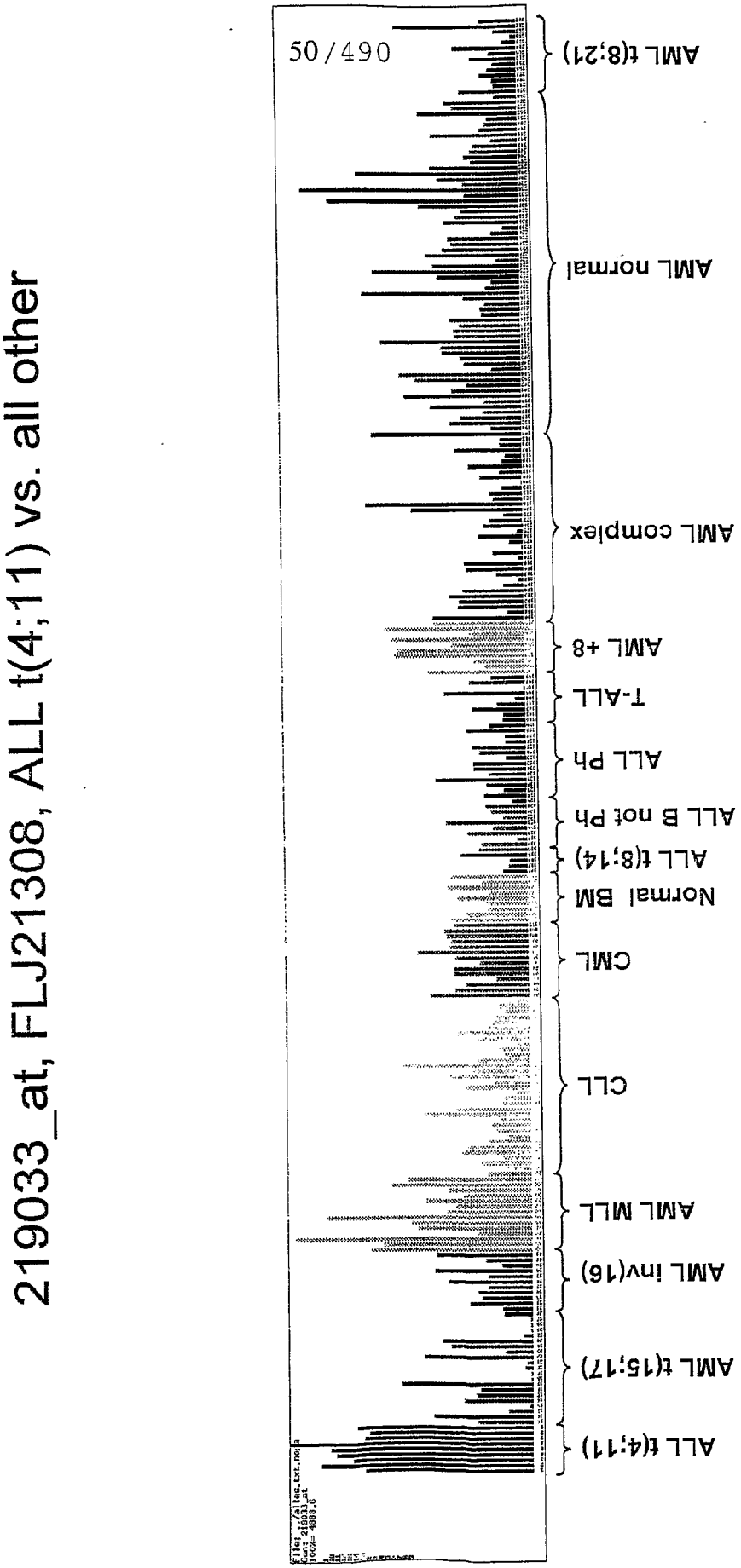

219033_at, FLJ21308, ALL t(4;11) vs. all other
50/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 24

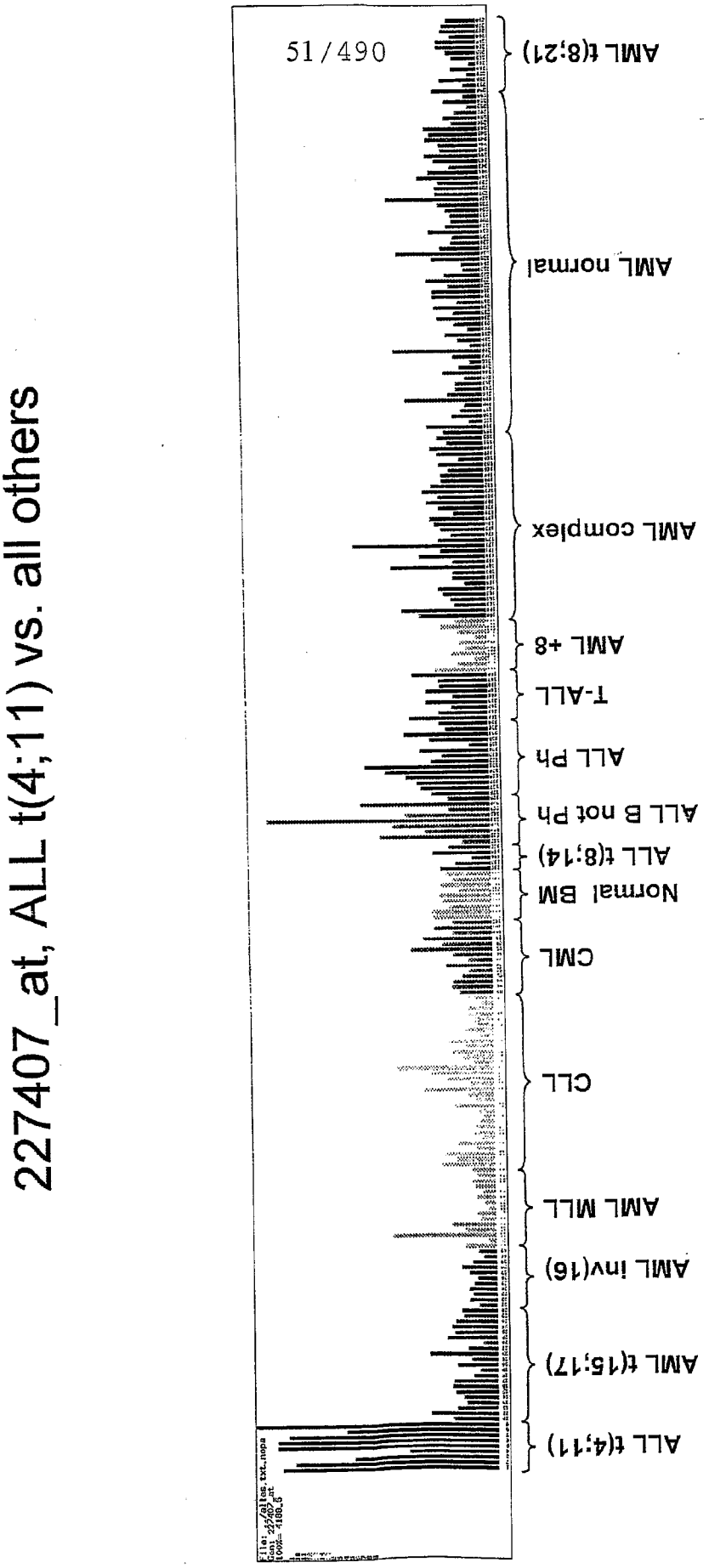

227407_at, ALL t(4;11) vs. all others
51/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 25

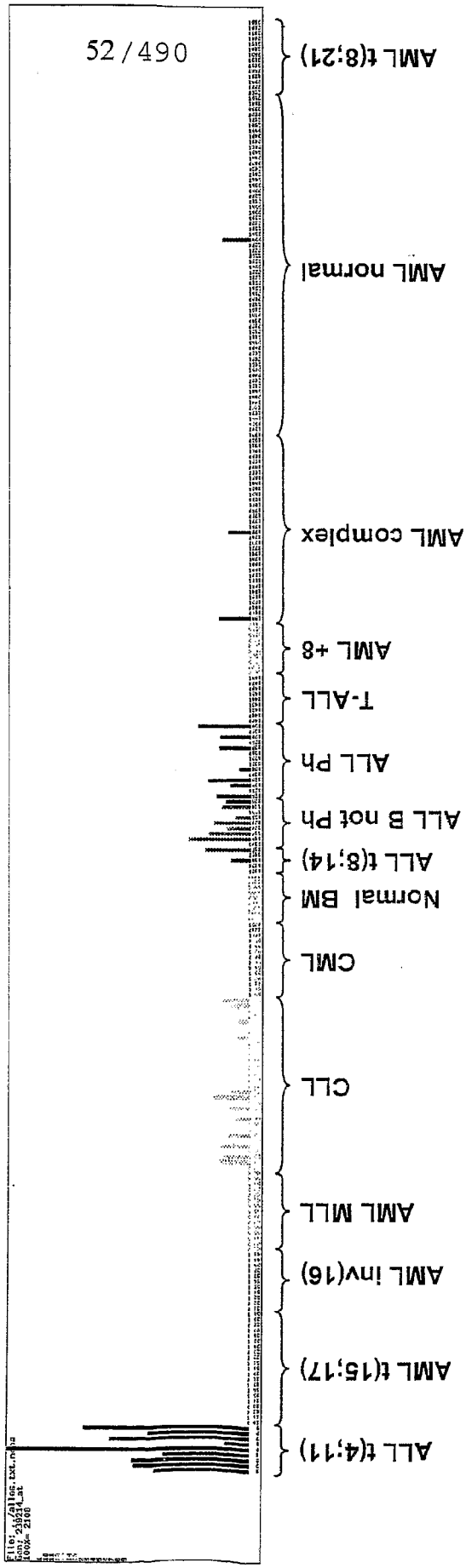

239214_at, ALL t(4;11) vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 26

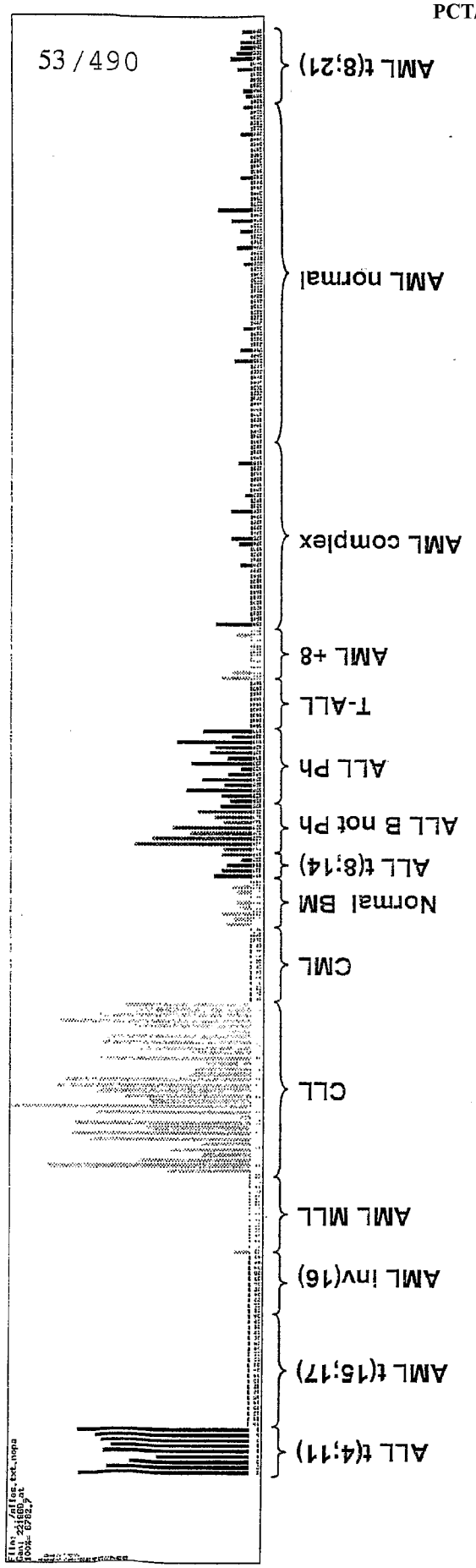

221969_at, PAX5, ALL t(4;11) vs. AML t(15;17)
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 27

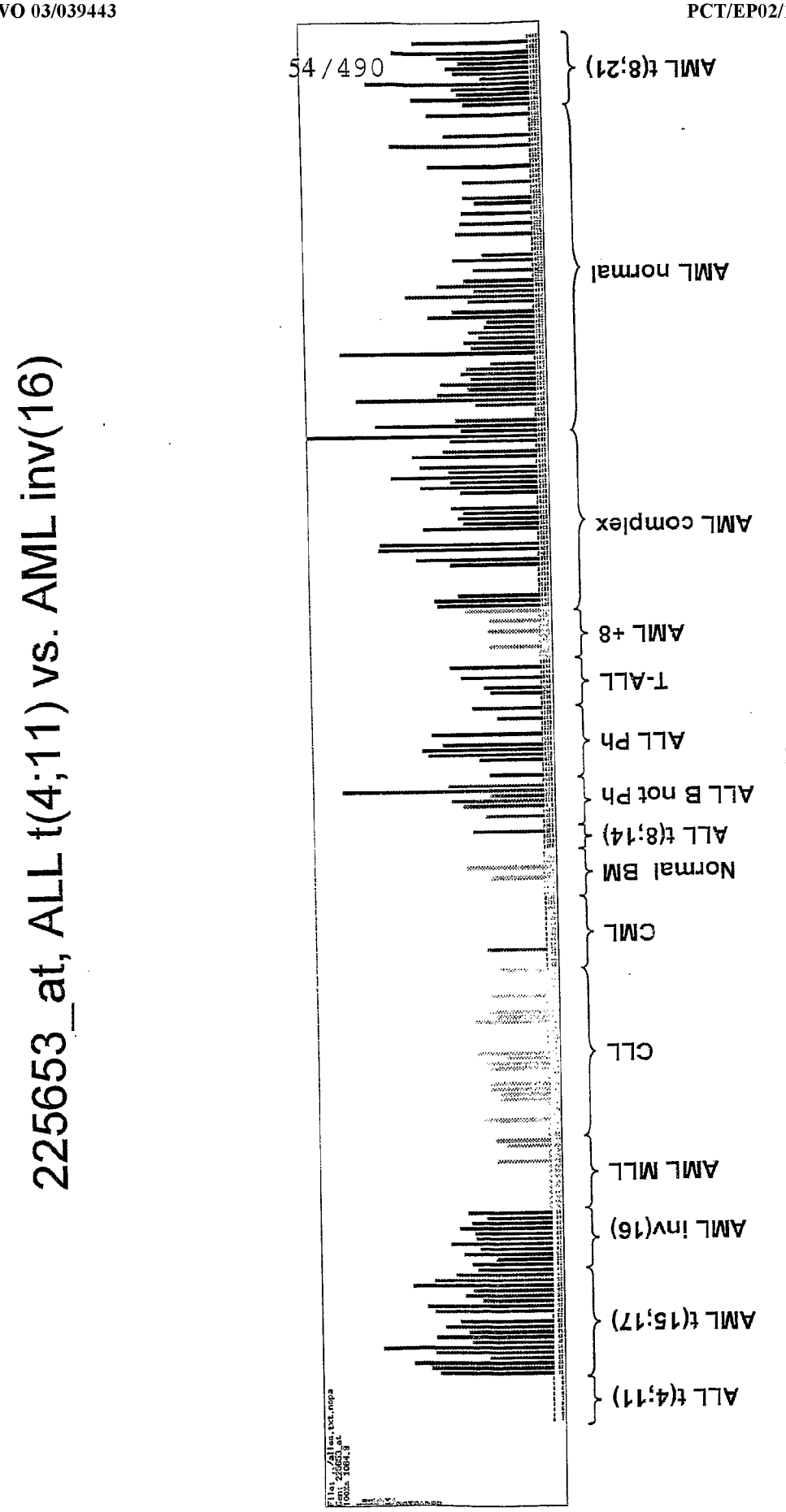
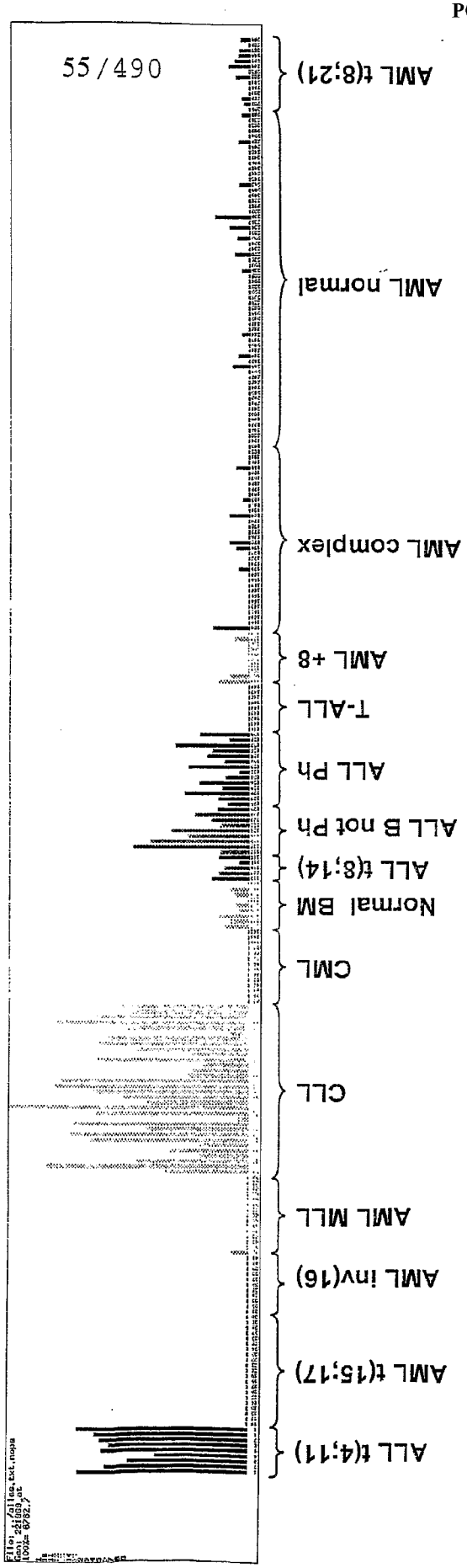

225653_at, ALL t(4;11) vs. AML inv(16)
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 28



221969_at, ALL t(4;11) vs. AML MLL

Figure 29

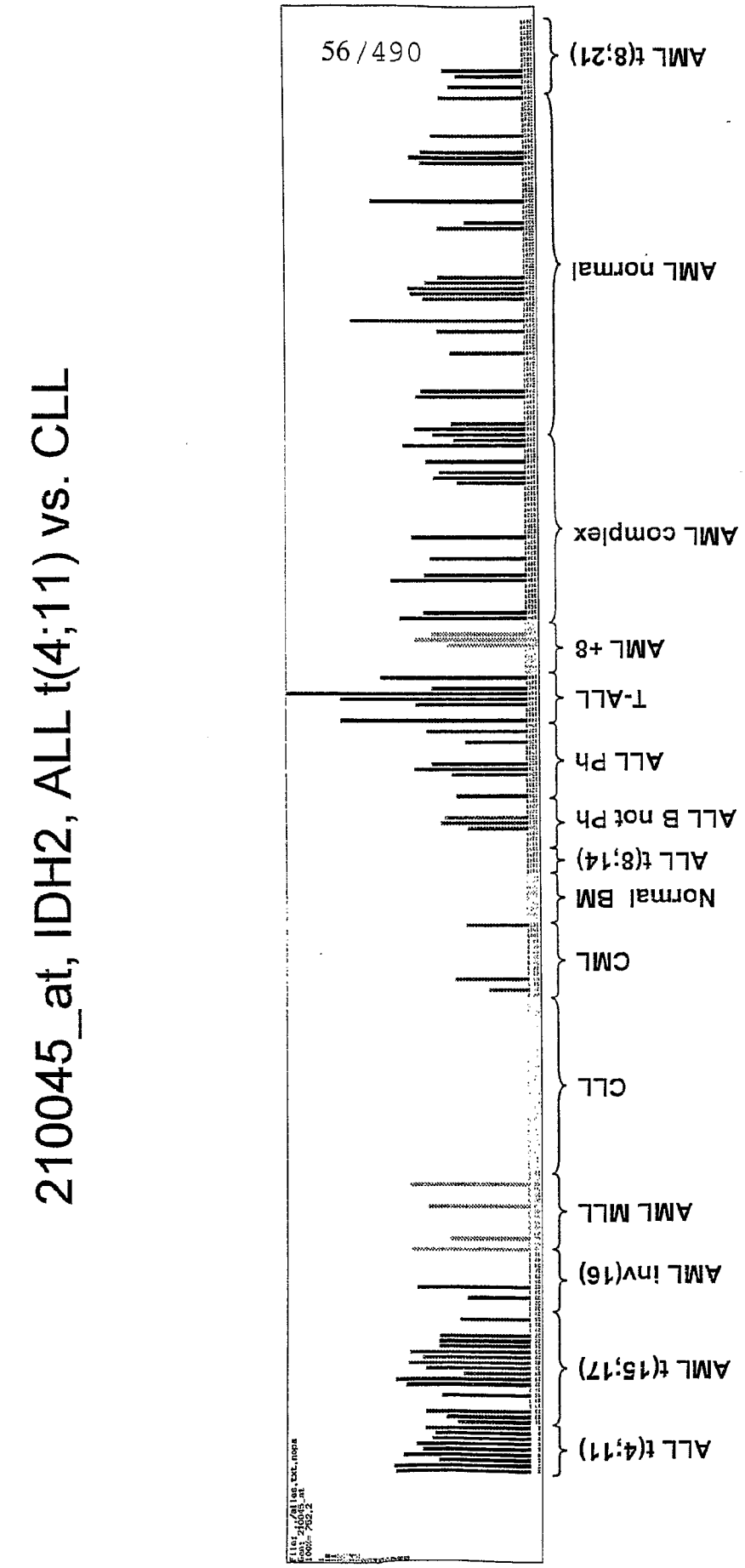
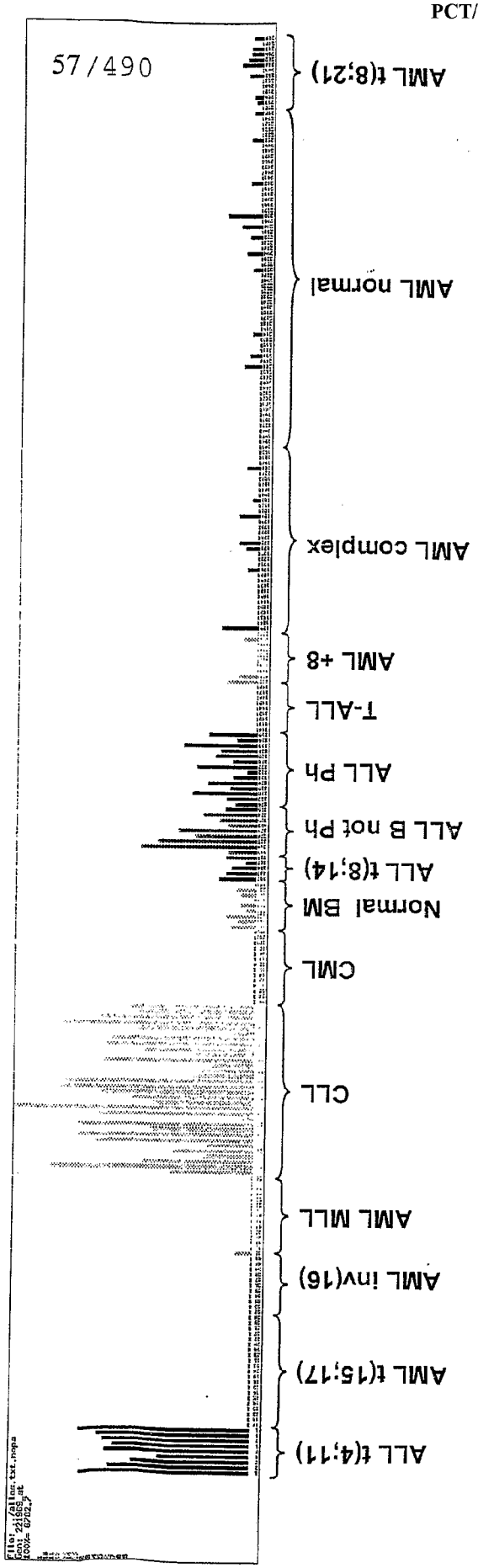
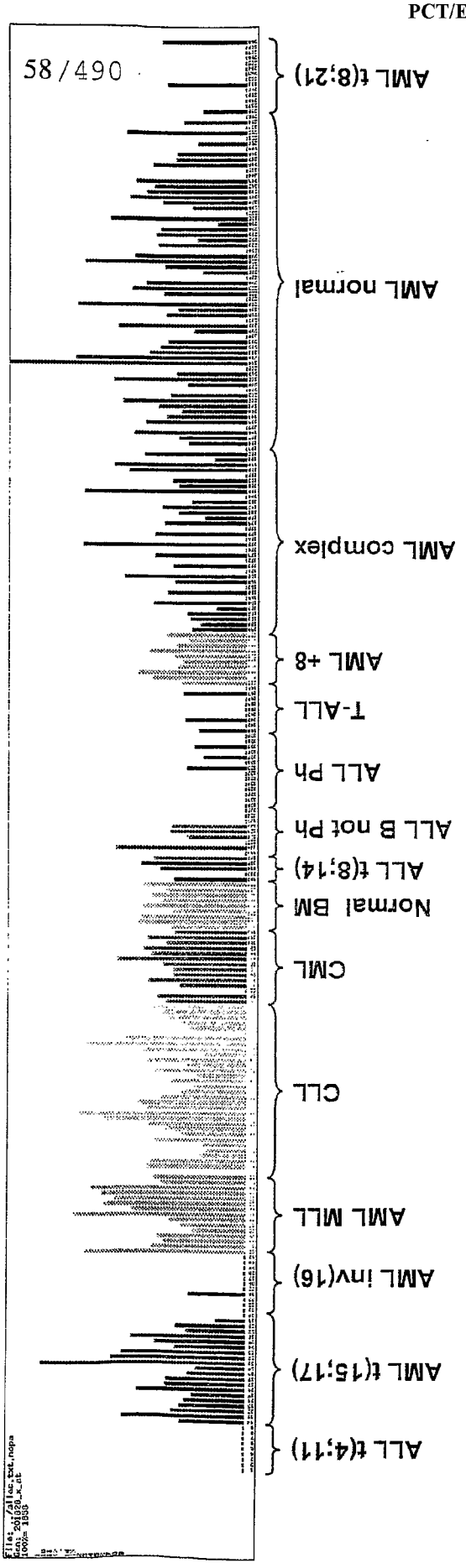

210045_at, IDH2, ALL t(4;11) vs. CLL
56/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 30



221969_at, PAX5, ALL t(4;11) vs. CML

Figure 31



201828_x_at, CXX1, ALL t(4;11) vs. normal BM

Figure 32

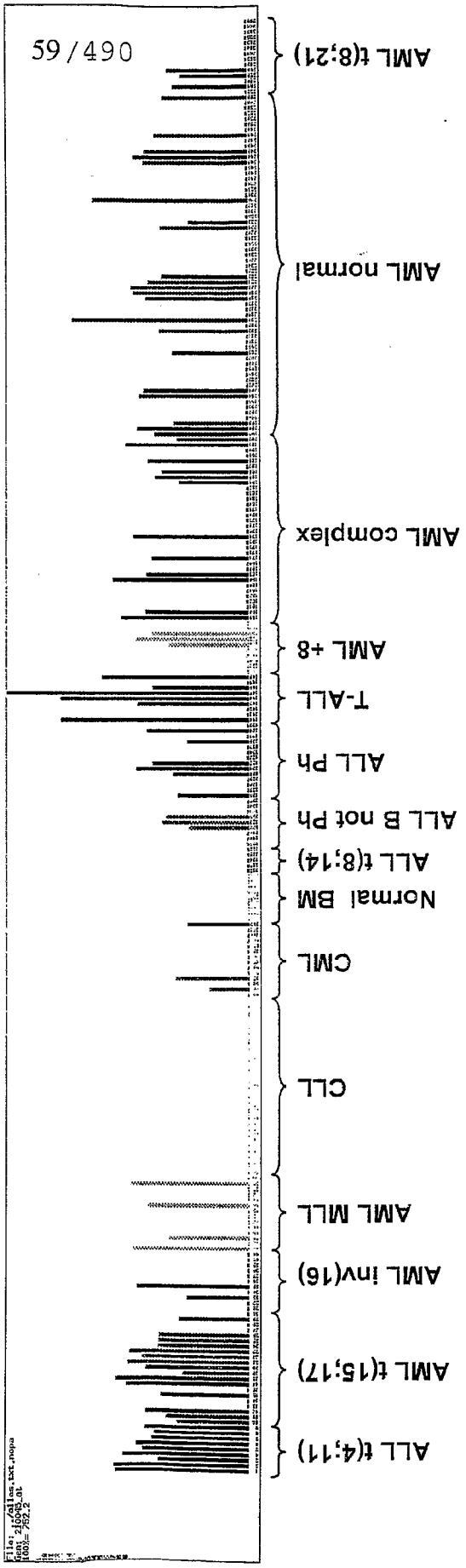

210045_at, IDH2, ALL t(4;11) vs. ALL t(8;14)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 33

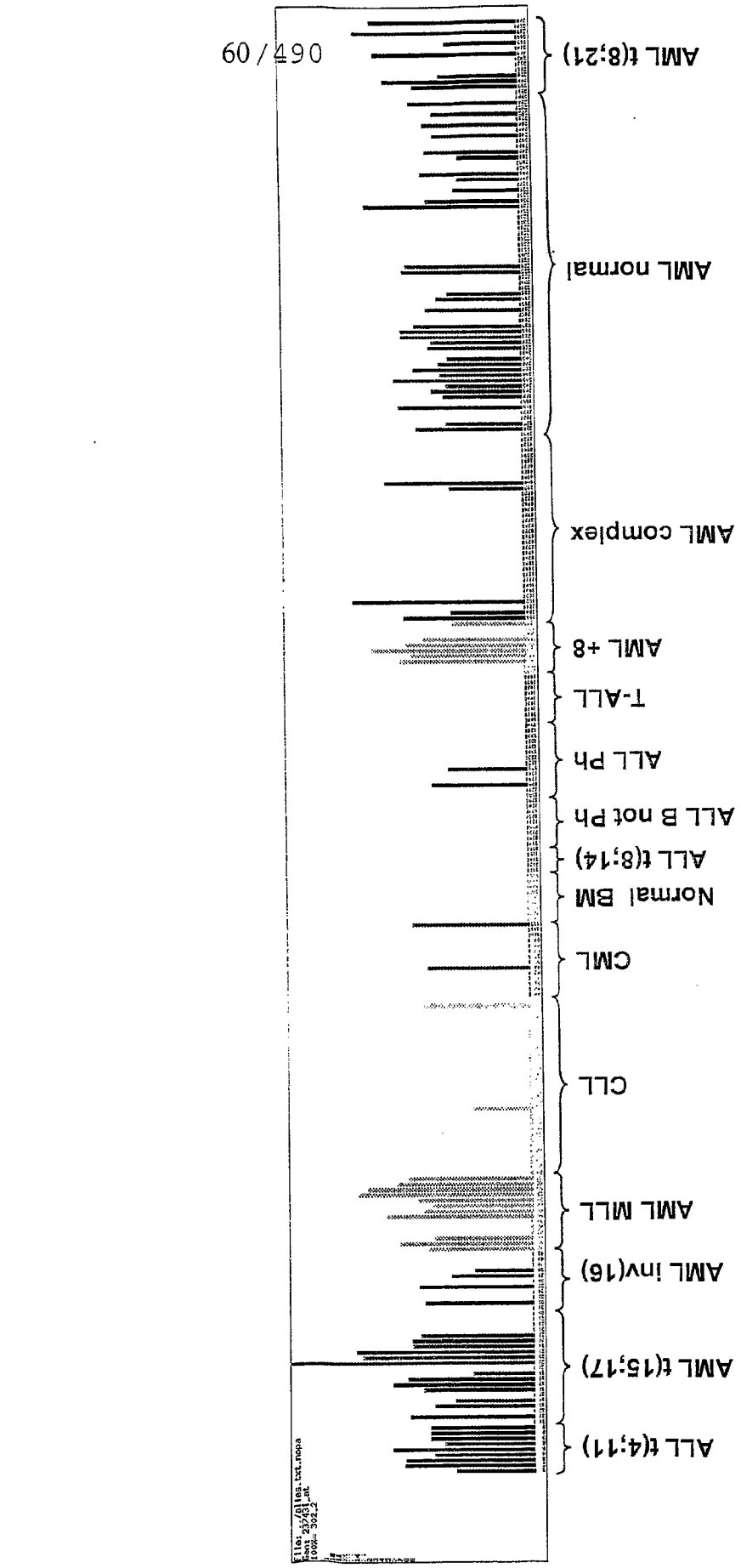

237431_at, ALL t(4;11) vs. ALL B not Ph
ALL t(4;11)
ALL t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 34

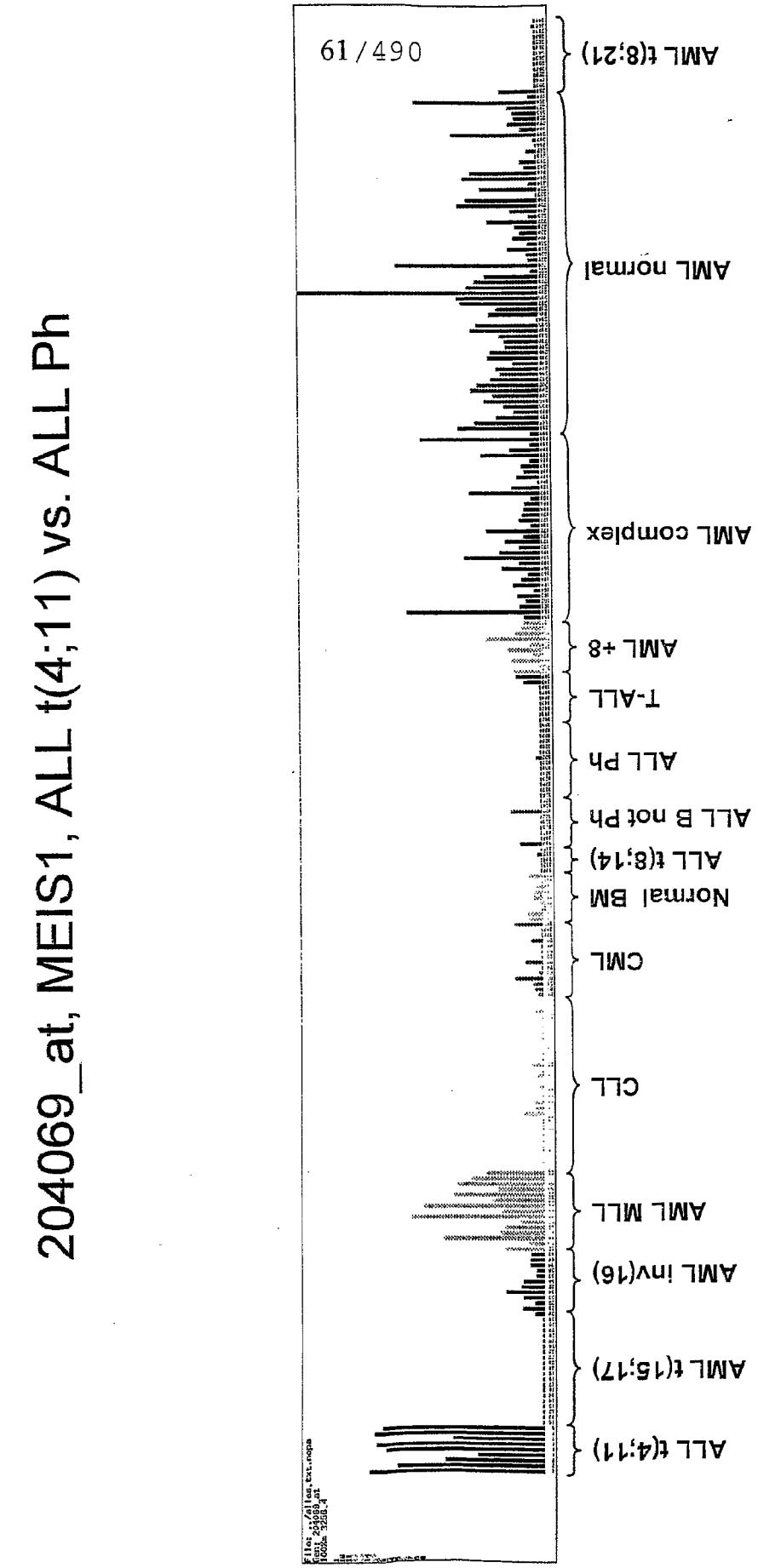

204069_at, MEIS1, ALL t(4;11) vs. ALL Ph
61/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 35

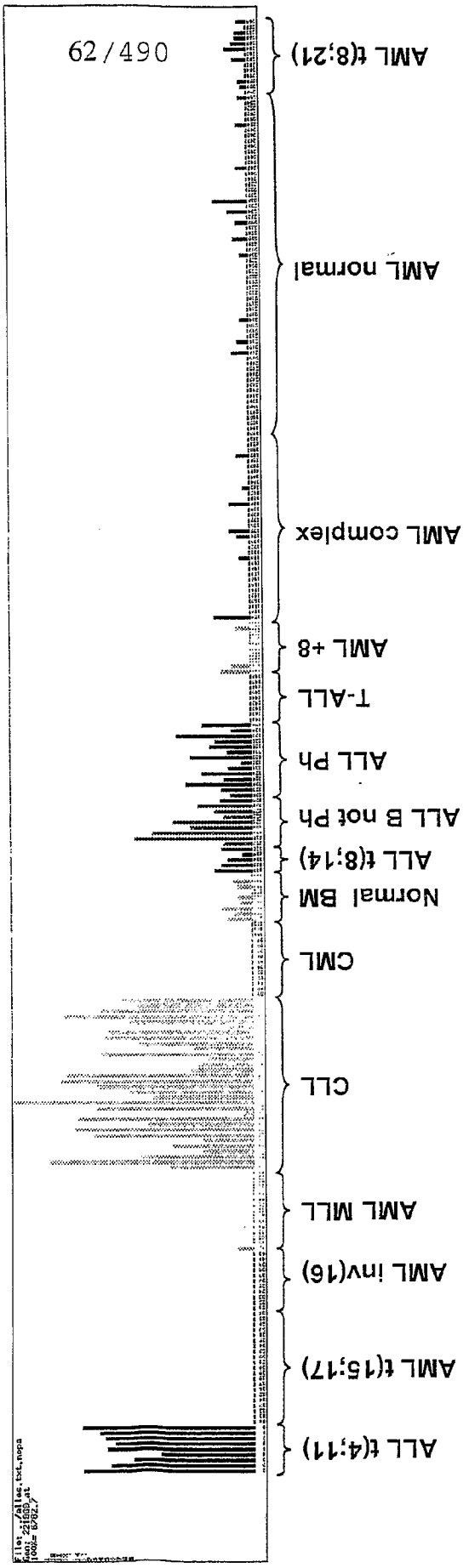

221969_at, PAX5, ALL t(4;11) vs. T-ALL
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 36

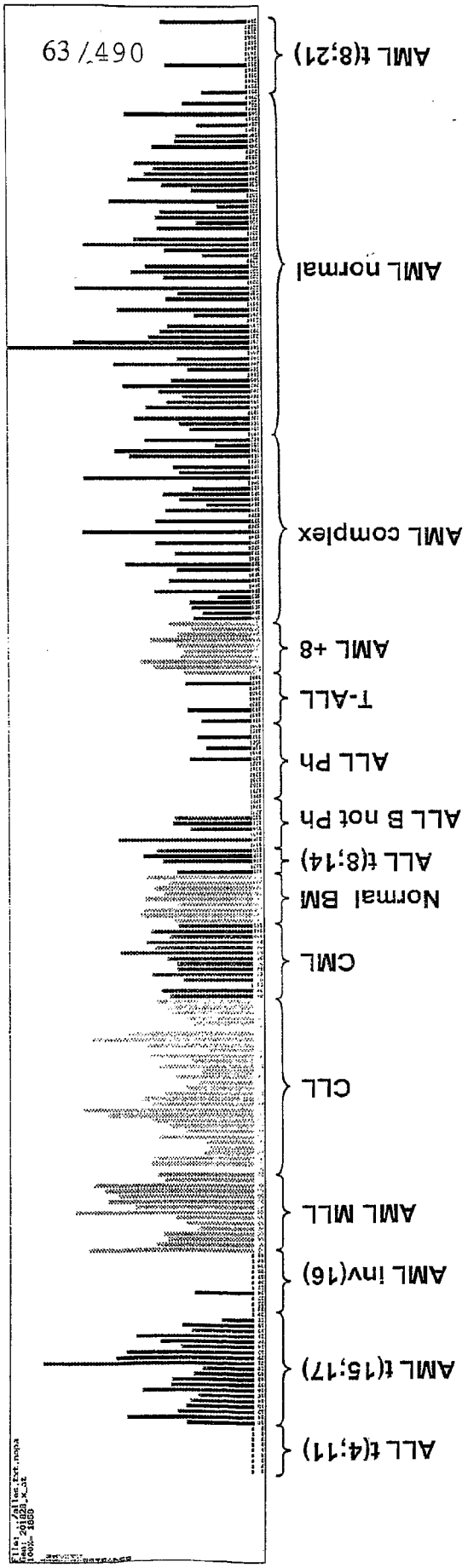

201828_x_at, CXX1, ALL t(4;11) vs. AML +8
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 37

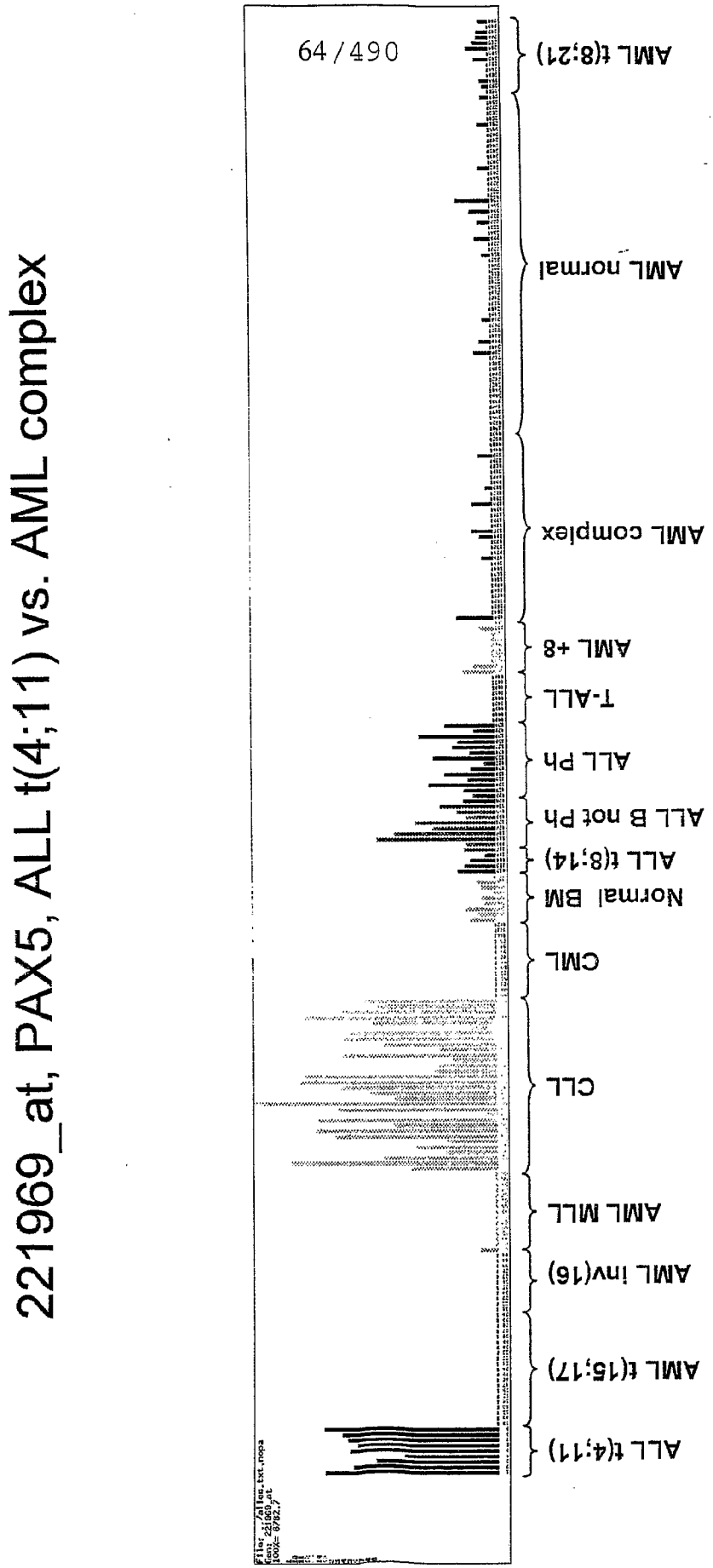

221969_at, PAX5, ALL t(4;11) vs. AML complex
64/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 38

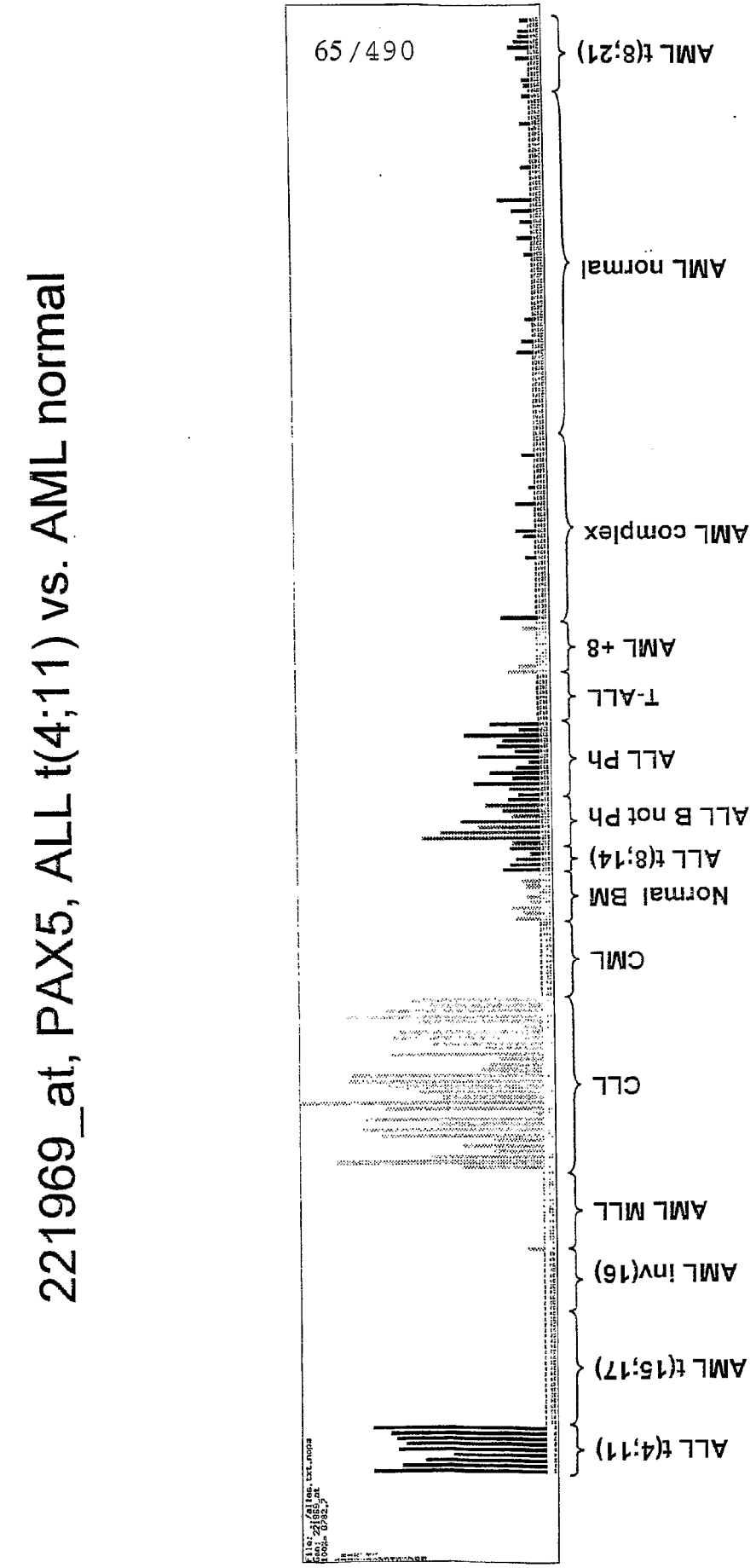

221969_at, PAX5, ALL t(4;11) vs. AML normal
65/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 39

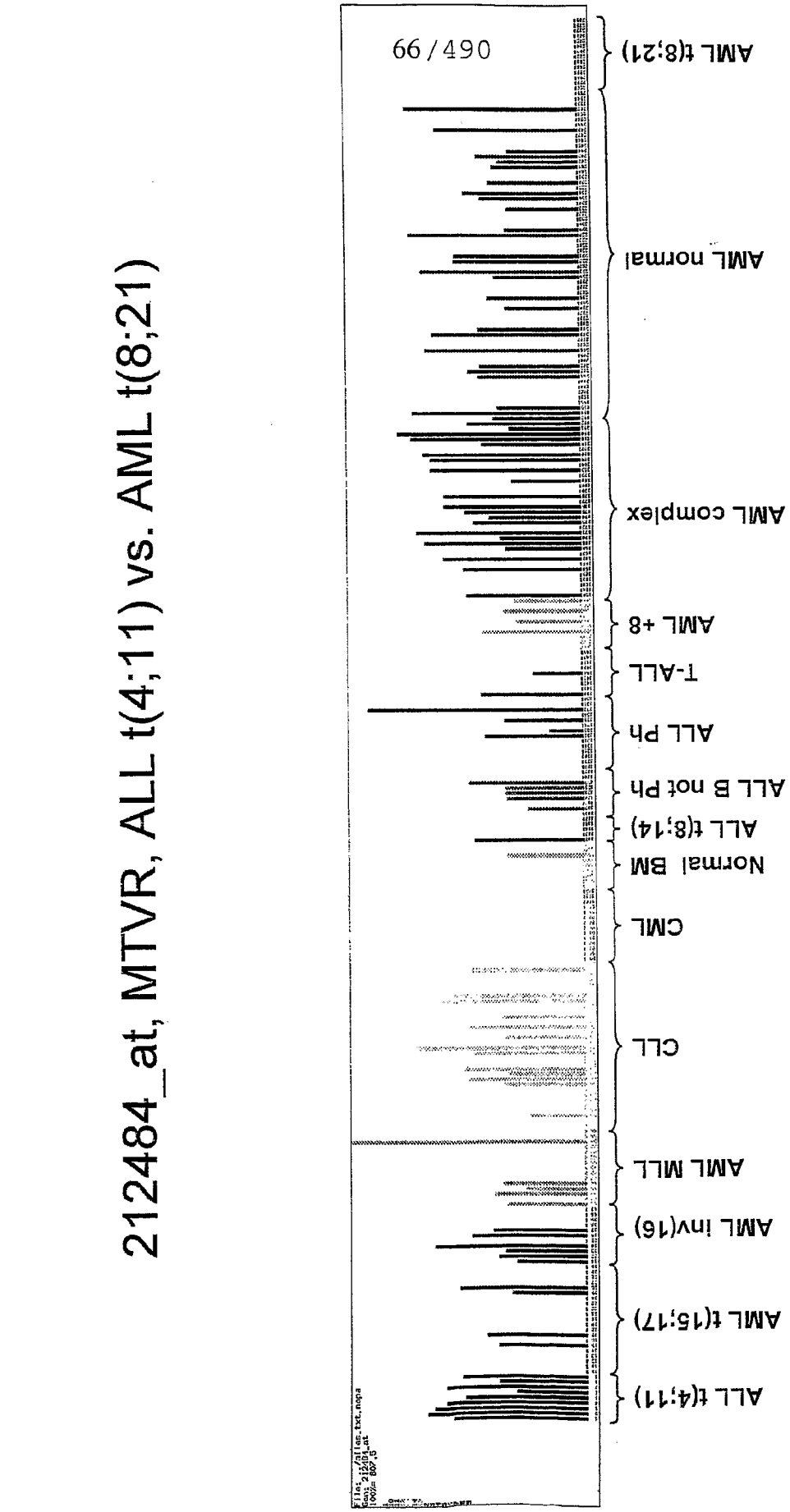

212484_at, MTVR, ALL t(4;11) vs. AML t(8;21)
66/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 40

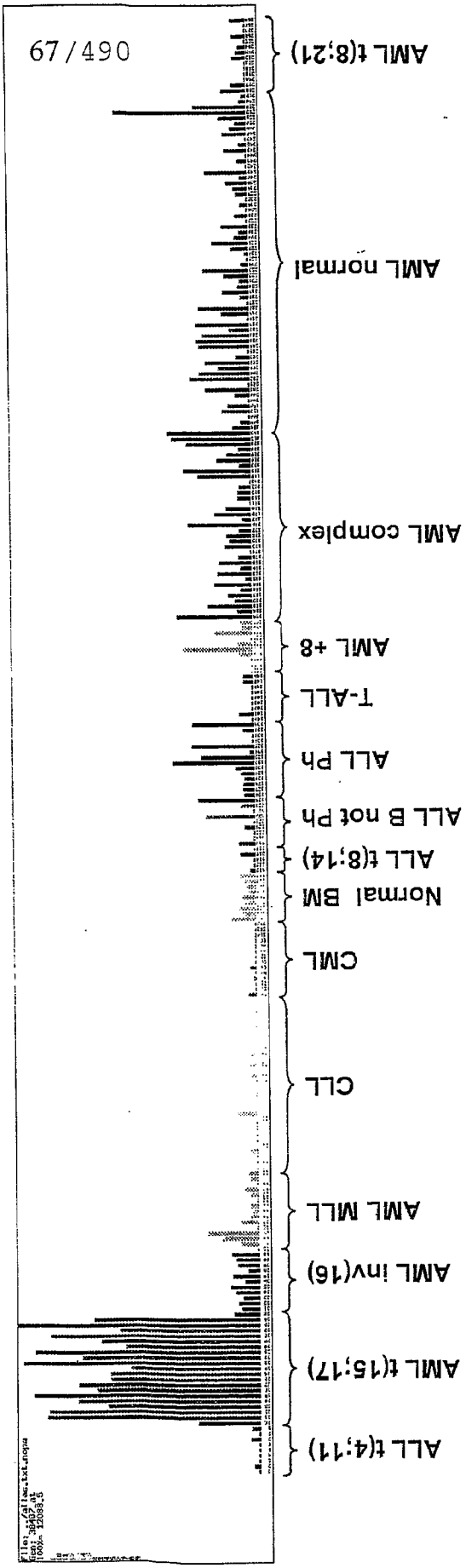

38487_at, FLJ12442, AML t(15;17) vs. all others
67/490
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 41

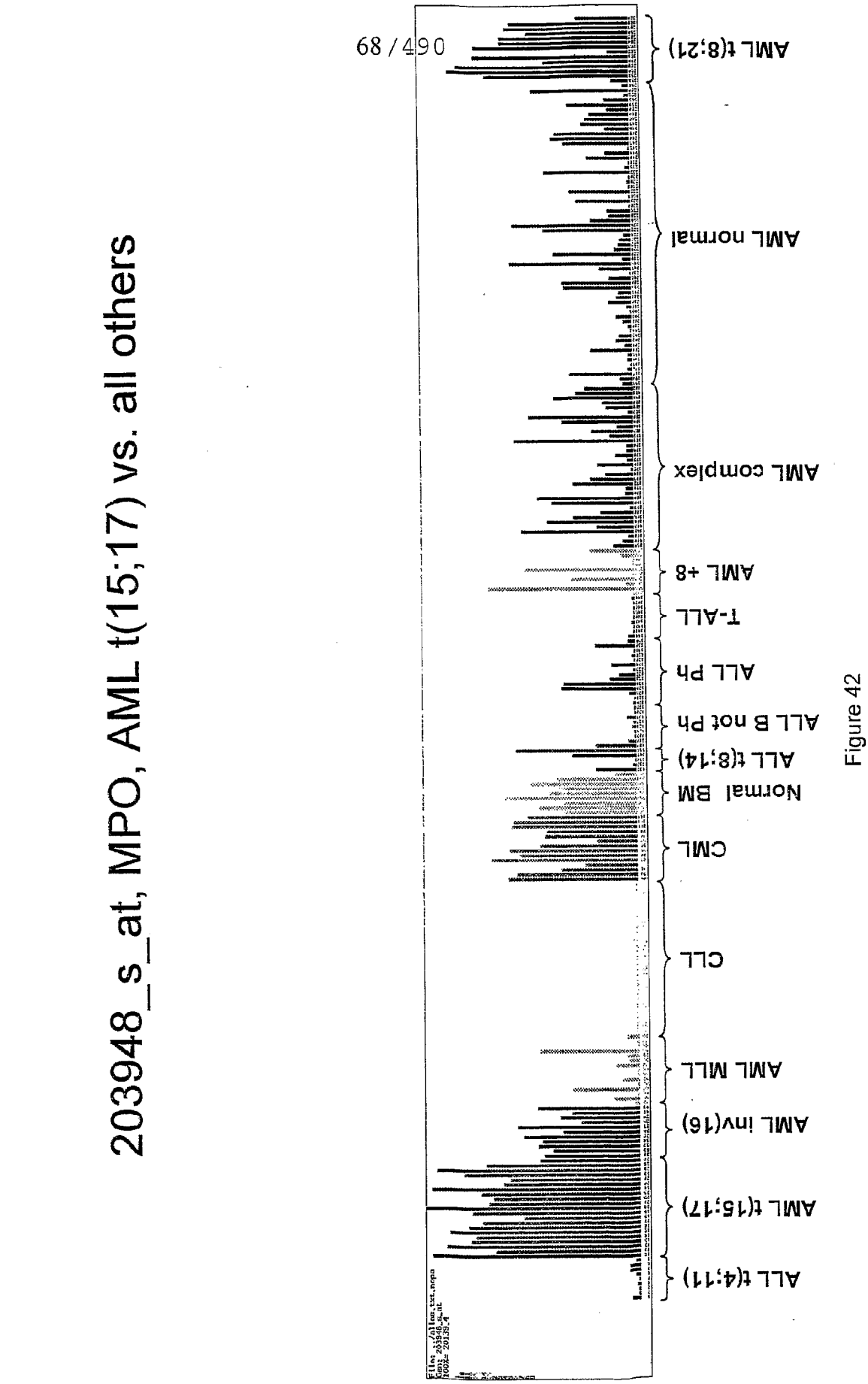

203948_s_at, MPO, AML t(15;17) vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 42

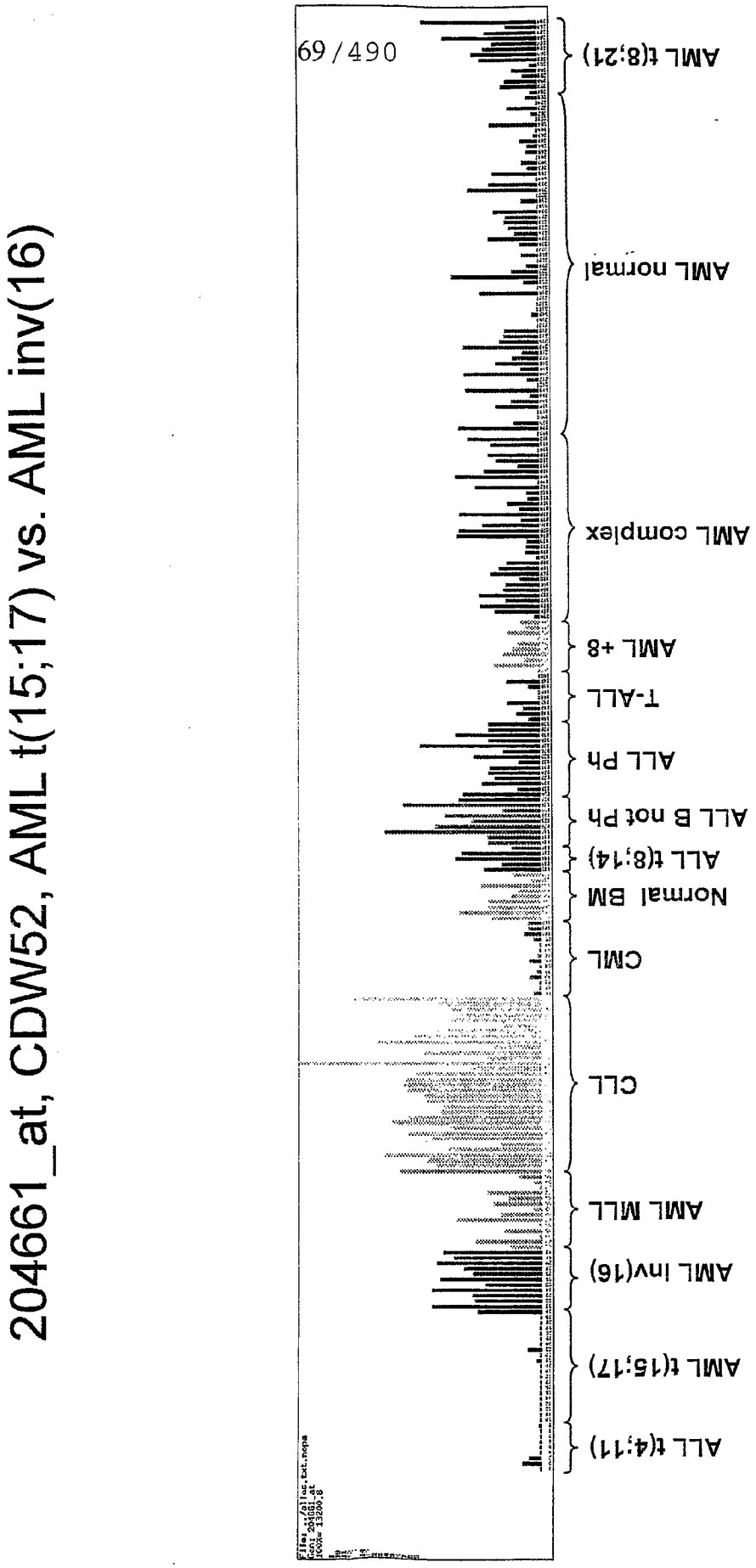

204661_at, CDW52, AML t(15;17) vs. AML inv(16)
69/490
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML Inv(16)
AML t(15;17)
ALL t(4;11)

Figure 43

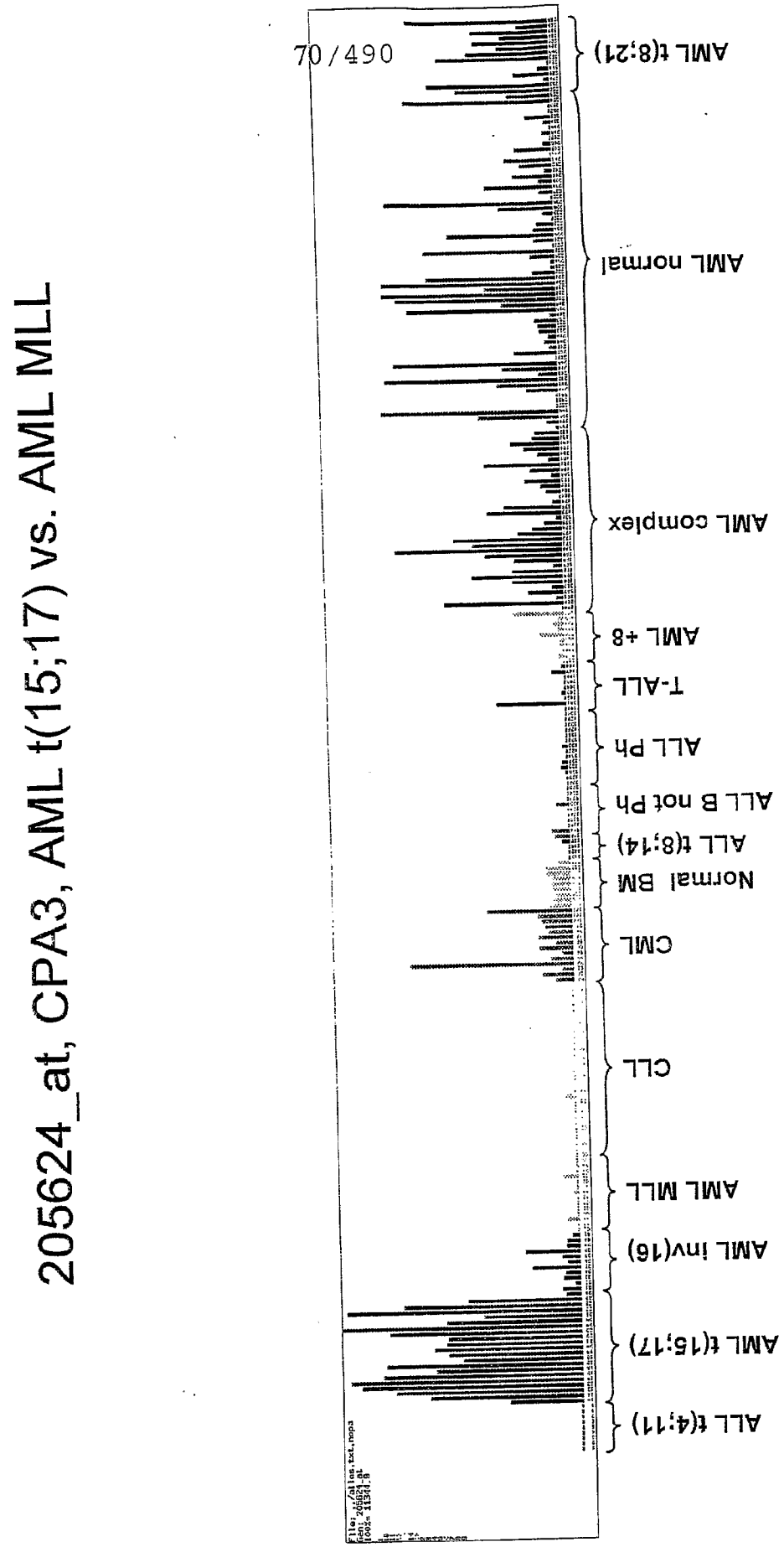

205624_at, CPA3, AML t(15;17) vs. AML MLL
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 44

203949_at, MPO, AML t(15;17) vs. CLL

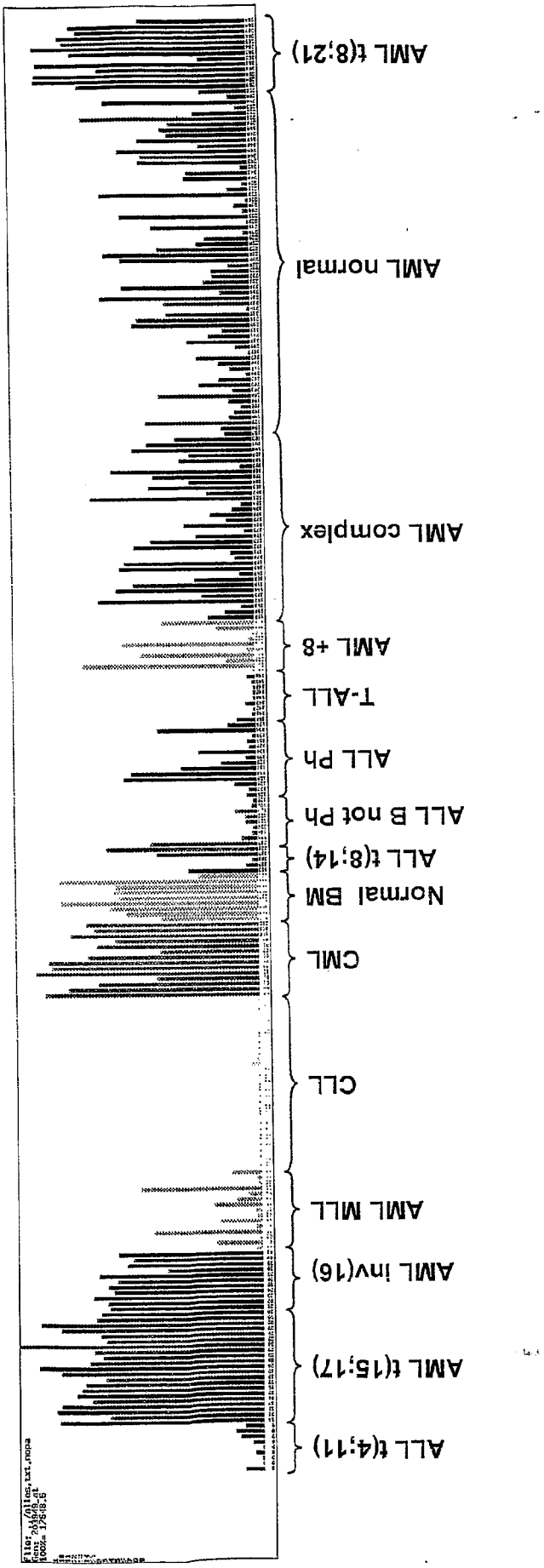


Figure 45

201029_s_at, MIC2, AML t(15;17) vs. CML

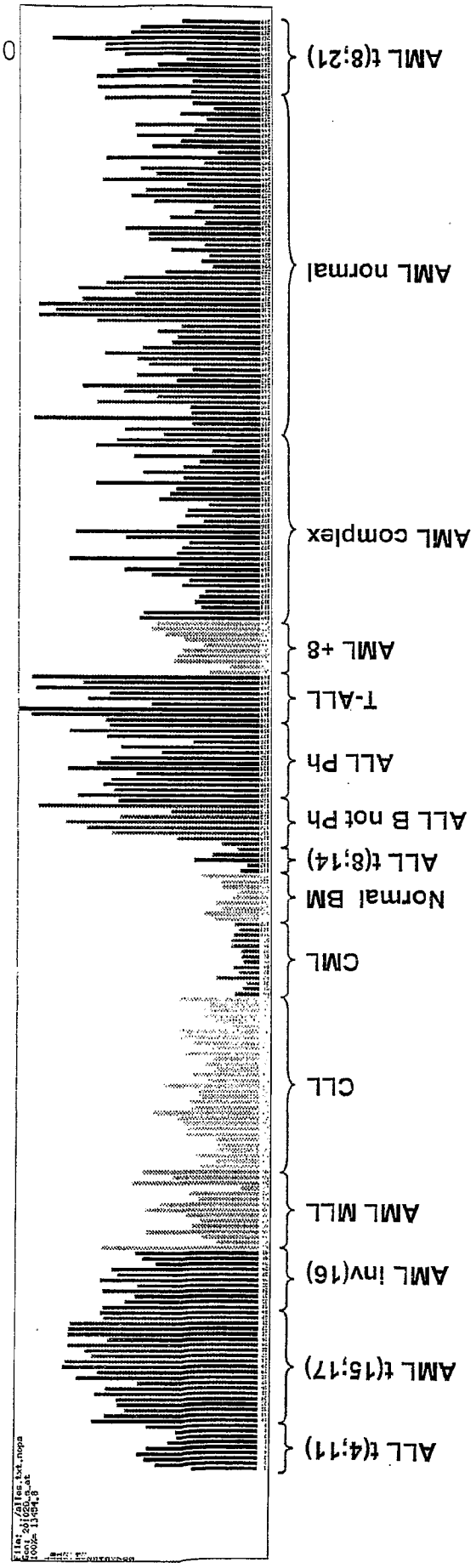


Figure 46

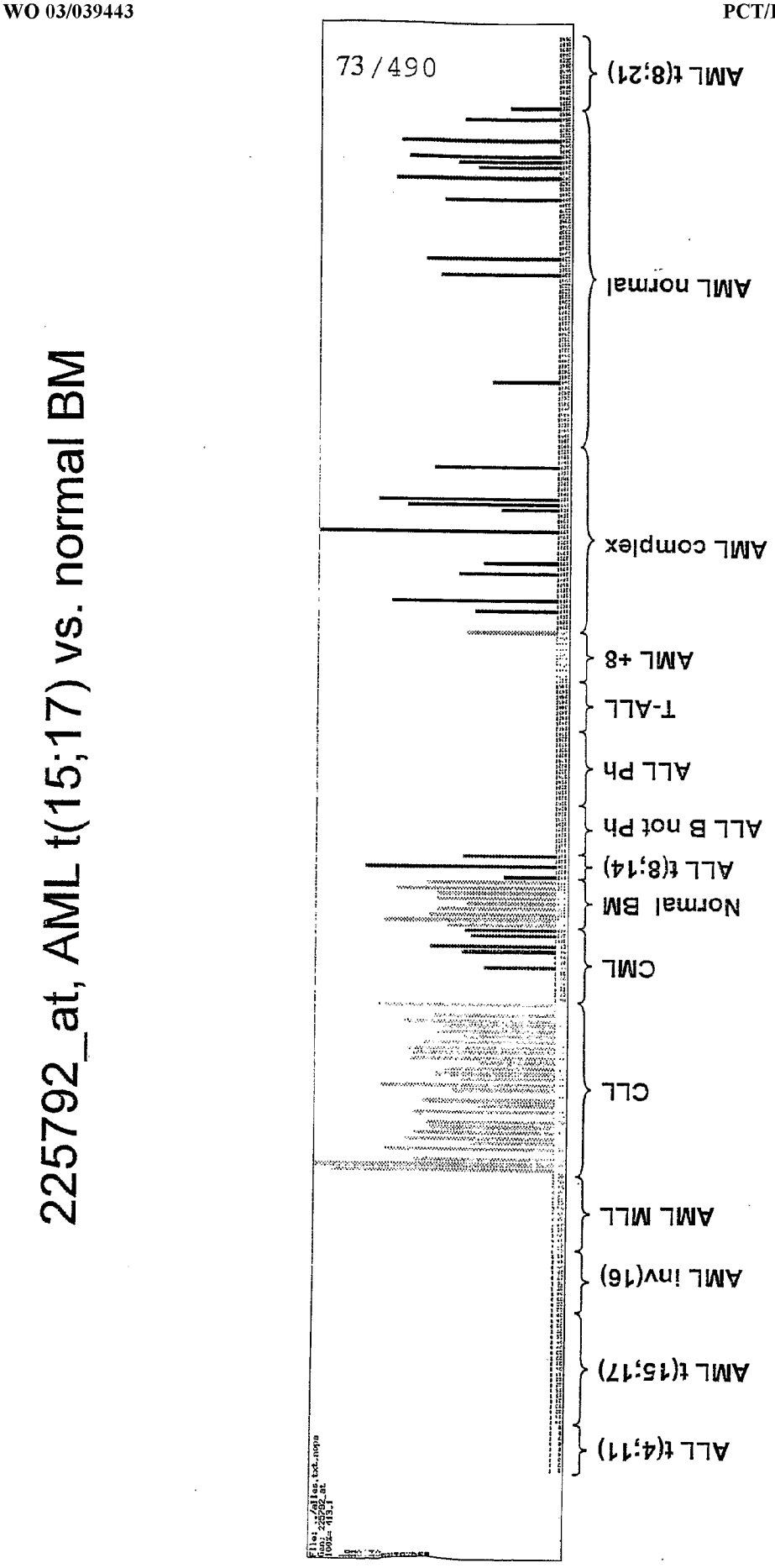

225792_at, AML t(15;17) vs. normal BM
73 / 490
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 47

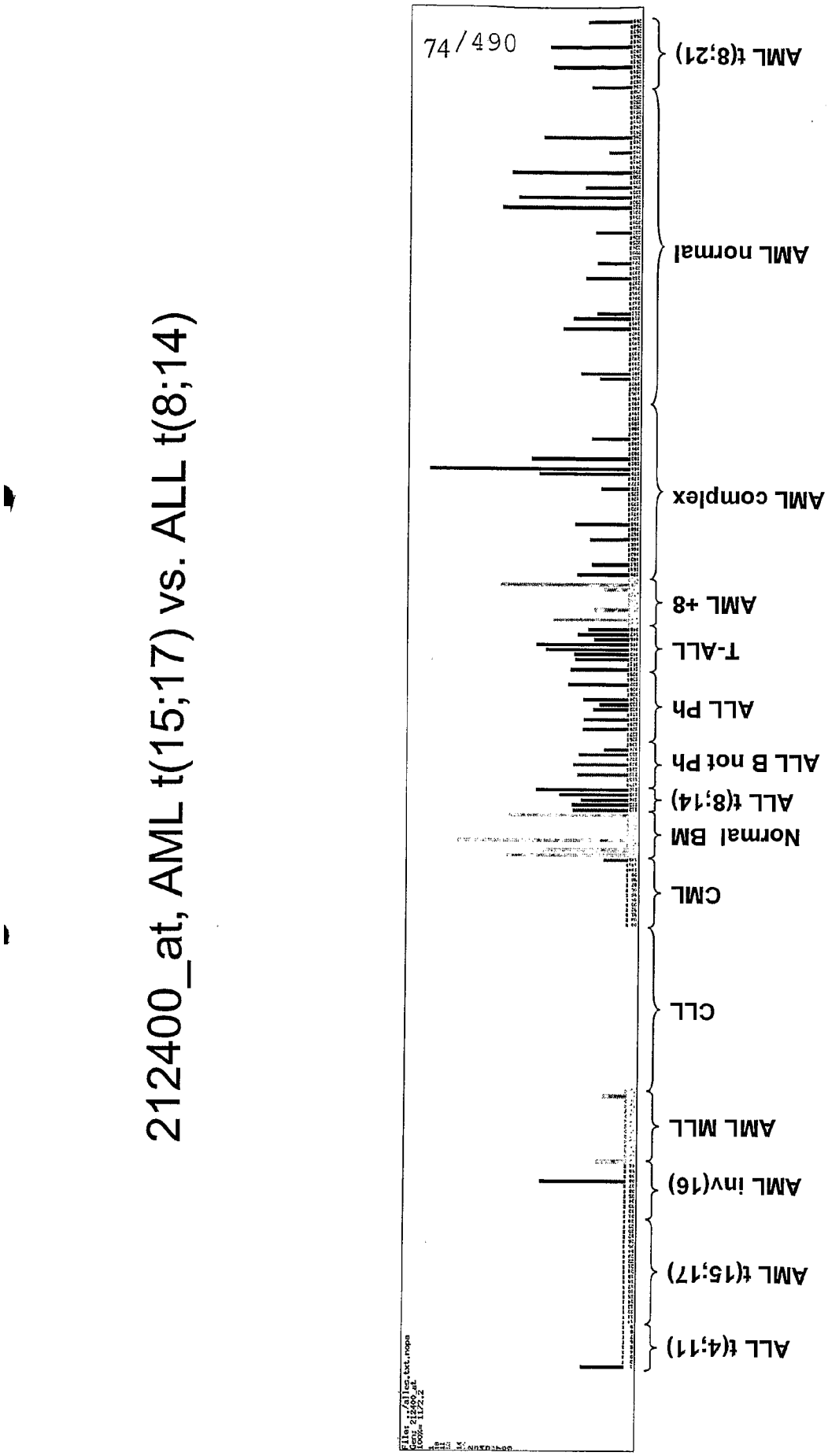

212400_at, AML t(15;17) vs. ALL t(8;14)
74/490
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 48

205382_s_at, DF, AML t(15;17) vs. ALL B not Ph

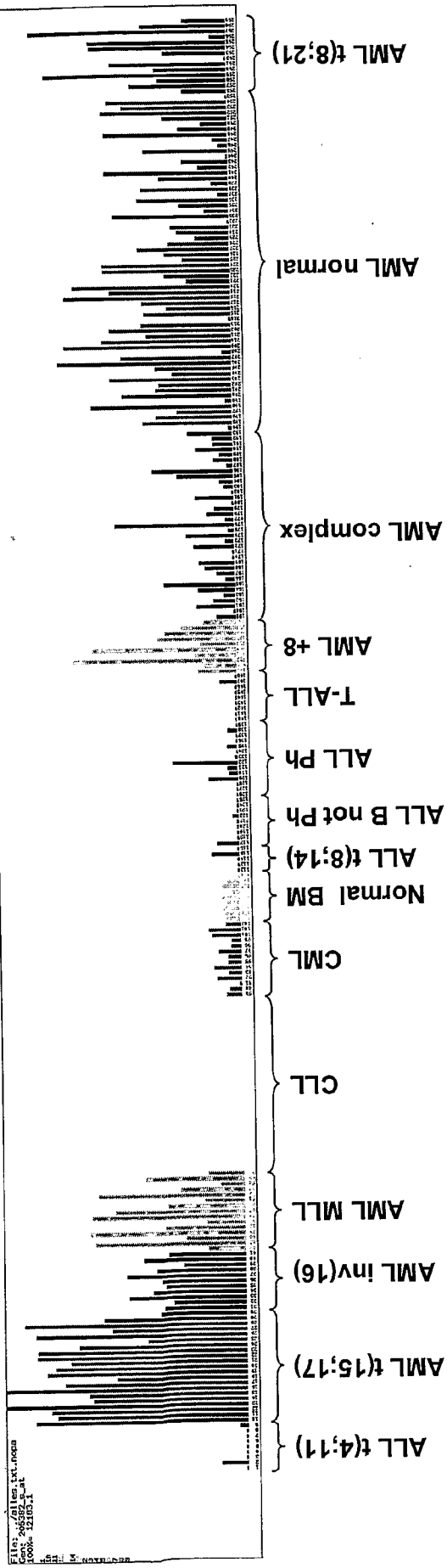


Figure 49

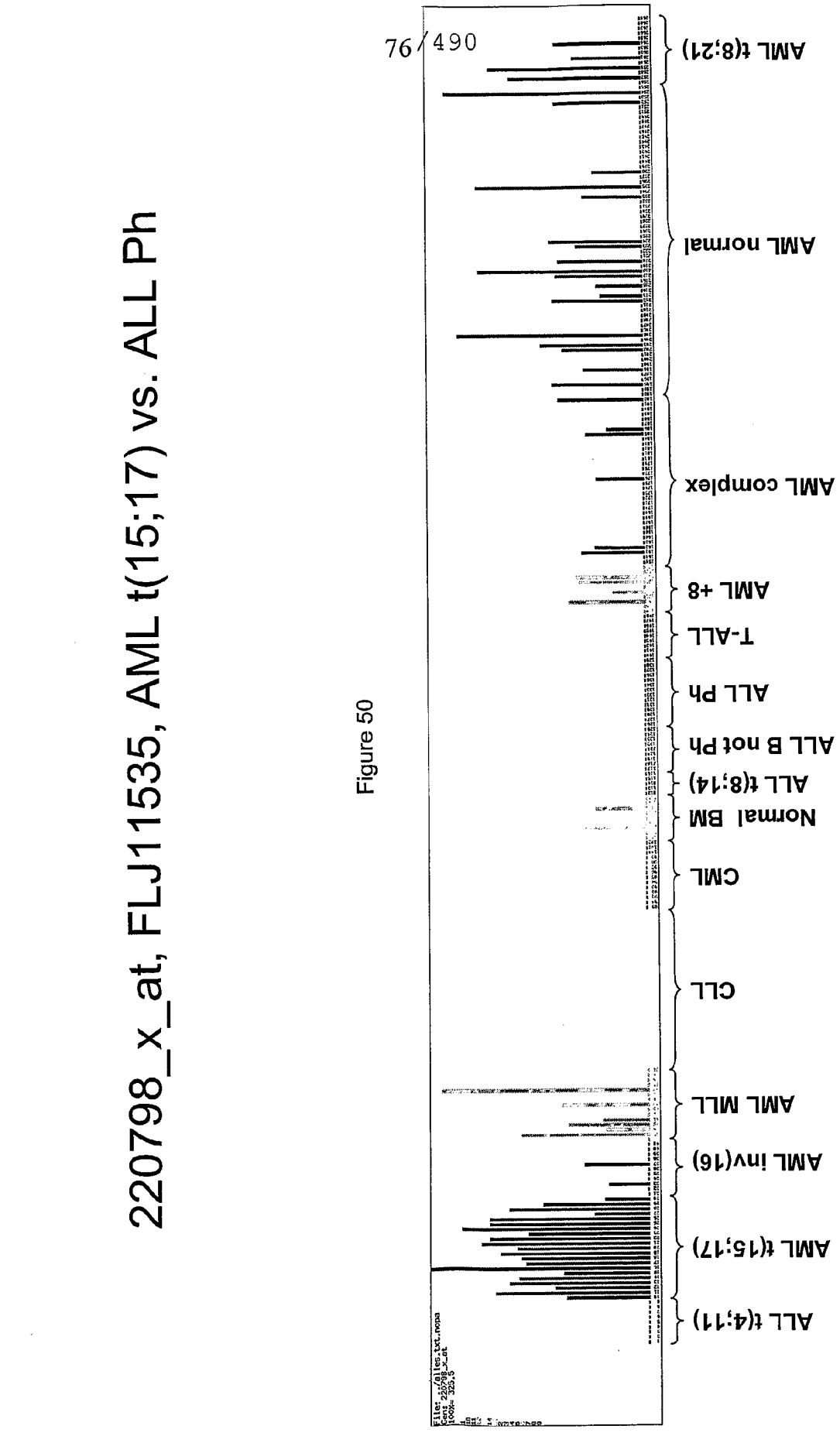

220798_x_at, FLJ11535, AML t(15;17) vs. ALL Ph
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 50

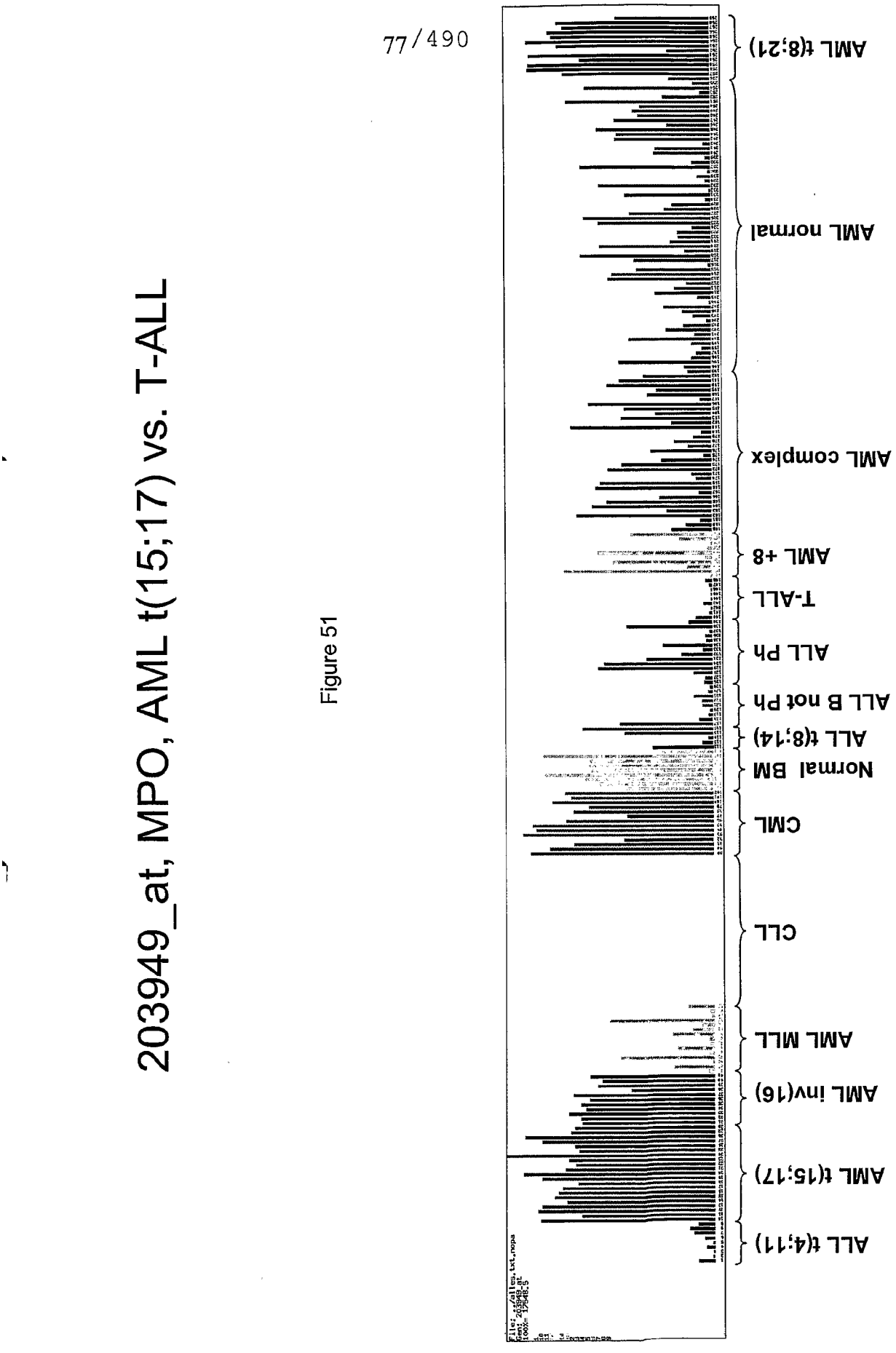

203949_at, MPO, AML t(15;17) vs. T-ALL
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 51

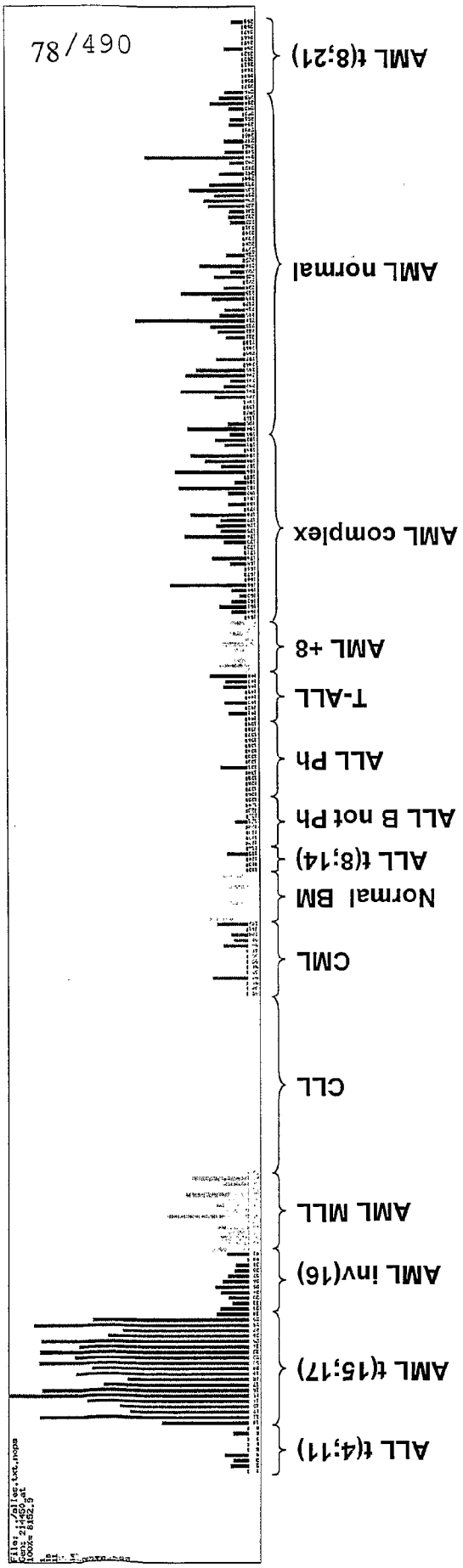

214450_at, CTSW, AML t(15;17) vs. AML +8
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 52

212953_x_at, CALR, AML t(15;17) vs. AML complex

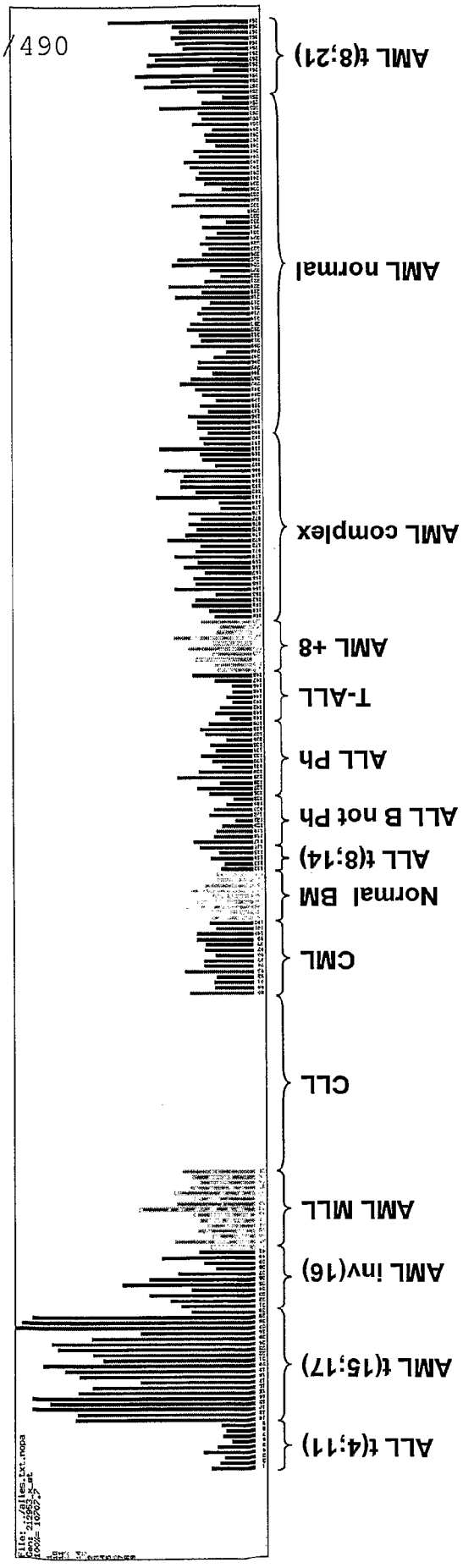


Figure 53

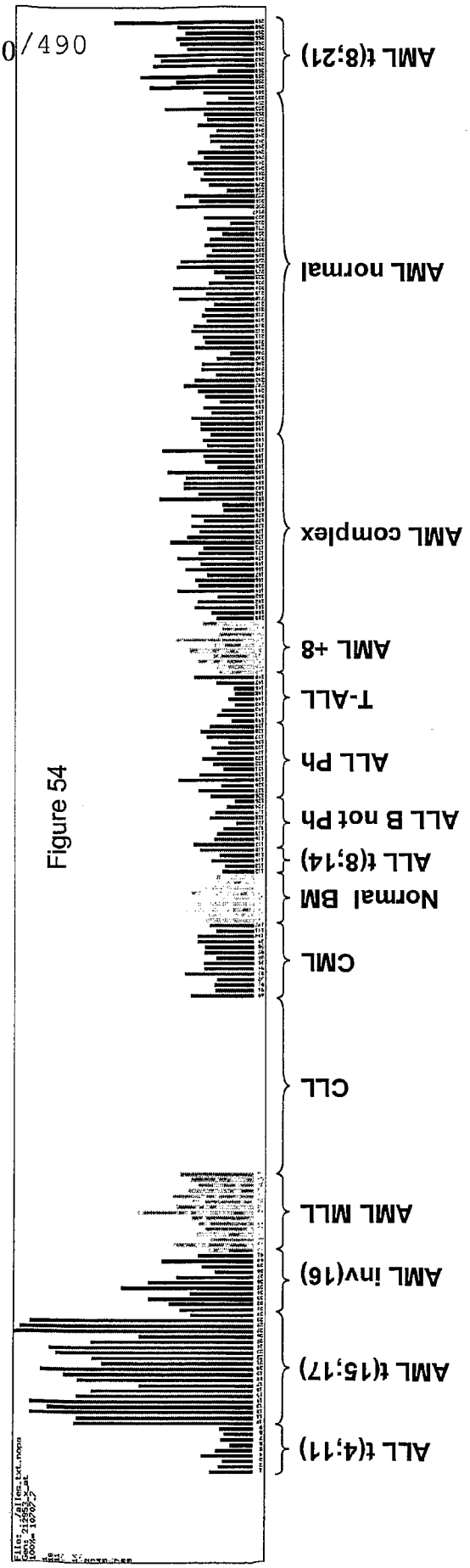

212953_x_at, CALR, AML t(15;17) vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 54

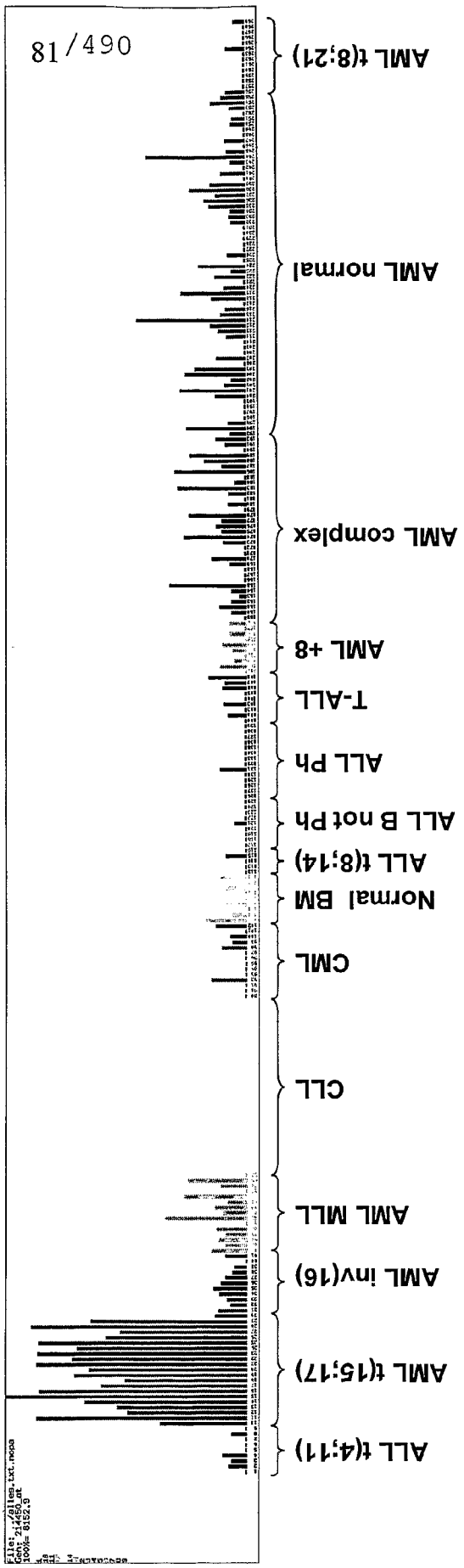

214450_at, CTSW, AML t(15;17) vs. AML t(8;21)
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 55

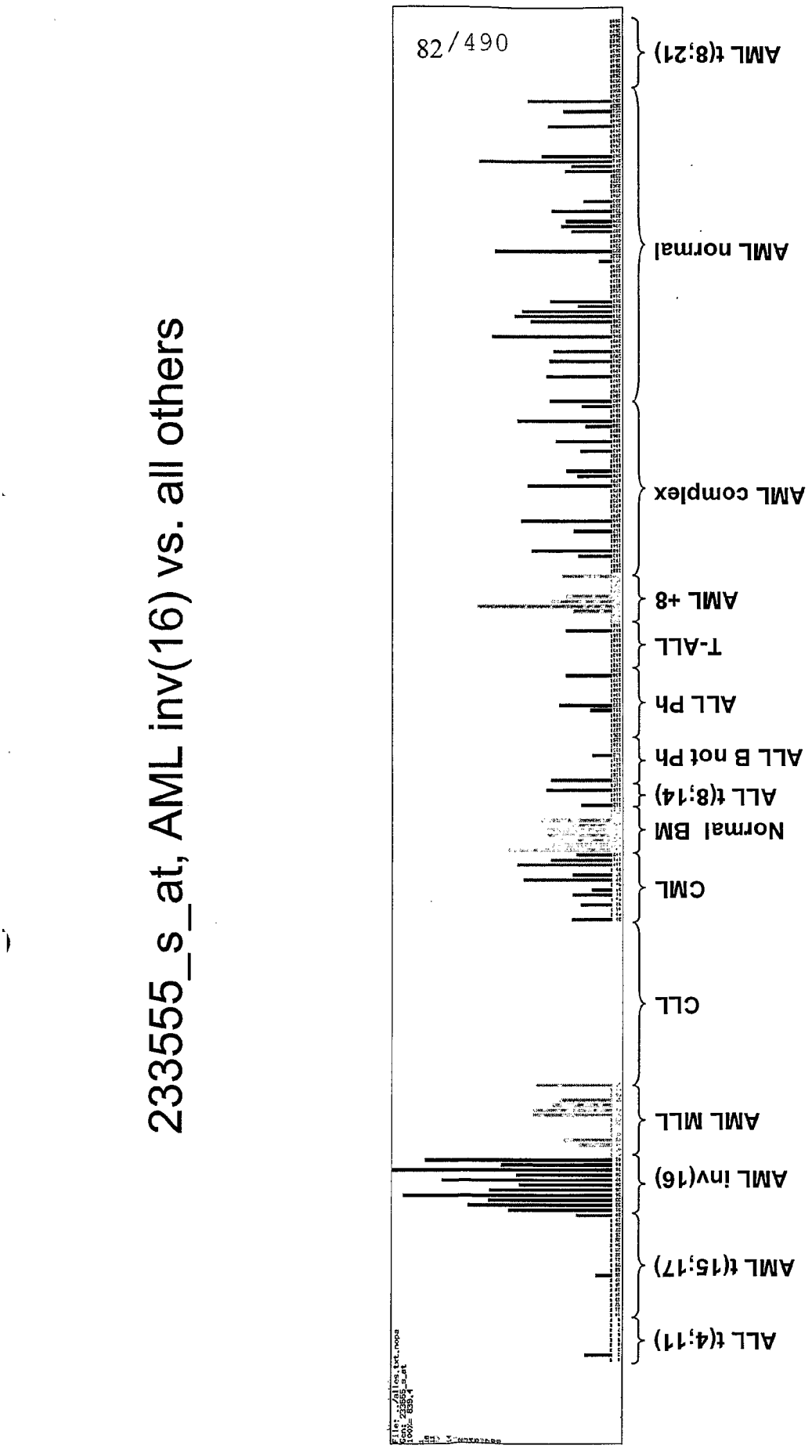

233555_s_at, AML inv(16) vs. all others
82/490
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 56

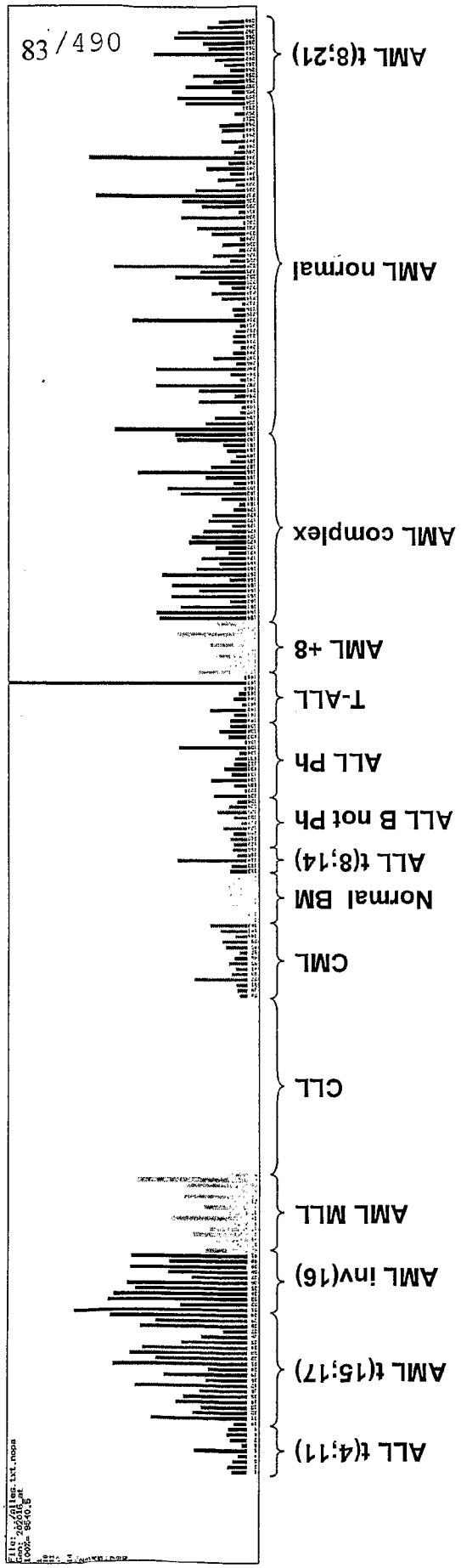

202016_at, MEST, AML inv(16) vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 57

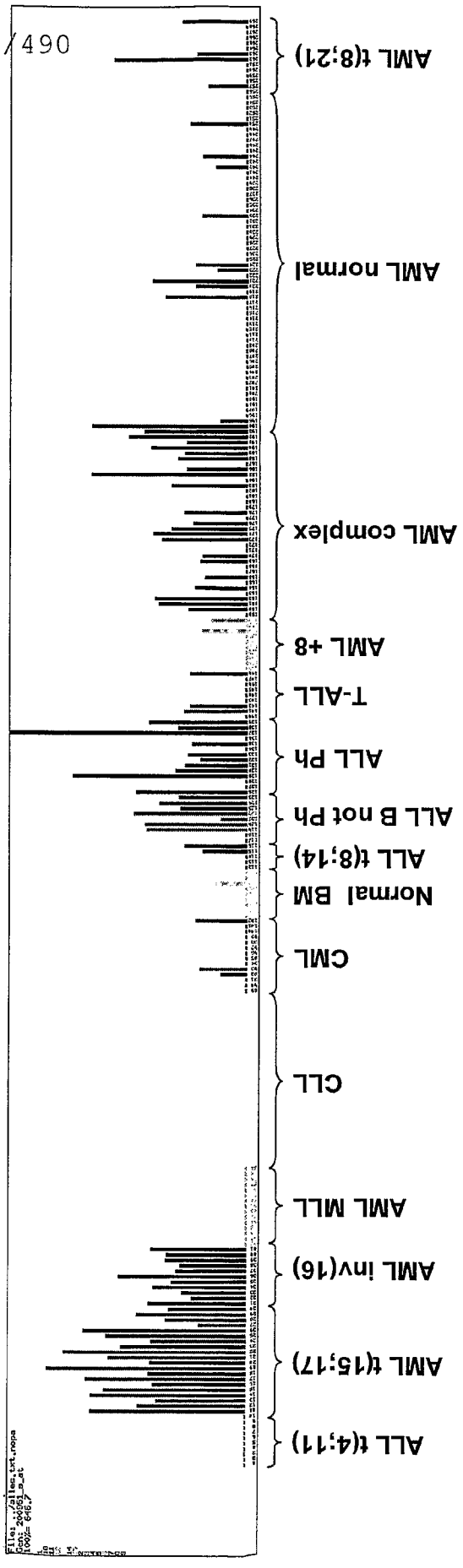

200951_s_at, CCND2, AML inv(16) vs. AML MLL
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 58

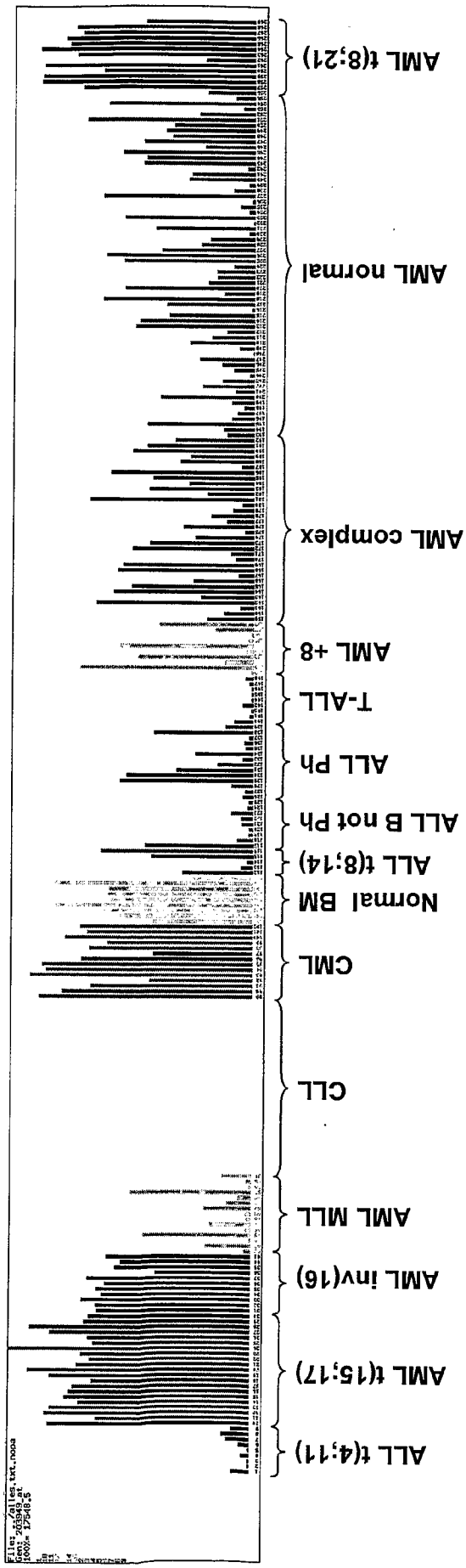

203949_at, MPO, AML inv(16) vs. CLL
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 59

201029_s_at, MIC2, AML inv(16) vs. CML

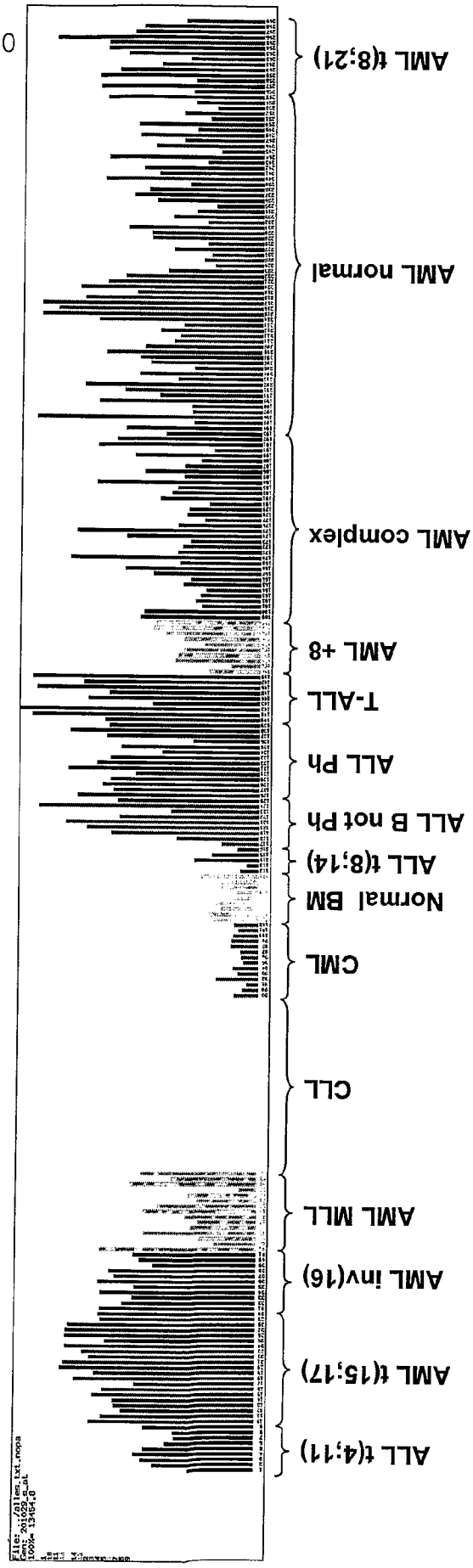
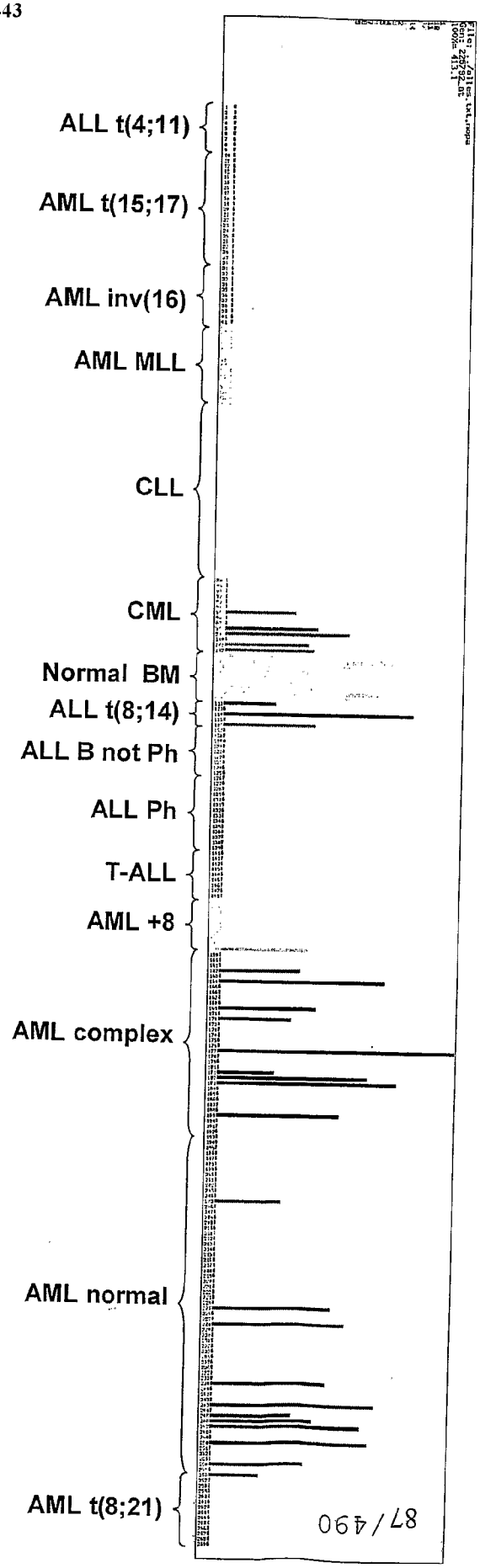


Figure 60



225792_at, AML inv(16) vs. normales KM

Figure 61

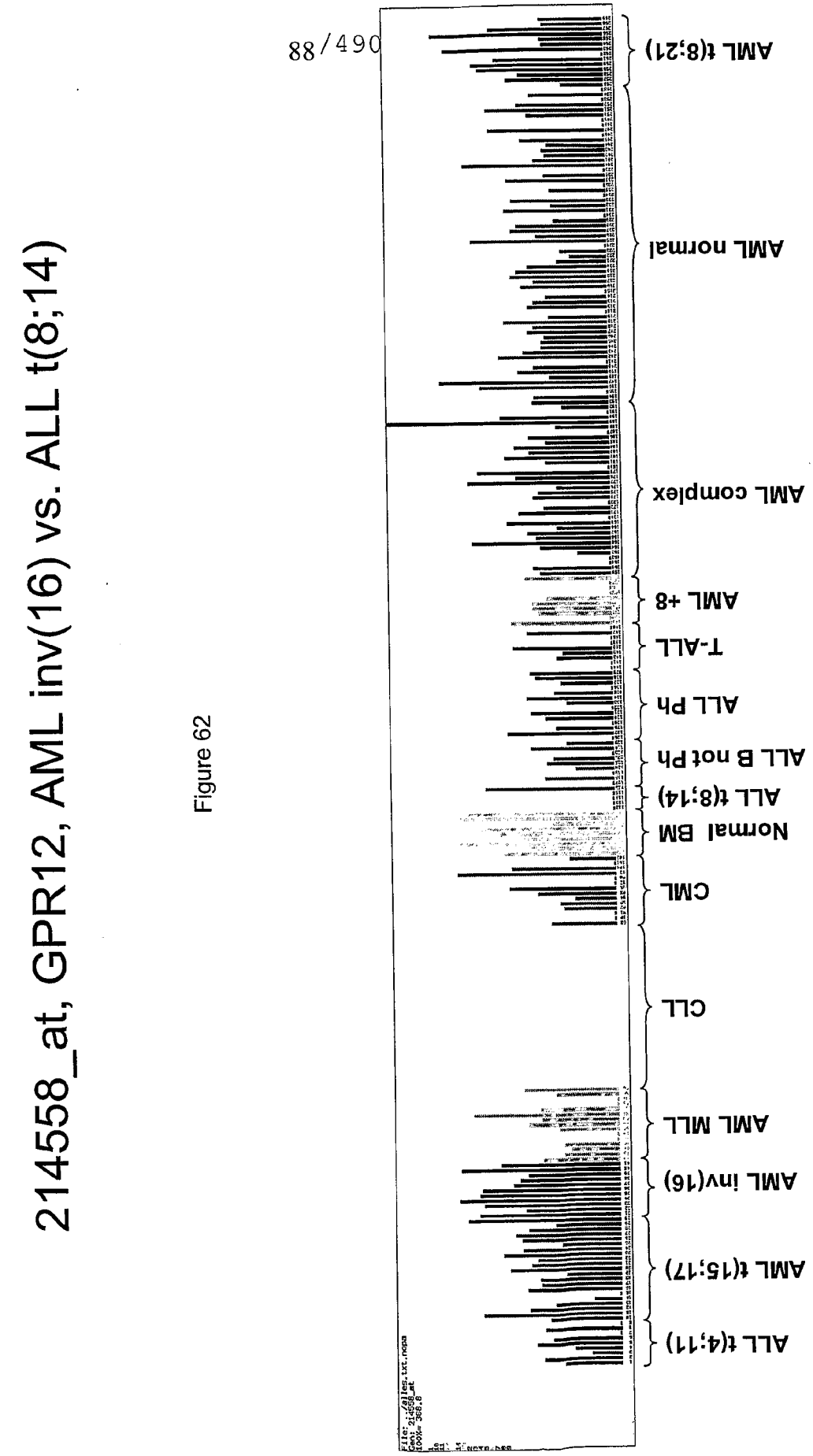

214558_at, GPR12, AML inv(16) vs. ALL t(8;14)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 62

205382_s_at, DF, AML inv(16) vs. ALL B not Ph

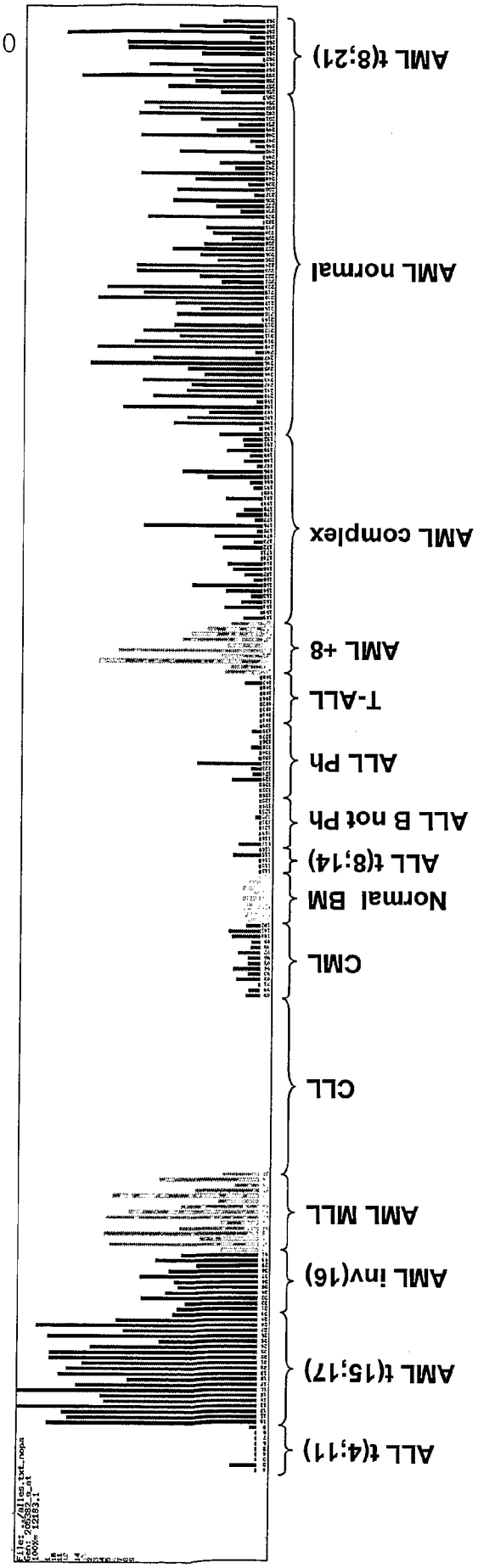


Figure 63

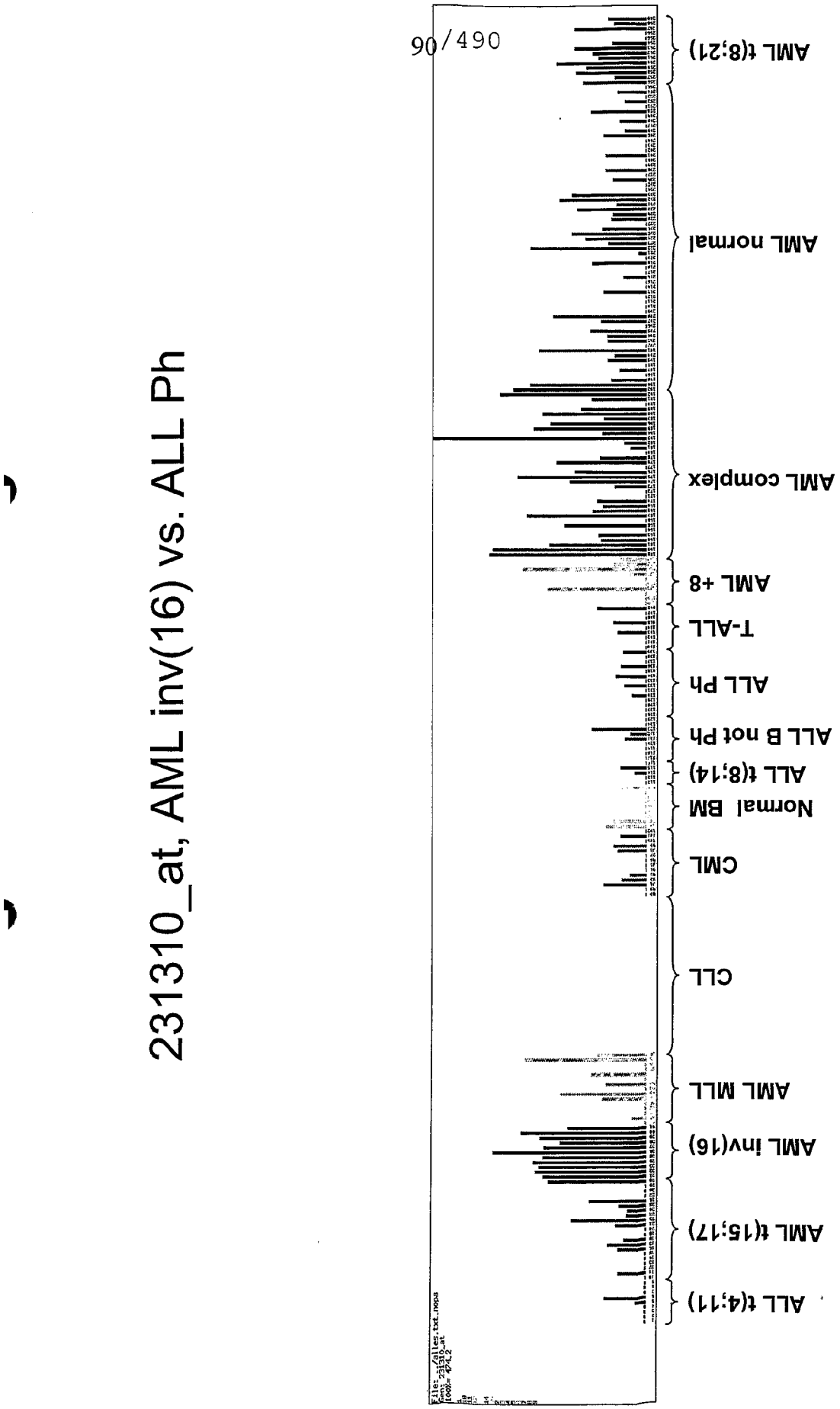

231310_at, AML inv(16) vs. ALL Ph
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 64

203949_at, MPO, AML inv(16) vs. T-ALL

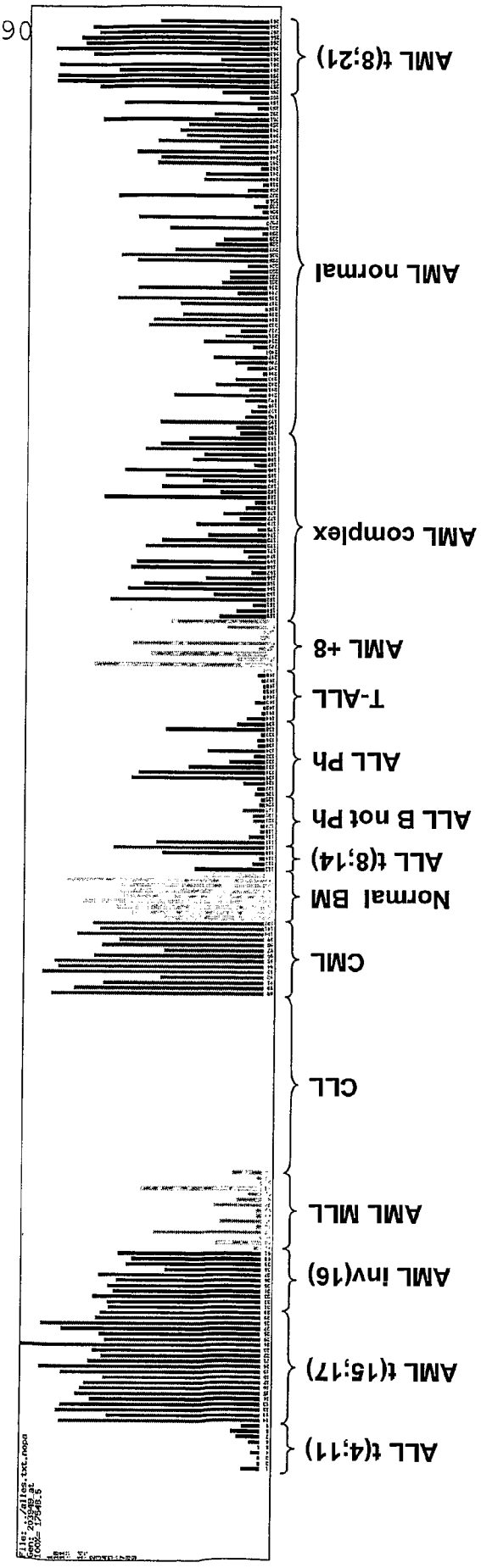


Figure 65

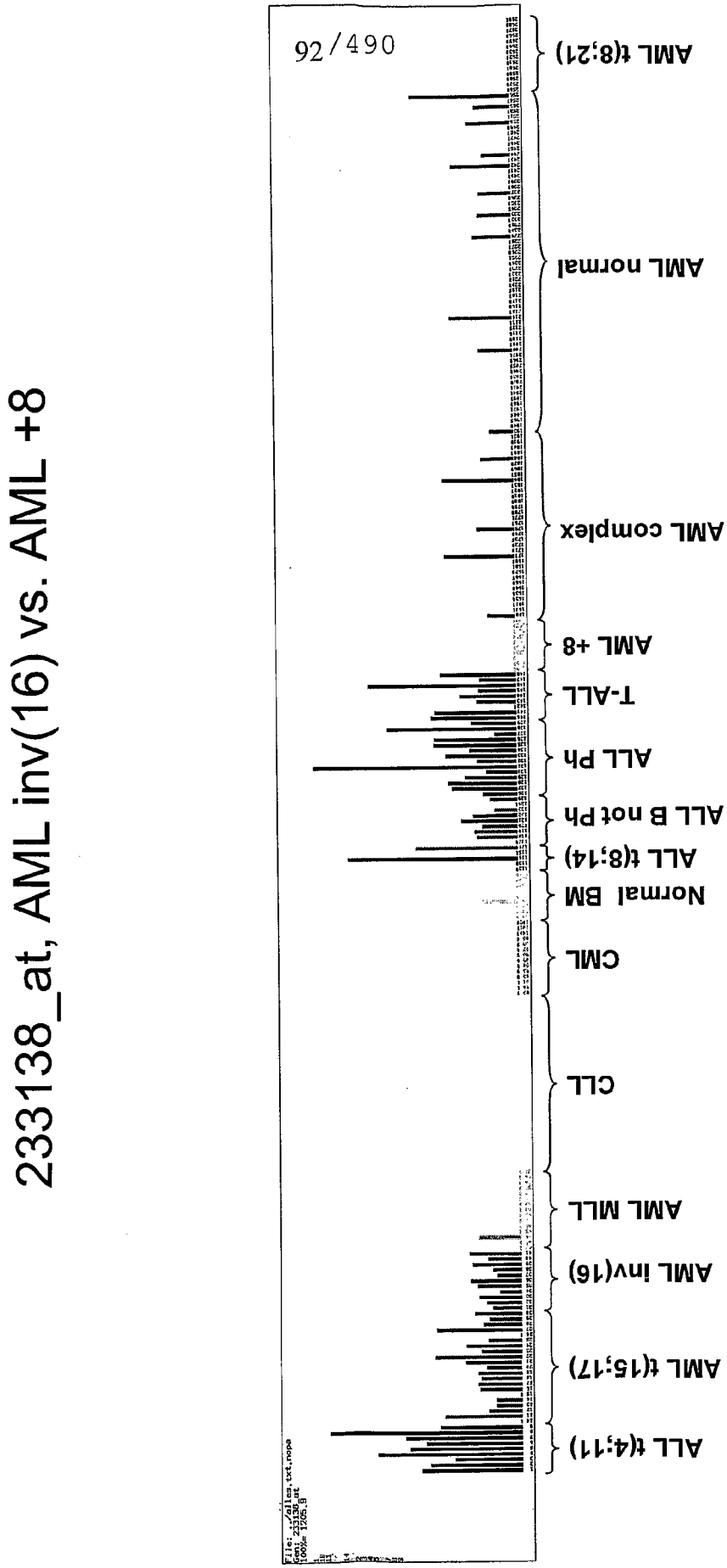

233138_at, AML inv(16) vs. AML +8
92/490
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 66

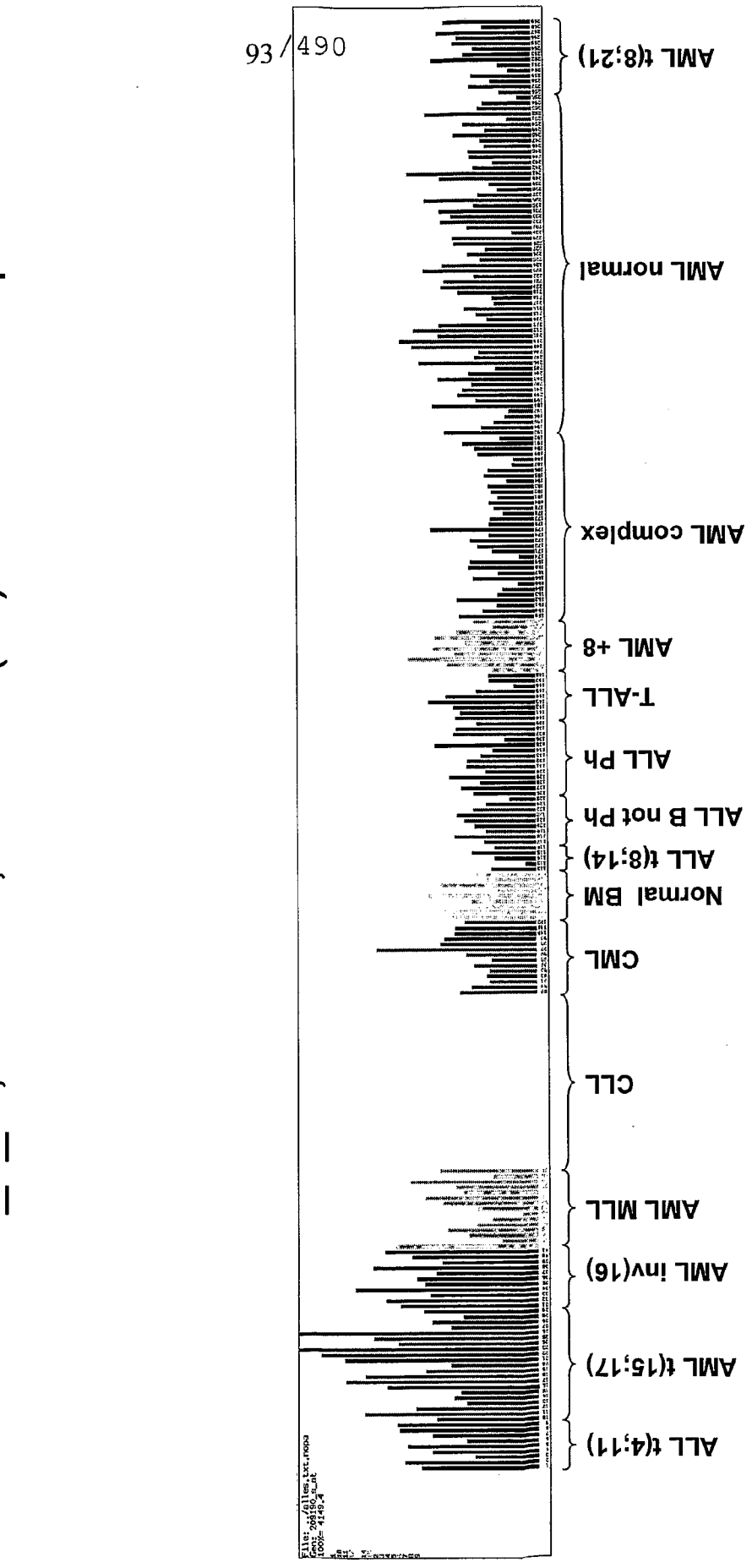

209190_s_at, DIAPH1, AML inv(16) vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 67

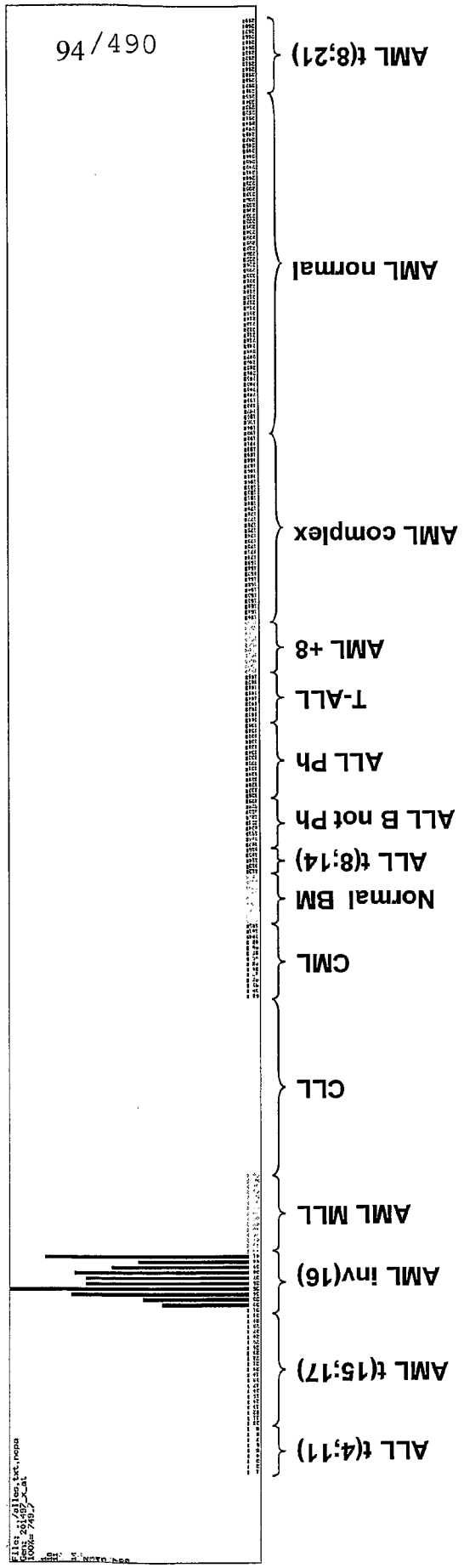

201497_x_at, MYH11, AML inv(16) vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 68

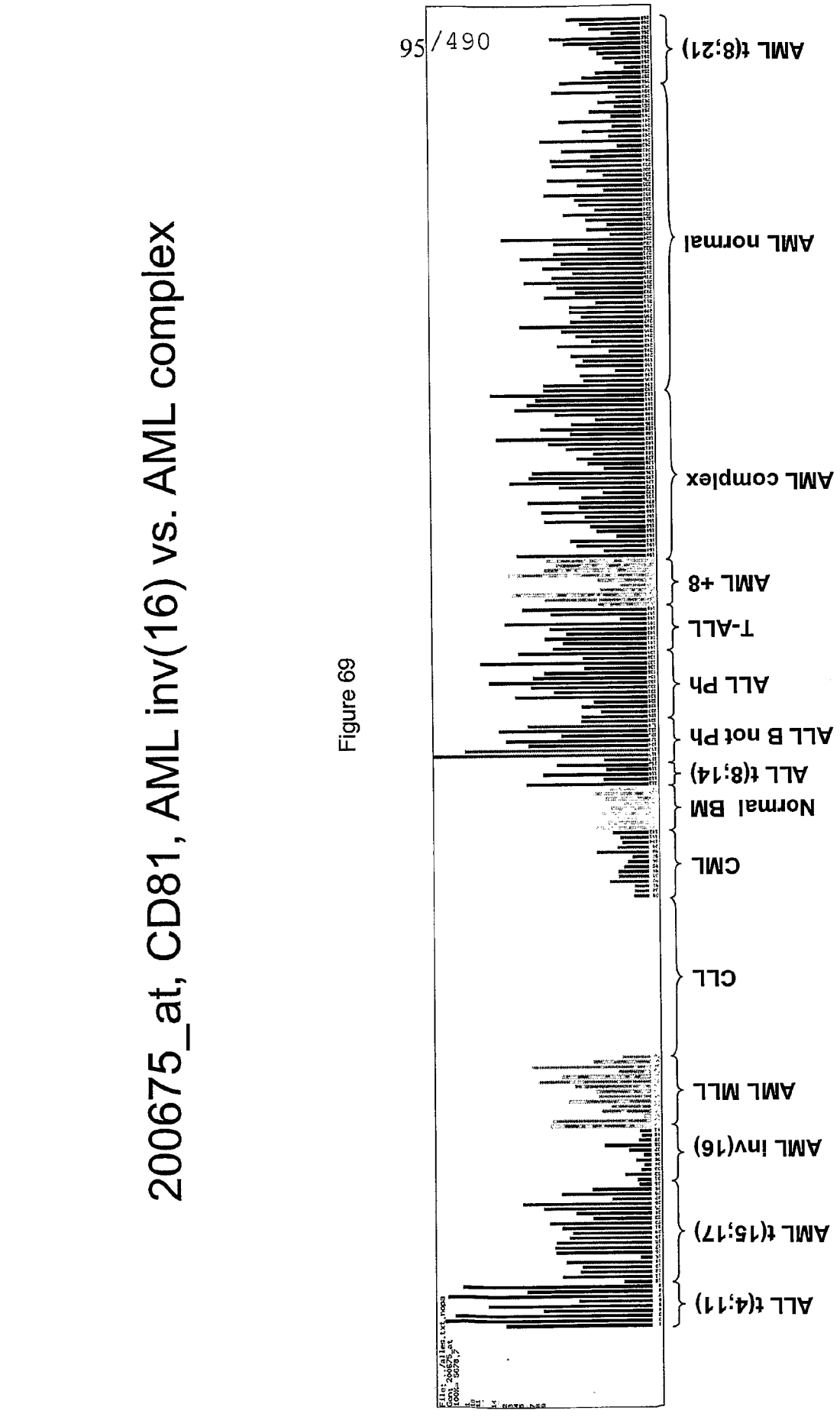

200675_at, CD81, AML inv(16) vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 69

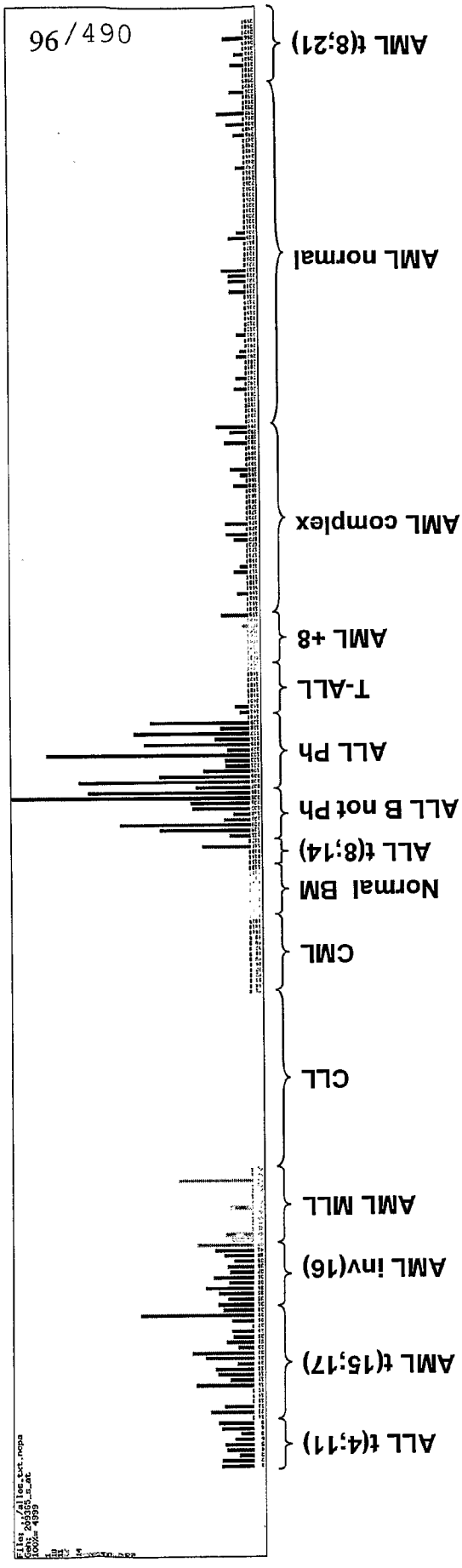

209365_s_at, ECM1, AML inv(16) vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 70

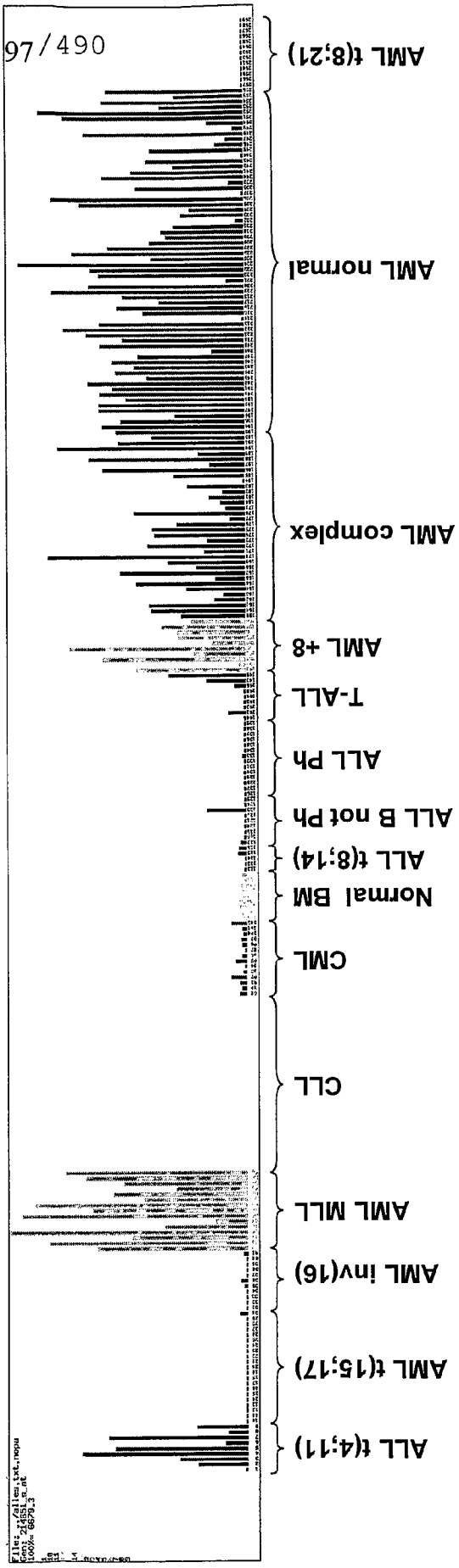

214641_s_at, HOXA9, AML inv(16) vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 71

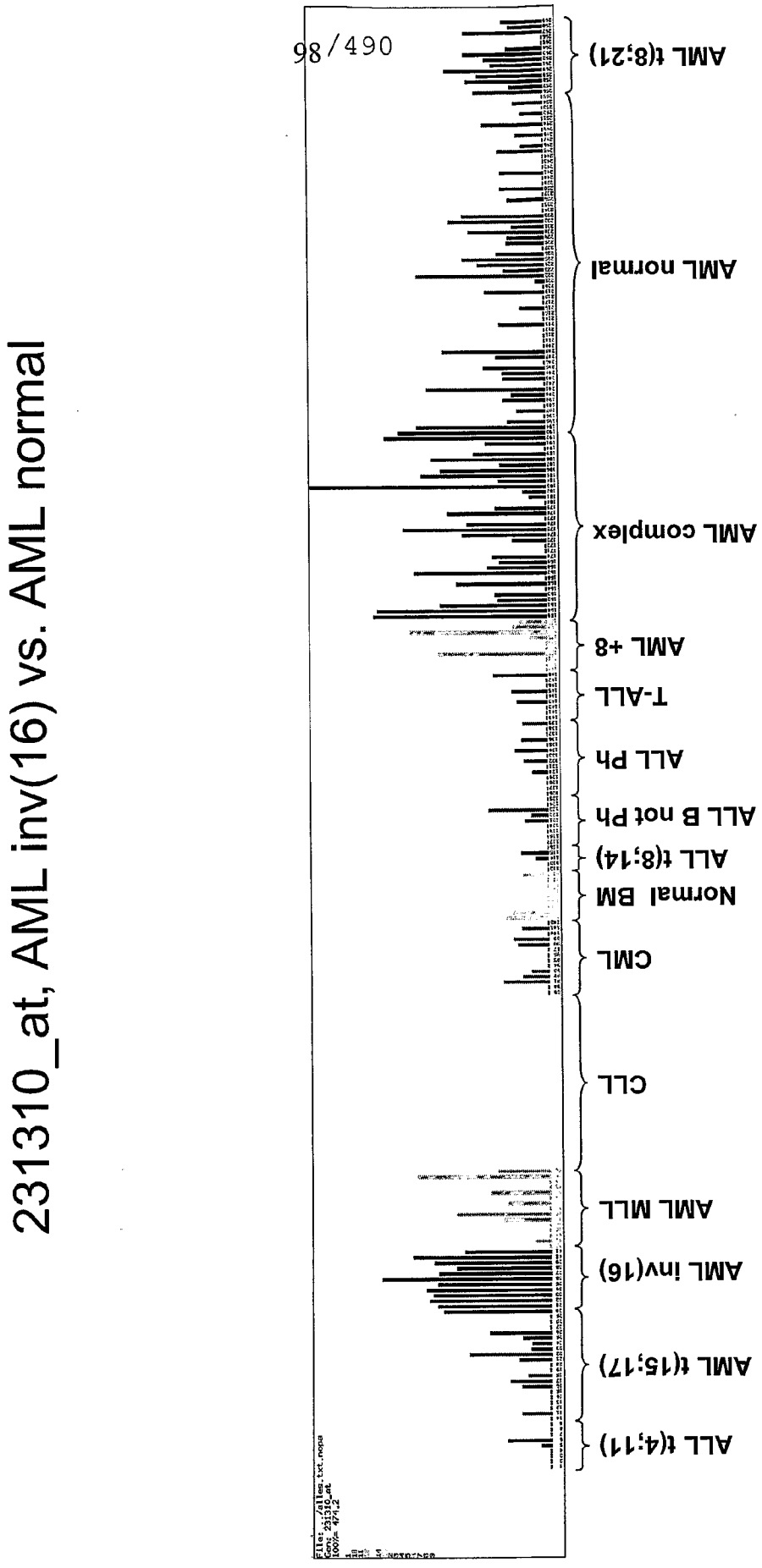

231310_at, AML inv(16) vs. AML normal
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 72

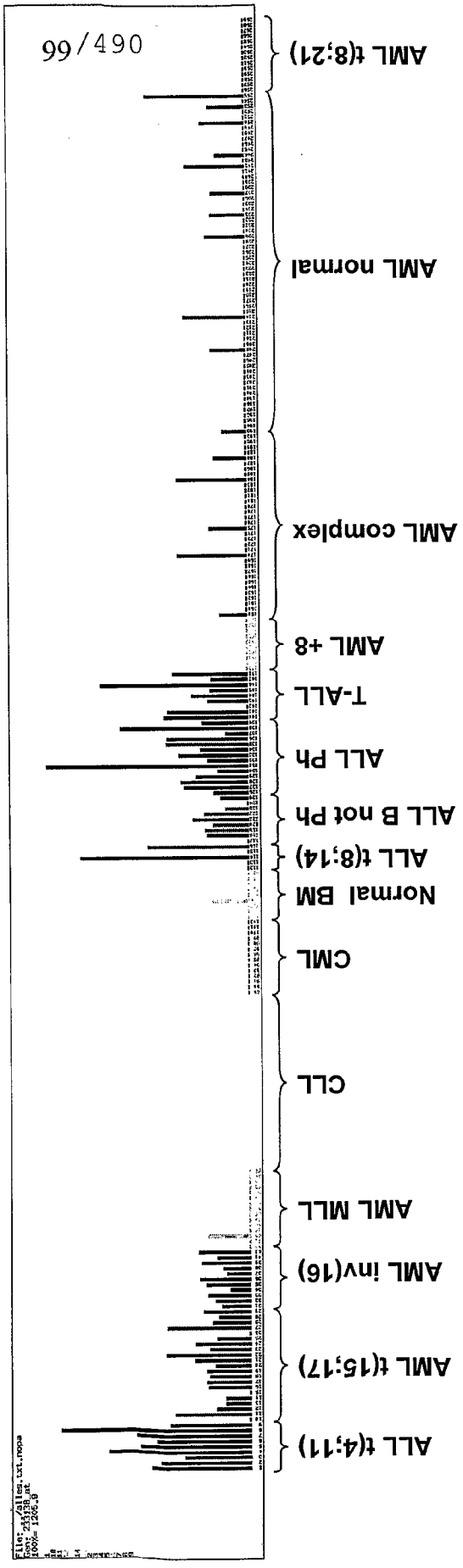
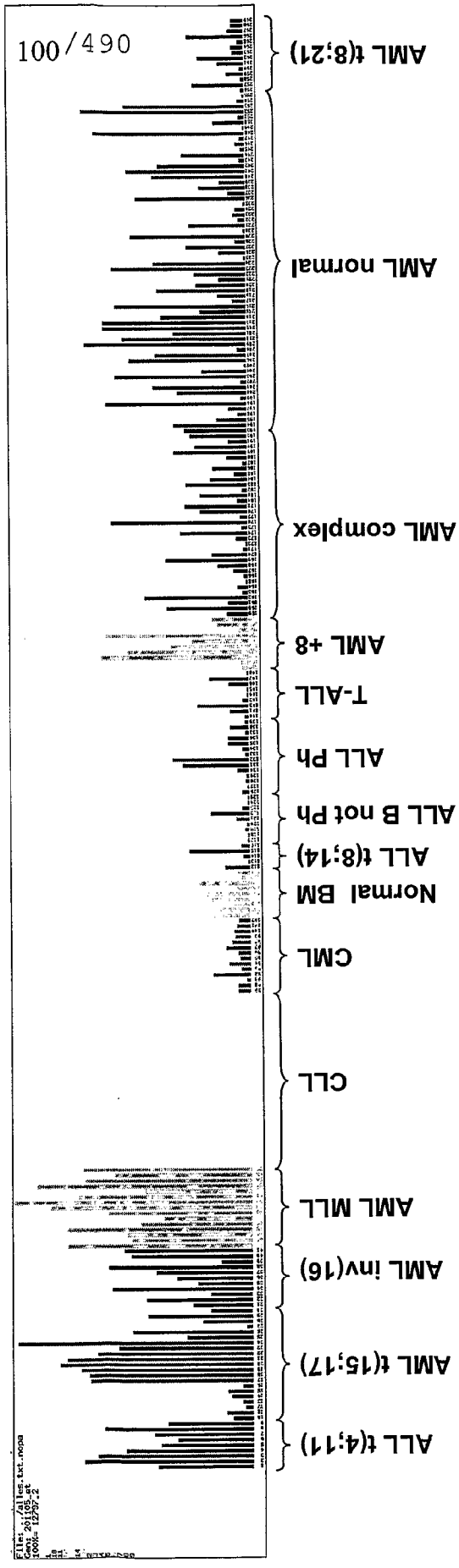

233138_at, AML inv(16) vs. AML t(8;21)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 73



201105_at, LGALS1, AML MLL vs. all others

Figure 74

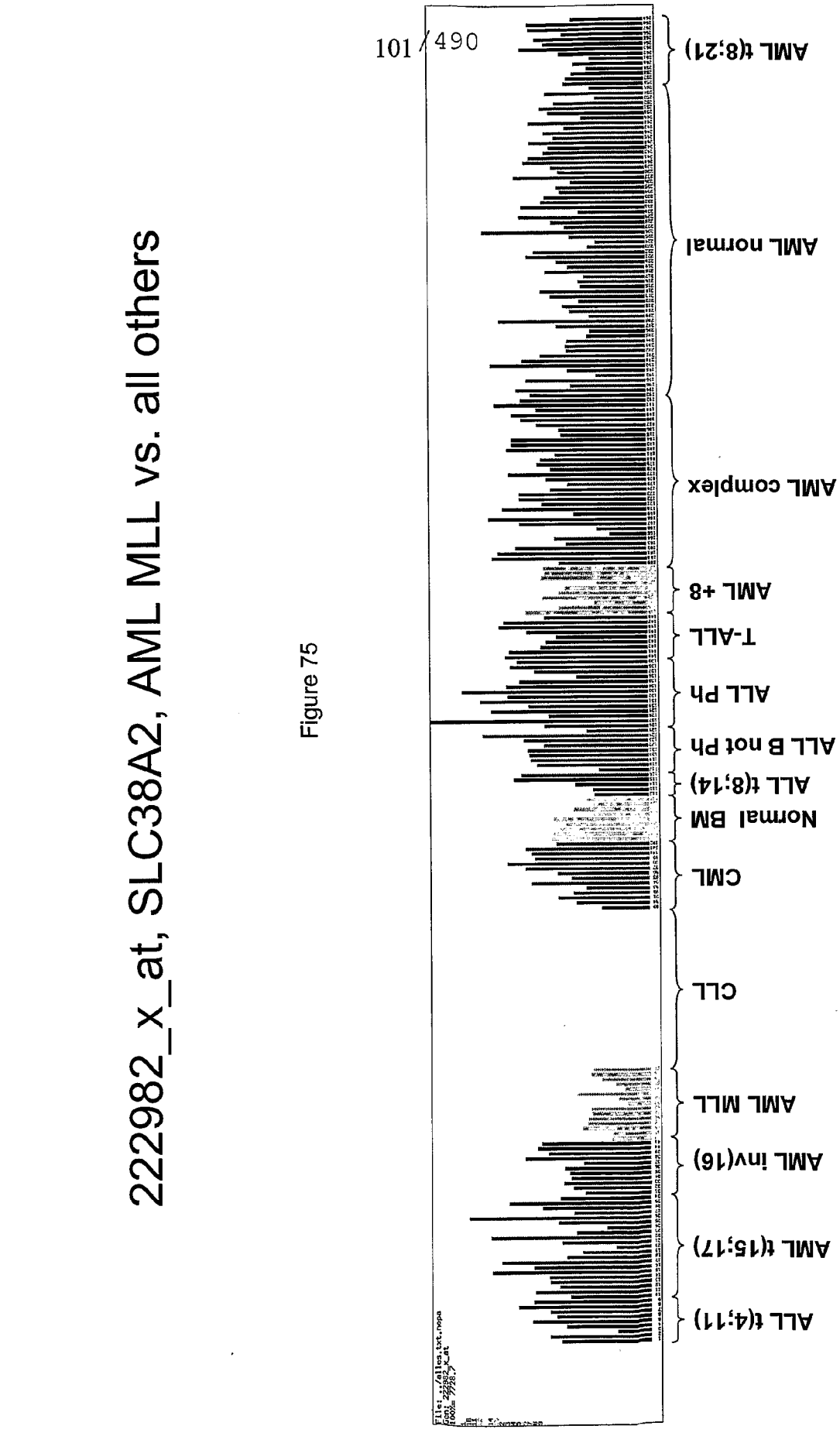

222982_x_at, SLC38A2, AML MLL vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 75

238856_s_at, AML MLL vs. all others

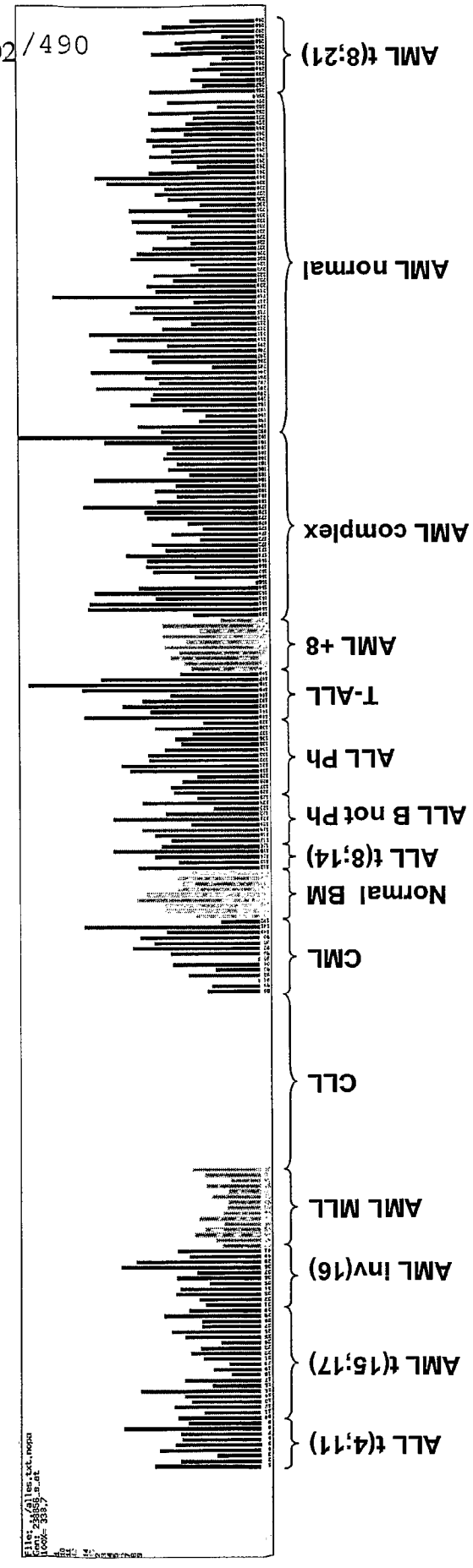


Figure 76

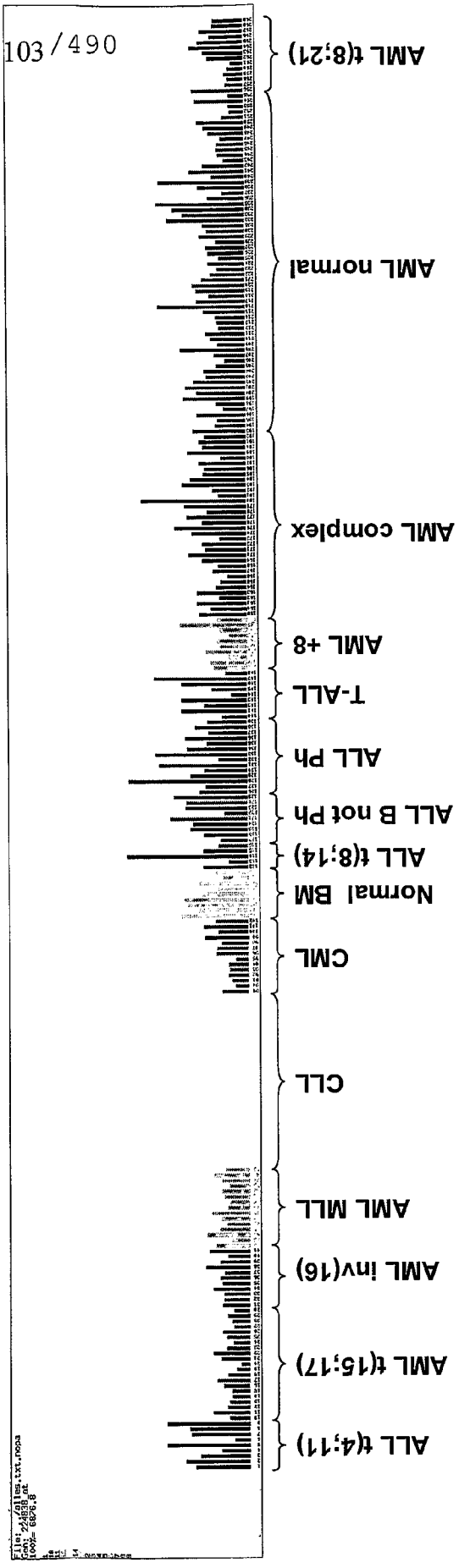

224838_at, AML MLL vs. CLL
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 77

209771_x_at, CD24, AML MLL vs. CML

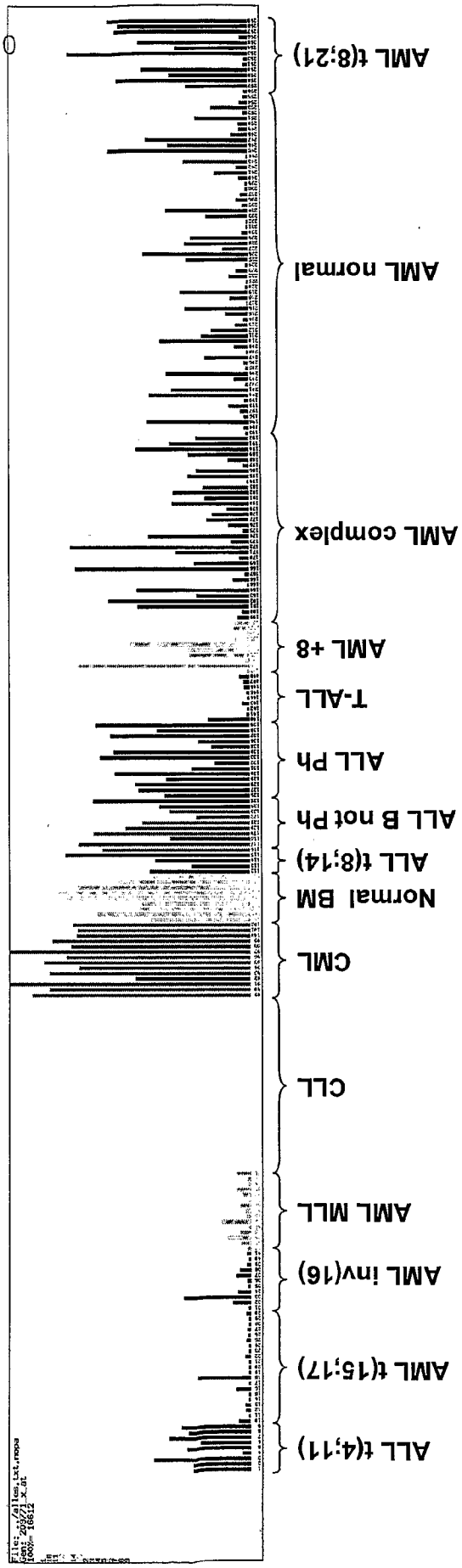


Figure 78

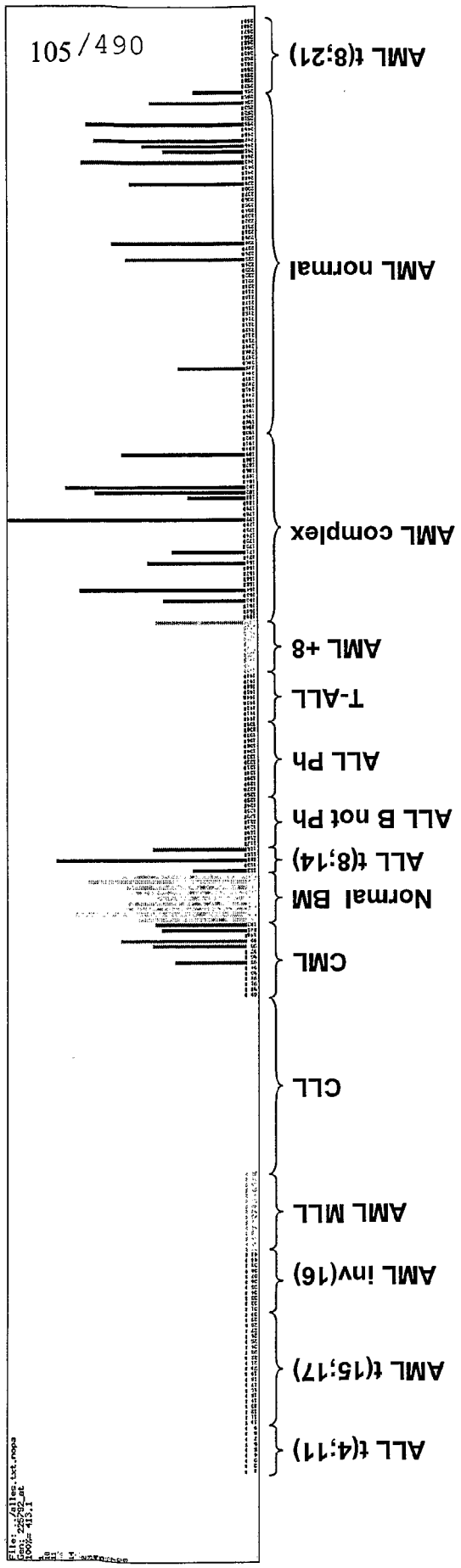

225792_at, AML MLL vs. normal BM
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 79

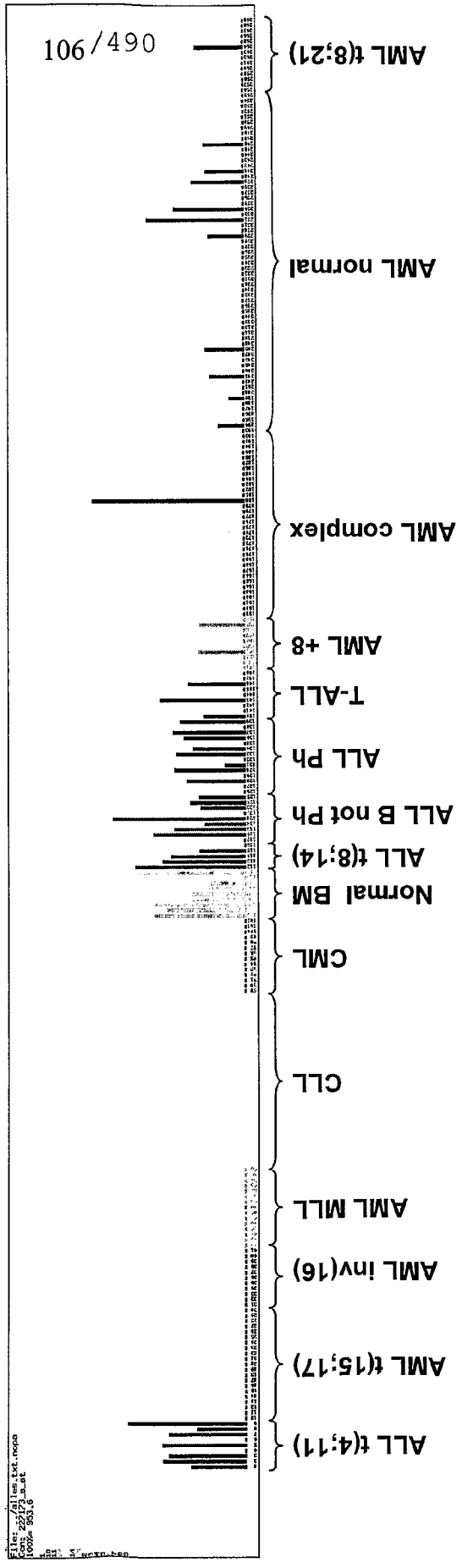

227173_s_at, BACH2, AML MLL vs. ALL t(8;14)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 80

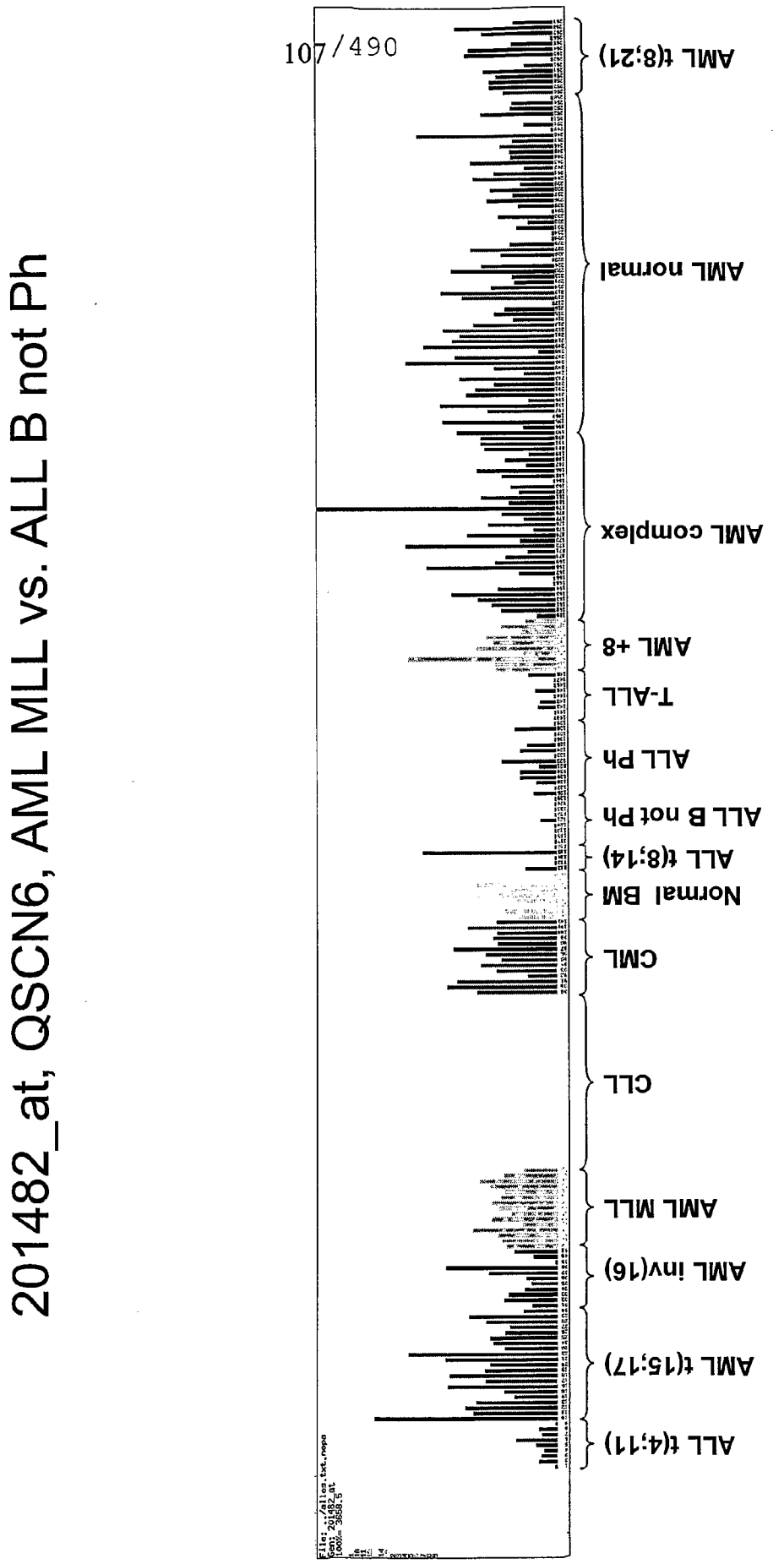

201482_at, QSCN6, AML MLL vs. ALL B not Ph
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 81

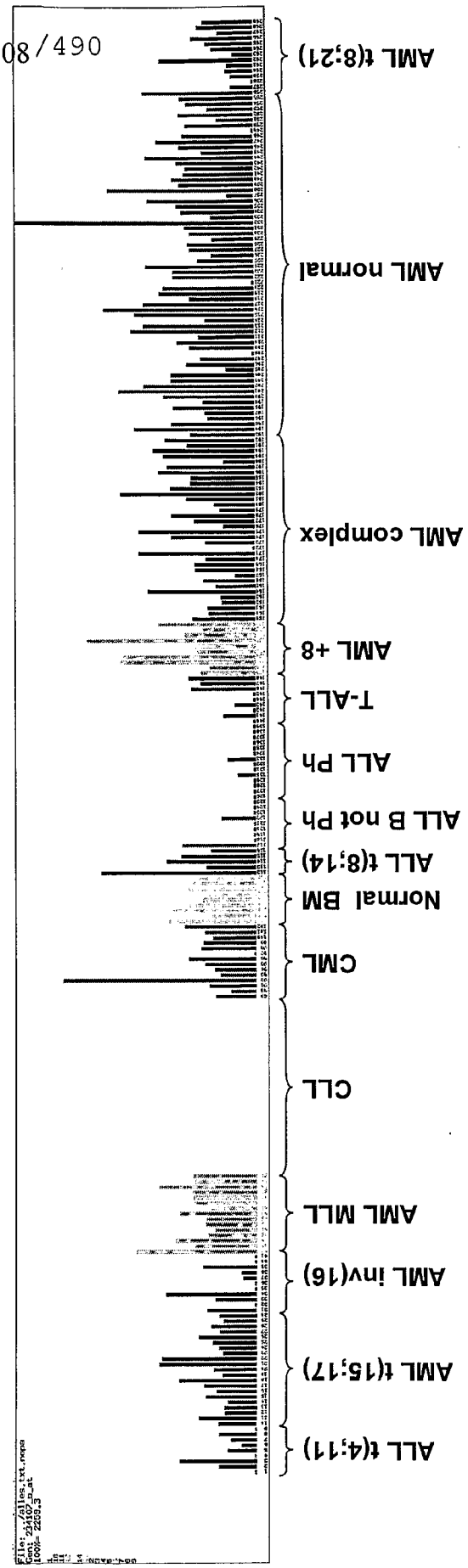

234107_s_at, AML MLL vs. ALL Ph
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 82

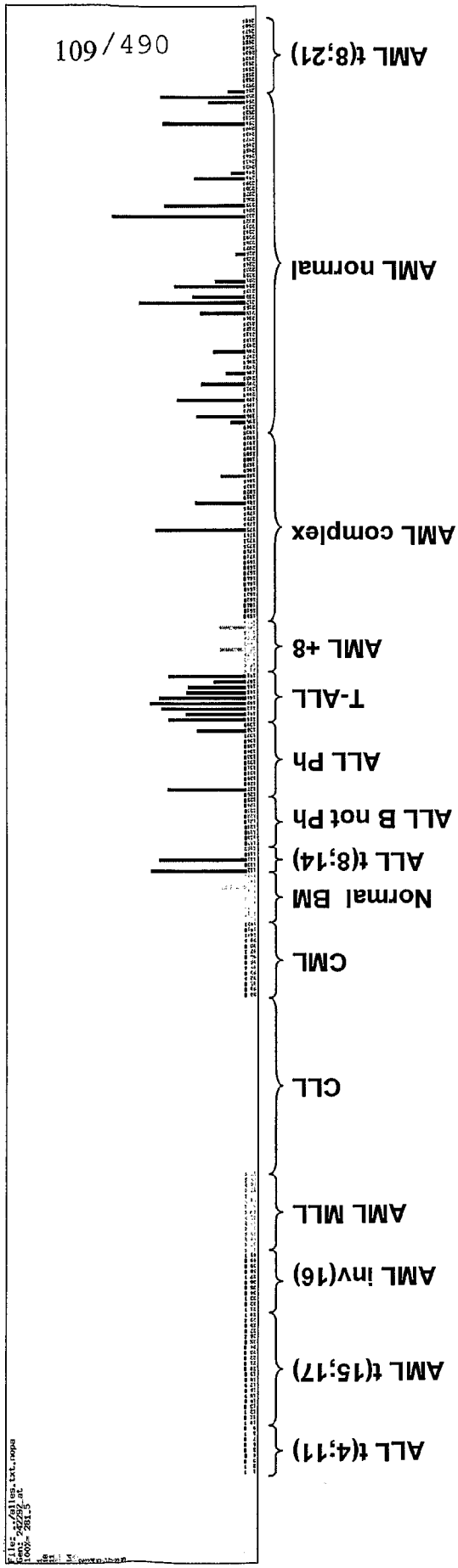

242292_at, AML MLL vs. T-ALL
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 83

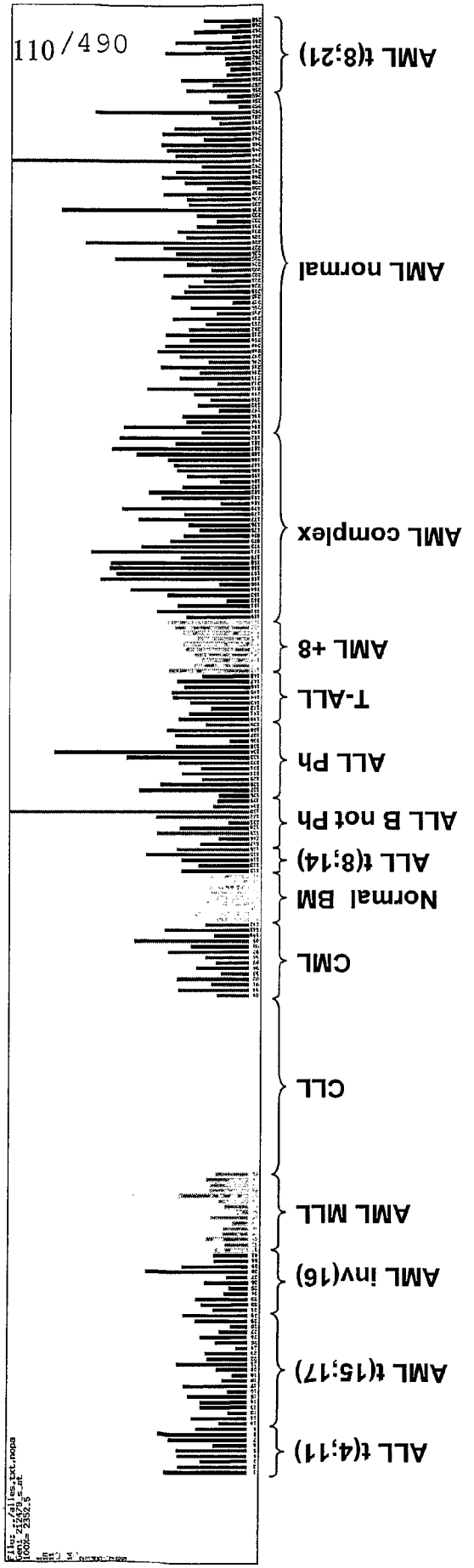

212479_s_at, FLJ13910, AML MLL vs. AML +8
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 84

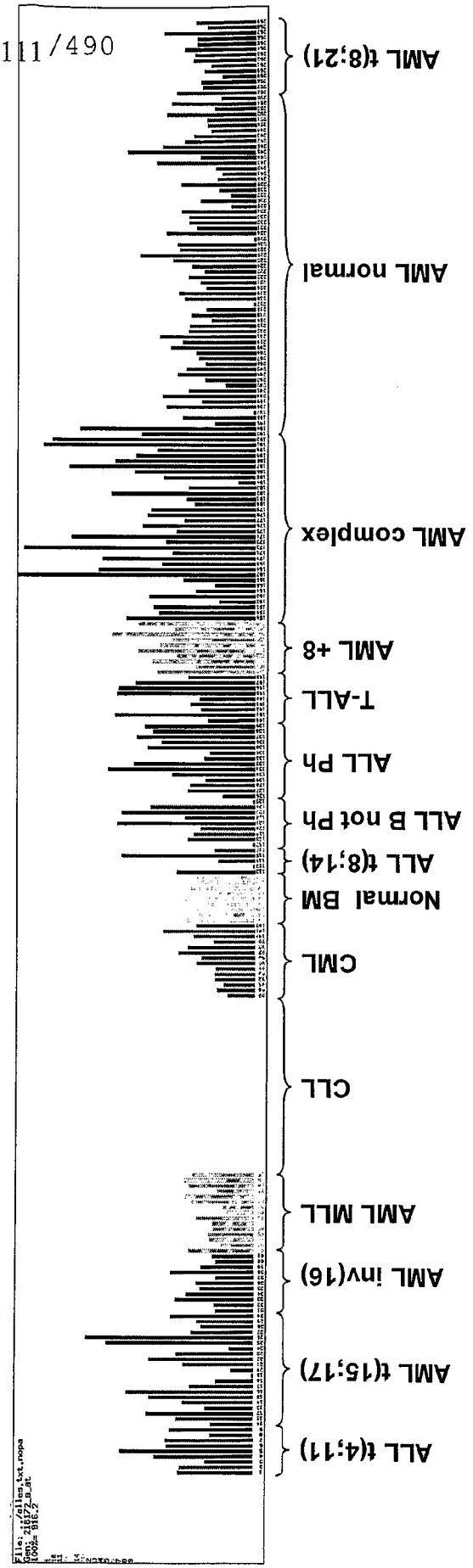

218172_s_at, PRO2577, AML MLL vs. AML +8
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 85

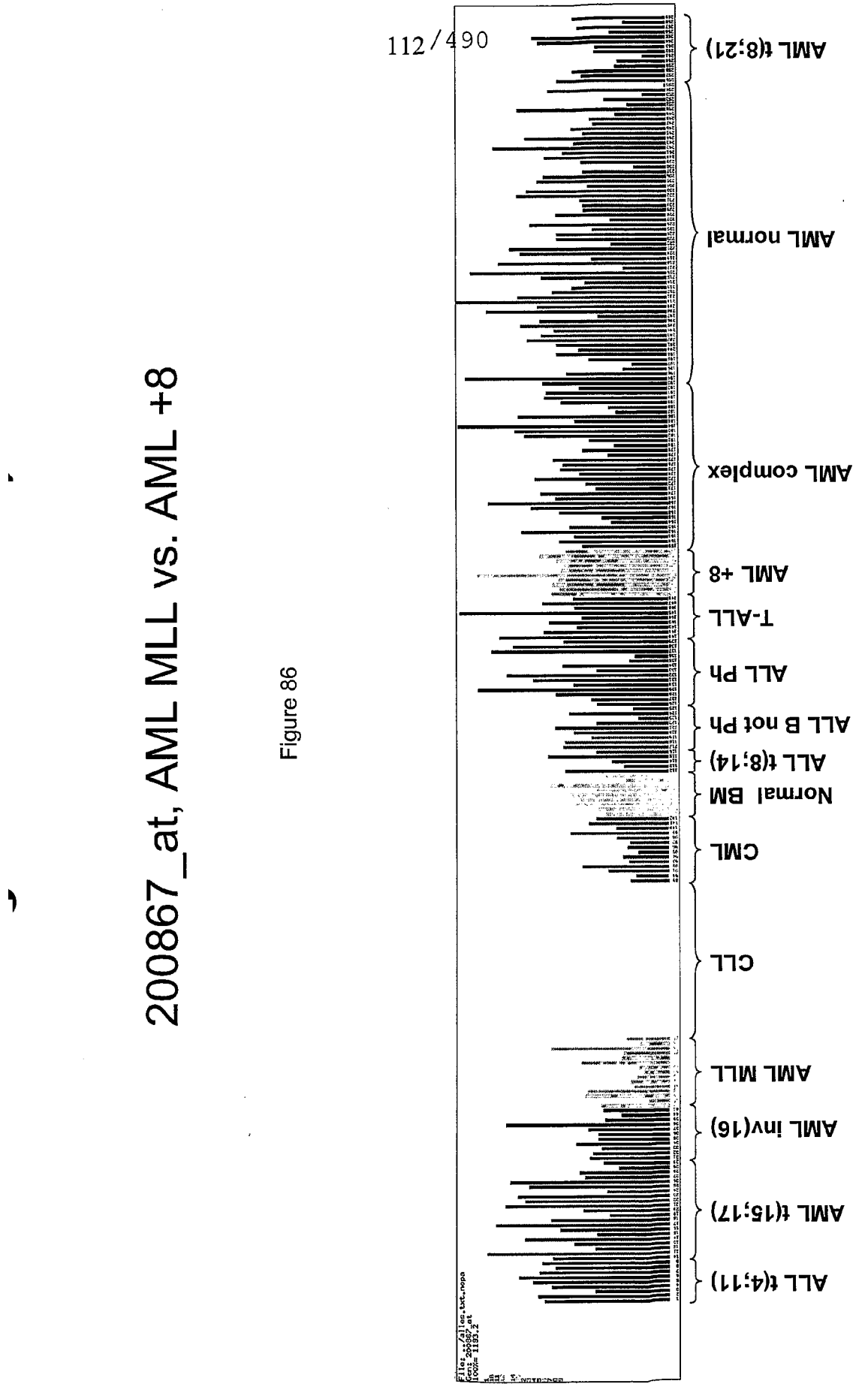

200867_at, AML MLL vs. AML +8
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 86

202956_at, BIG1, AML MLL vs. AML +8

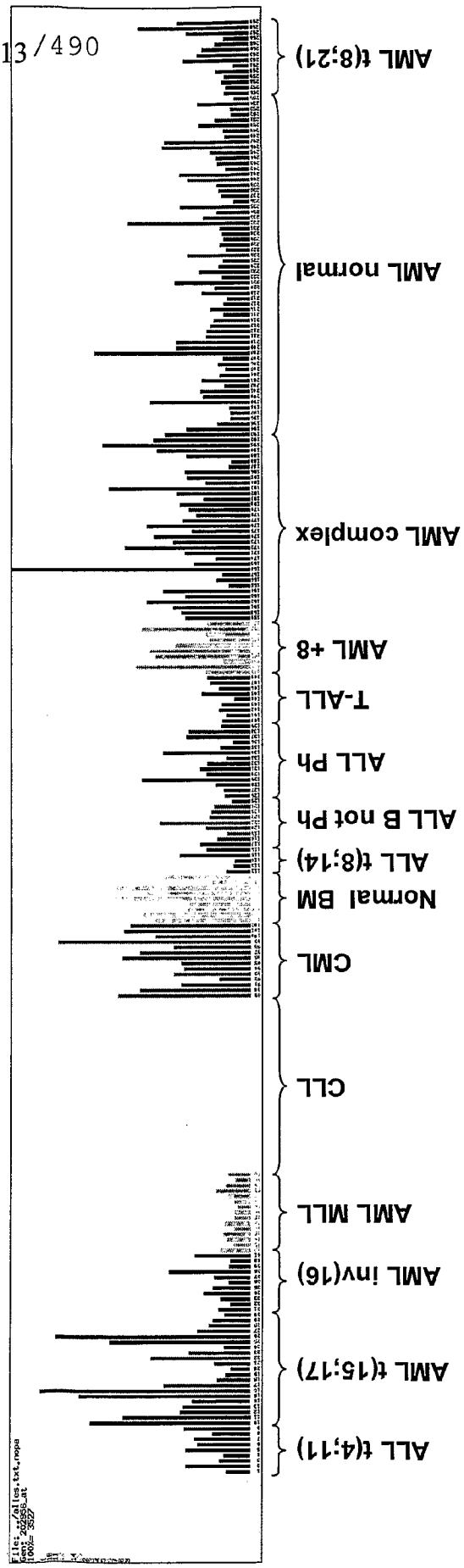


Figure 87

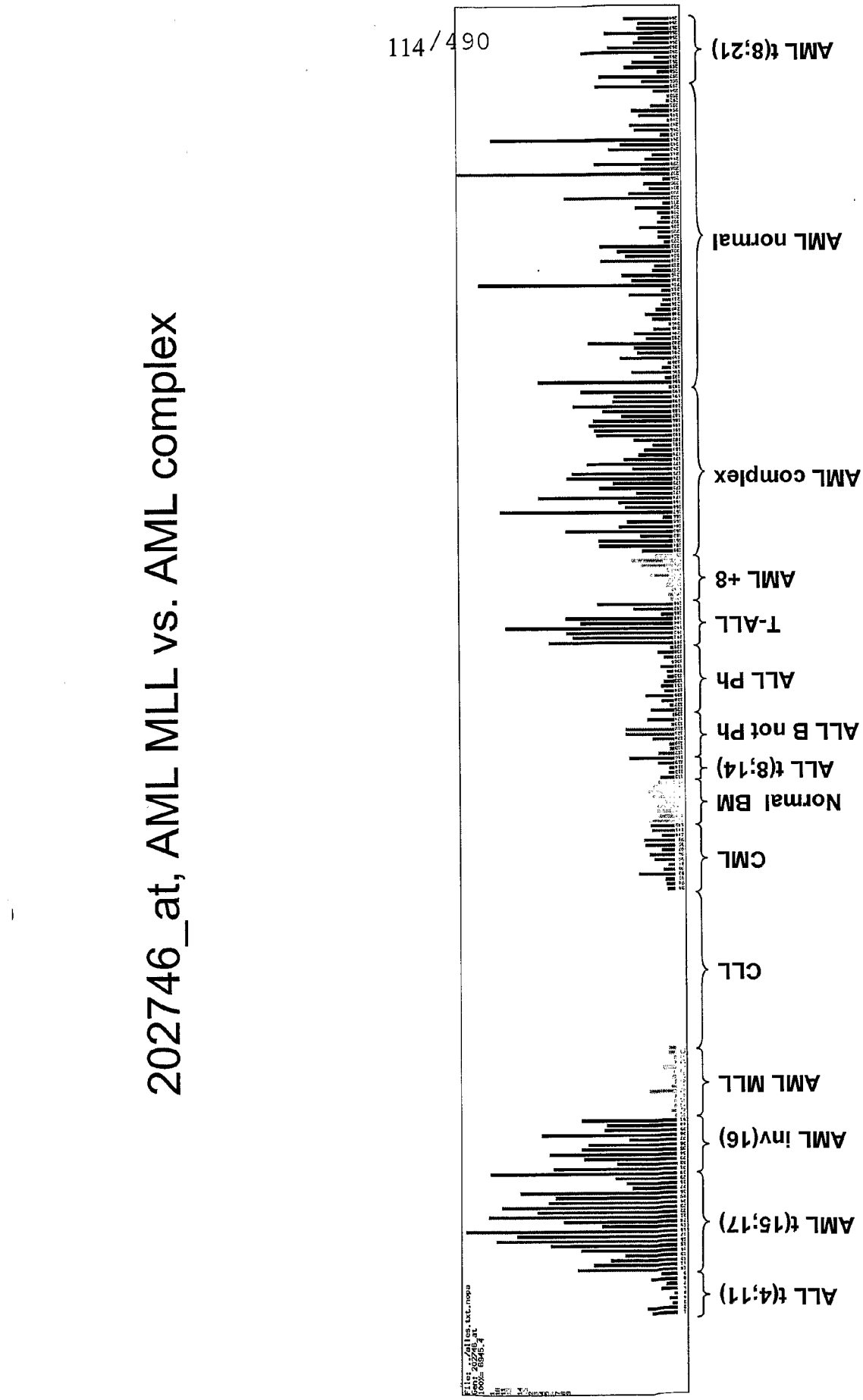

202746_at, AML MLL vs. AML complex
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 88

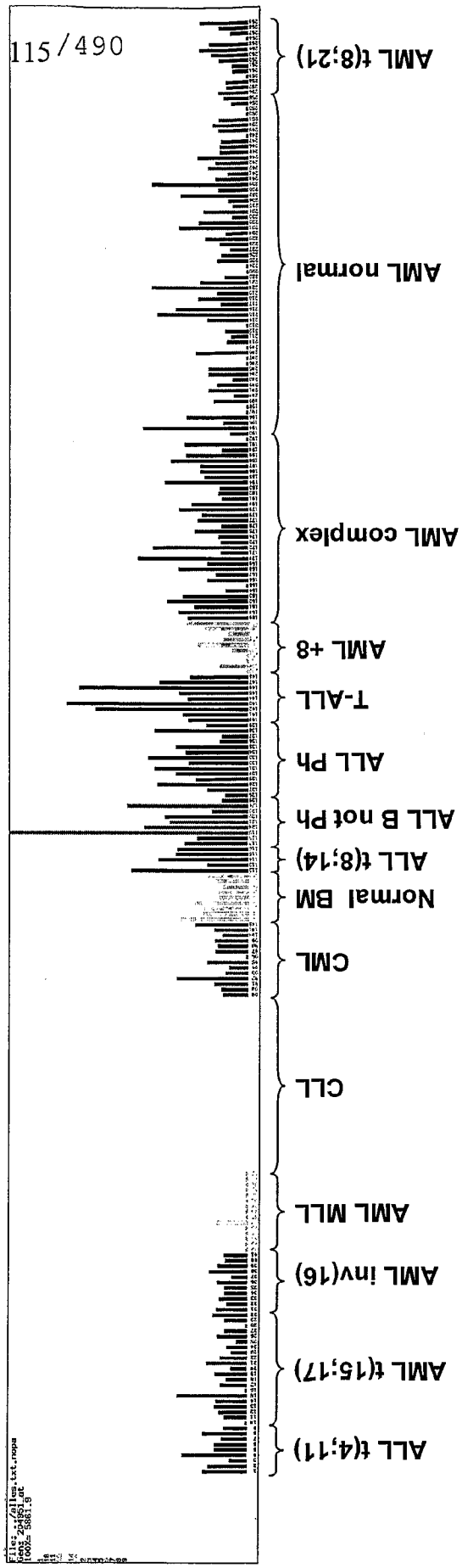

204951_at, ARHH, AML MLL vs. AML complex
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 89

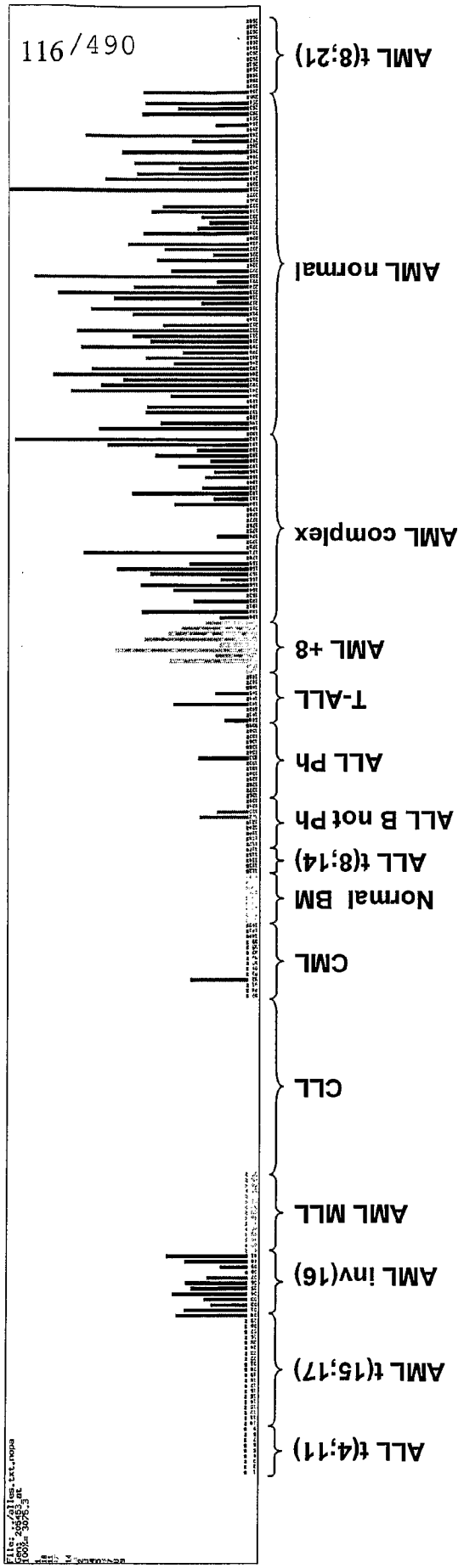

205453_at, HOXB2, AML MLL vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 90

225406_at, TSG, AML MLL vs. AML normal

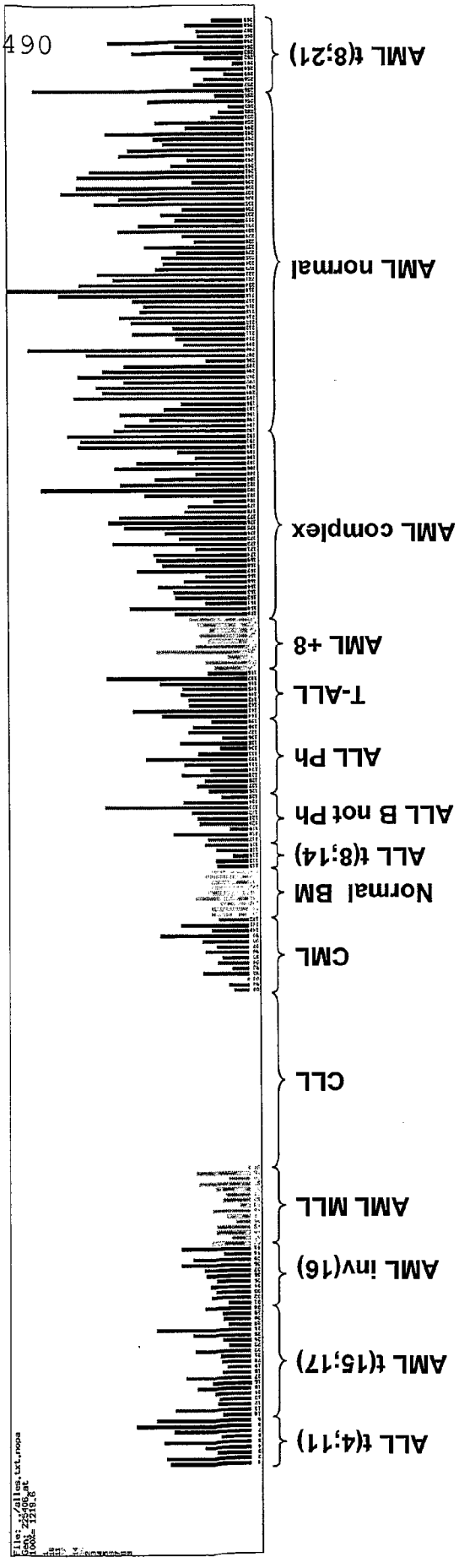


Figure 91

201105_at, LGALS1, AML MLL vs. AML t(8;21)

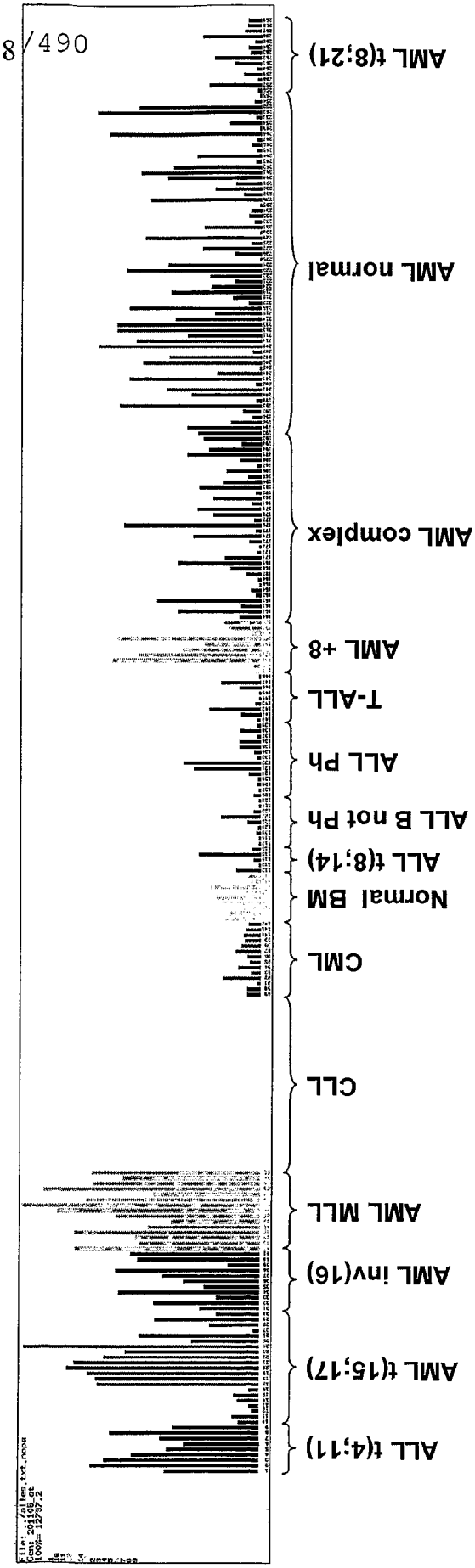


Figure 92

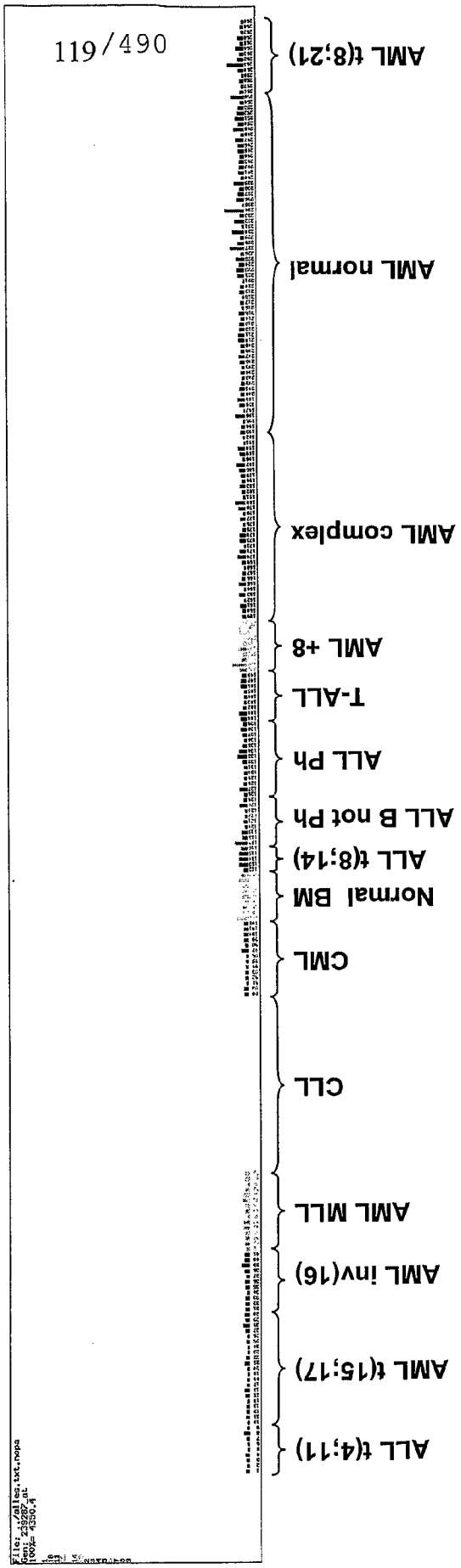

239287_at, CLL vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 93

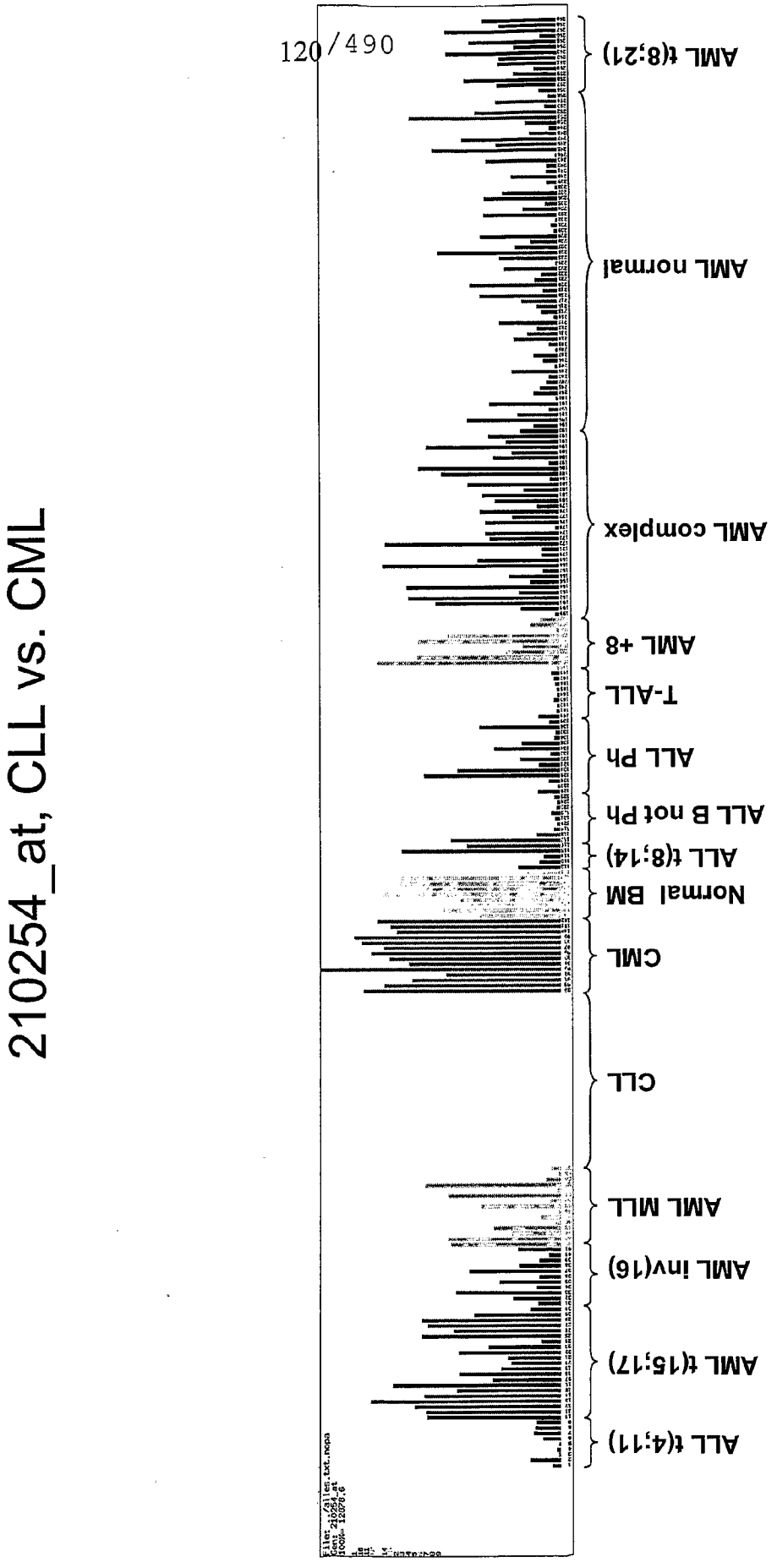

210254_at, CLL vs. CML
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 94

204776_at, THBS4, CLL vs. normal BM

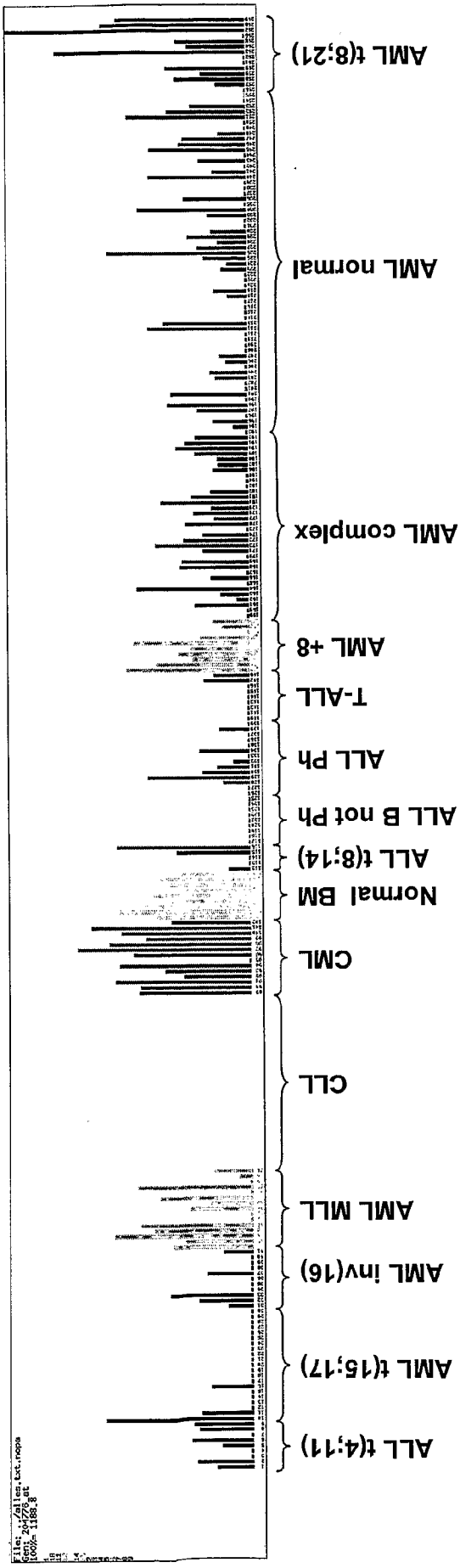


Figure 95

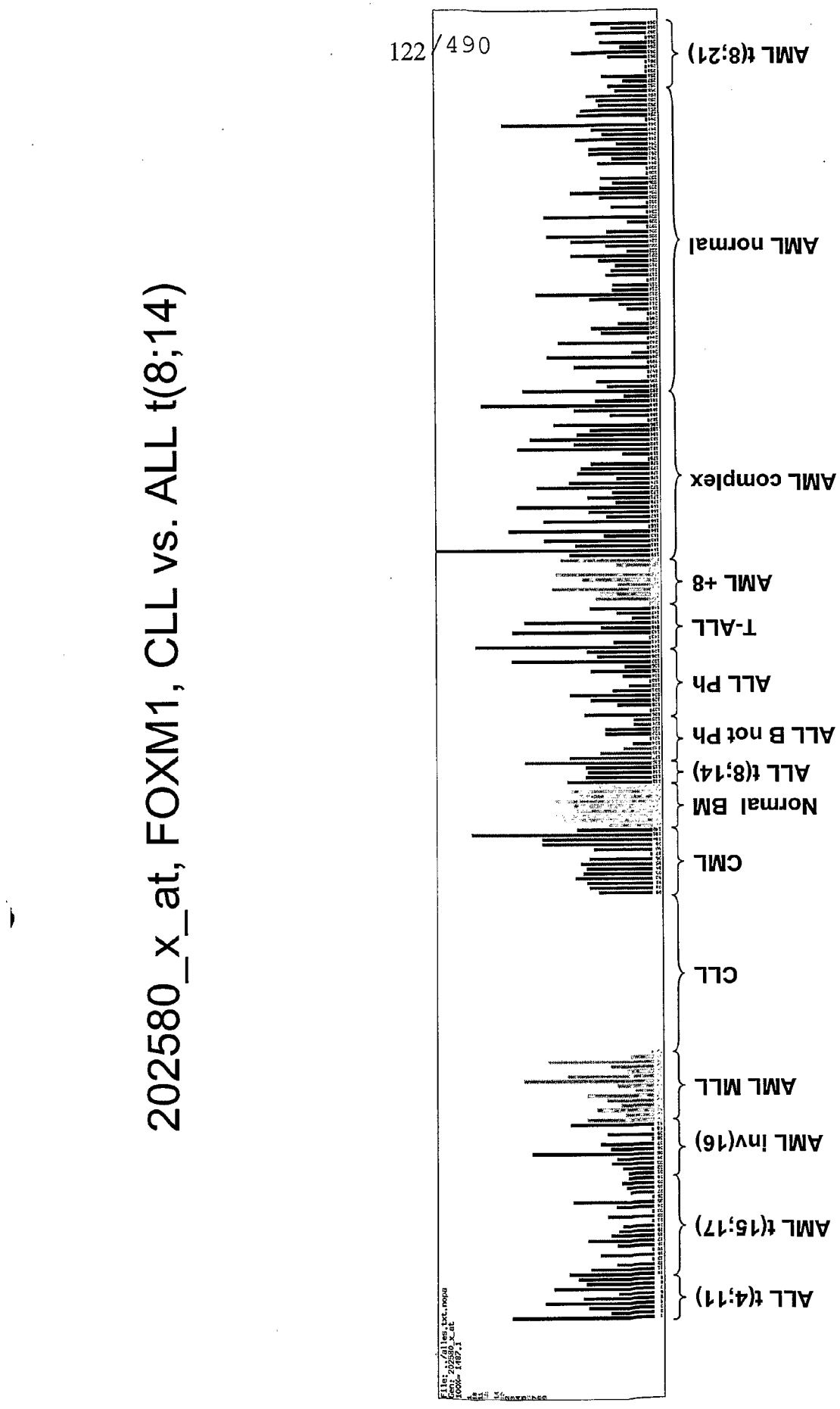

202580_x_at, FOXM1, CLL vs. ALL t(8;14)
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 96

225927_at, MAP3K1, CLL vs. ALL B not Ph

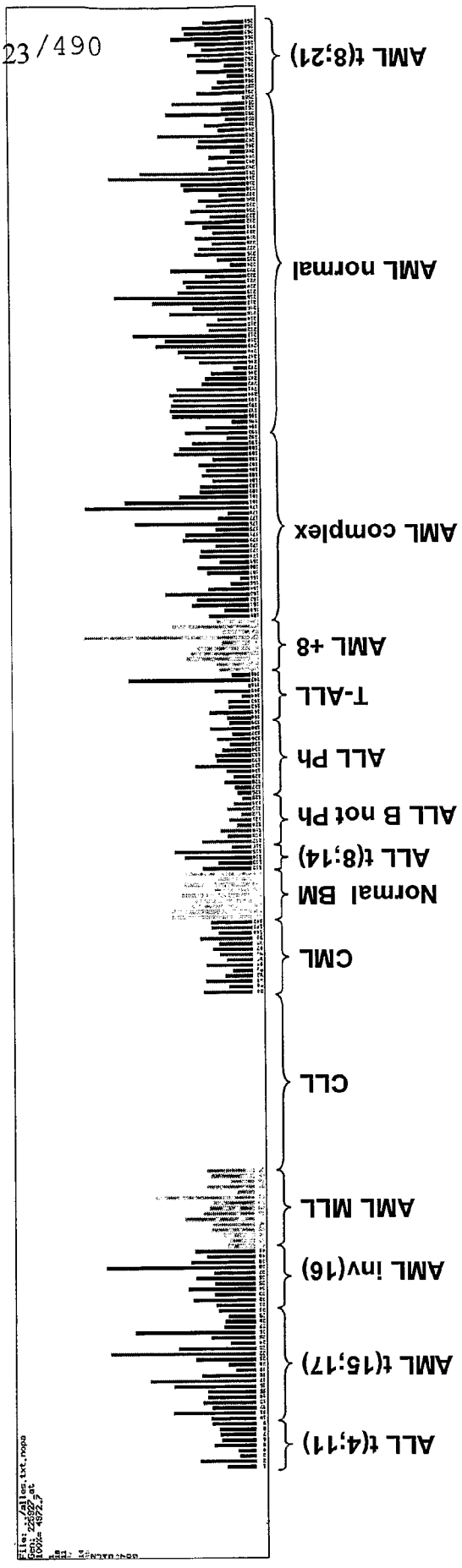


Figure 97

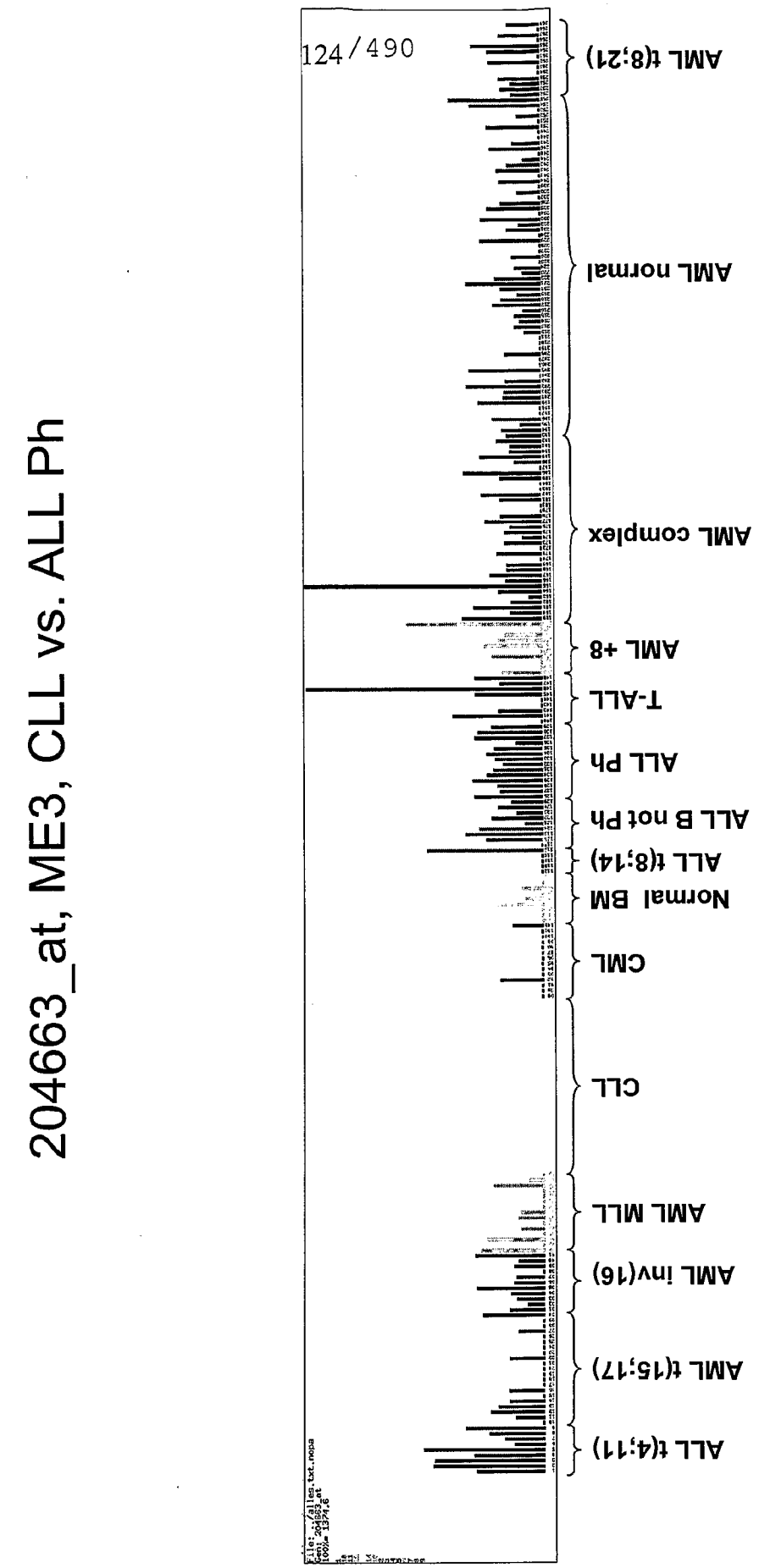

204663_at, ME3, CLL vs. ALL Ph
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 98

201417_at, CLL vs. T-ALL

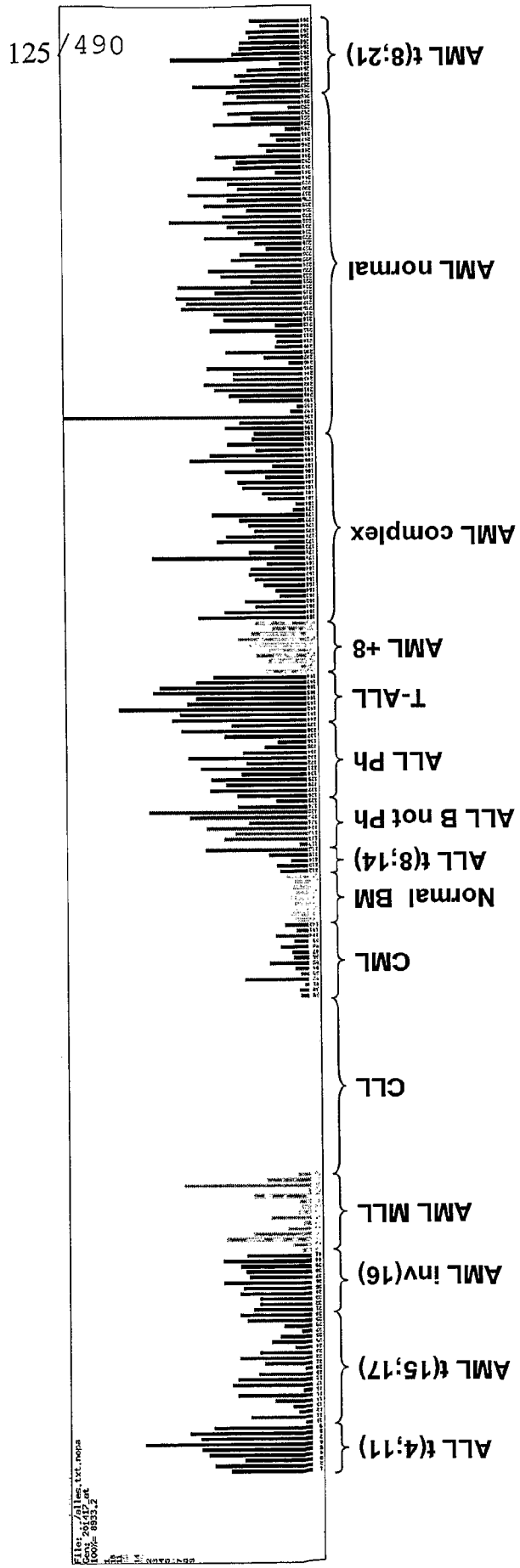


Figure 99

204215_at, MGC4175, CLL vs. AML +8

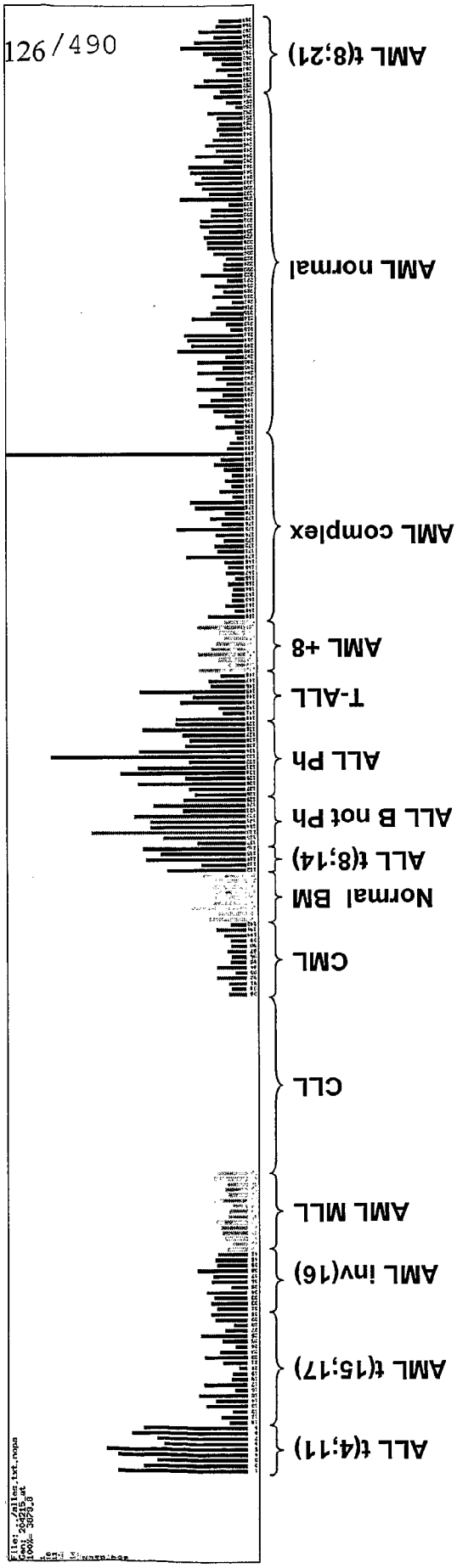
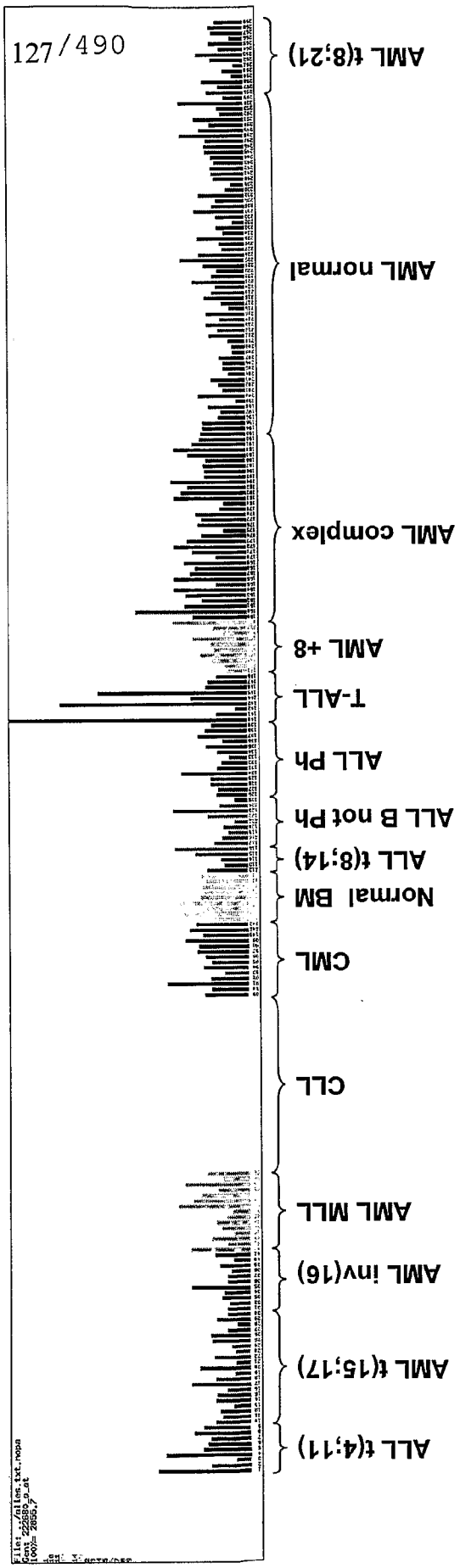


Figure 100



222680_s_at, RAMP, CLL vs. AML complex

Figure 101

224838_at, CLL vs. AML normal

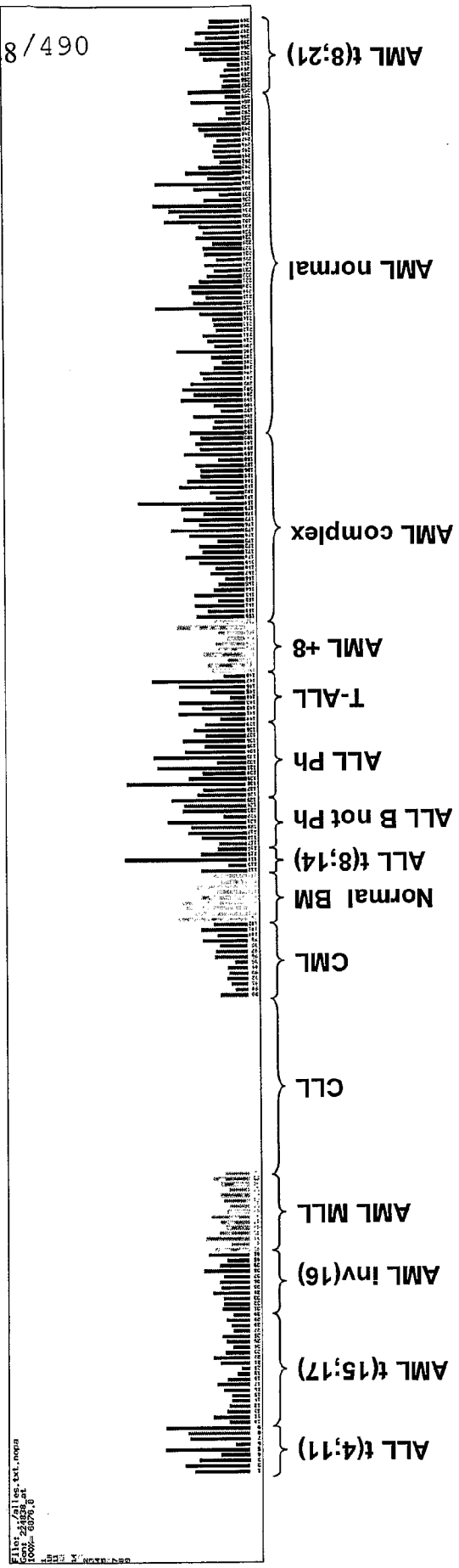


Figure 102

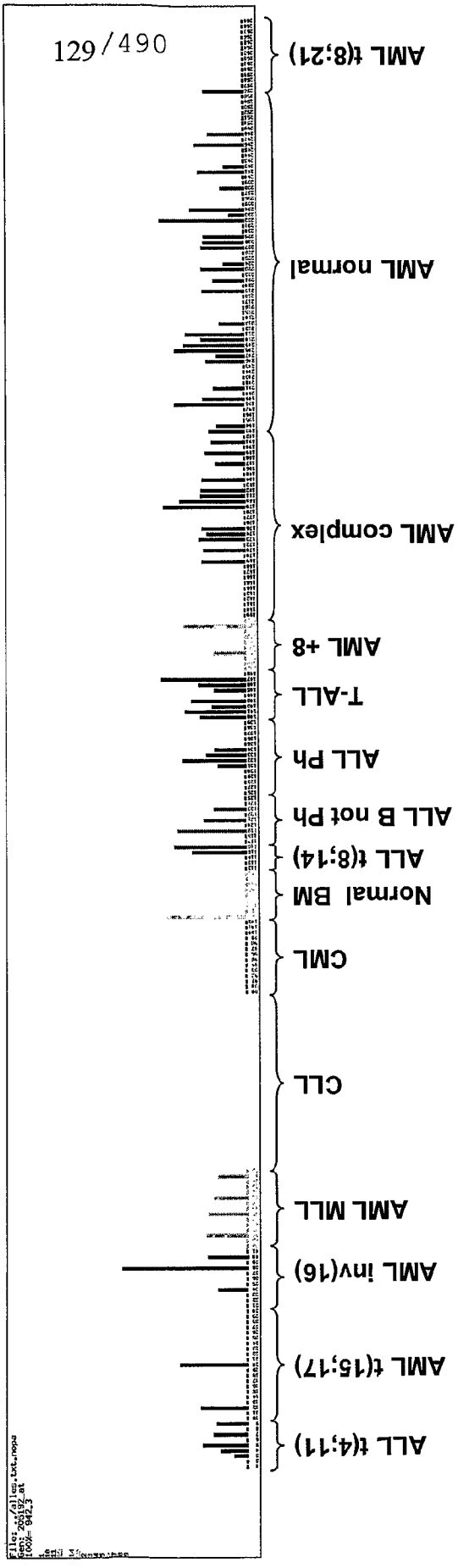

205192_at, MAP3K14, CLL vs. AML t(8;21)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 103

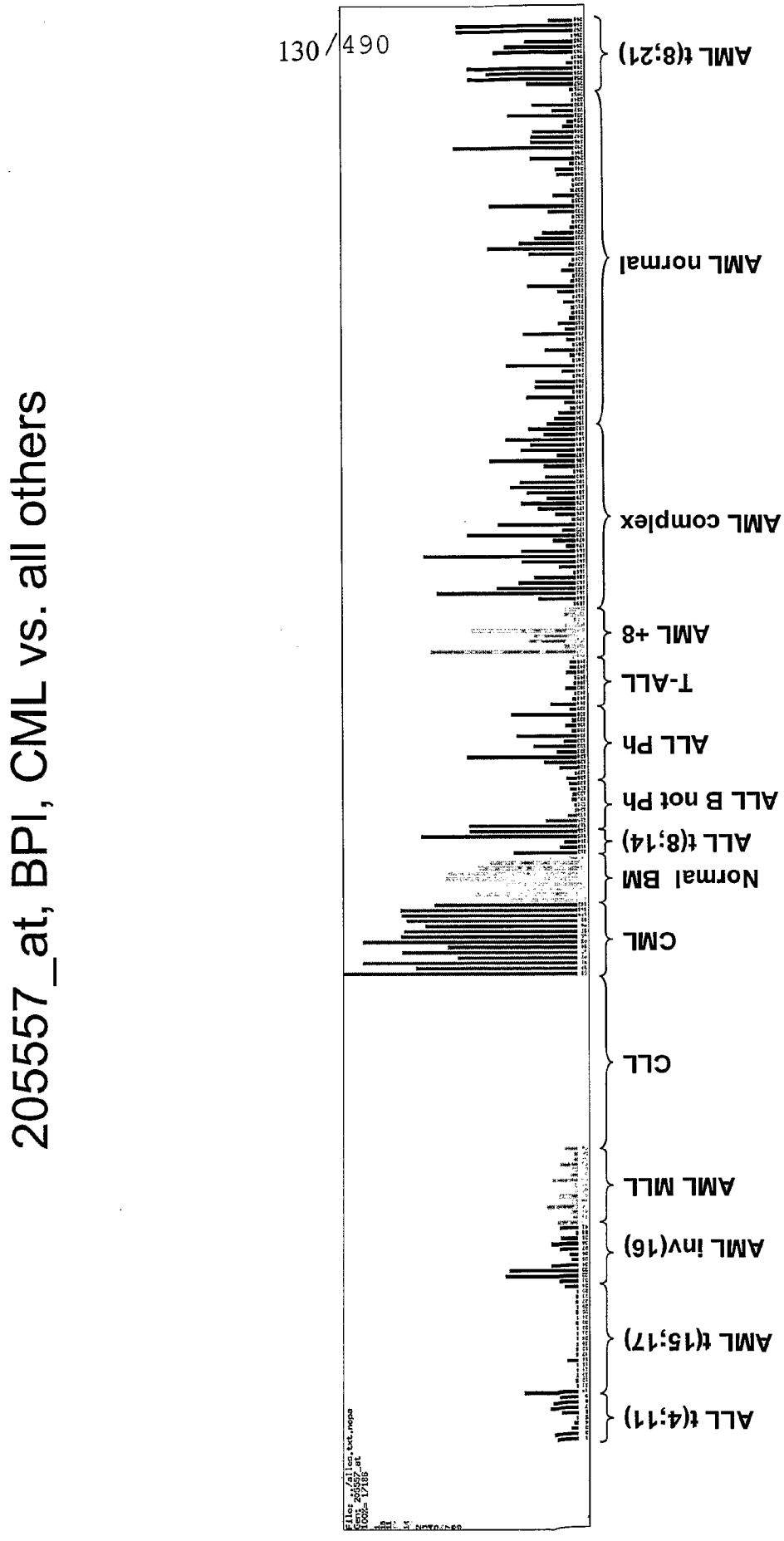

205557_at, BPI, CML vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 104

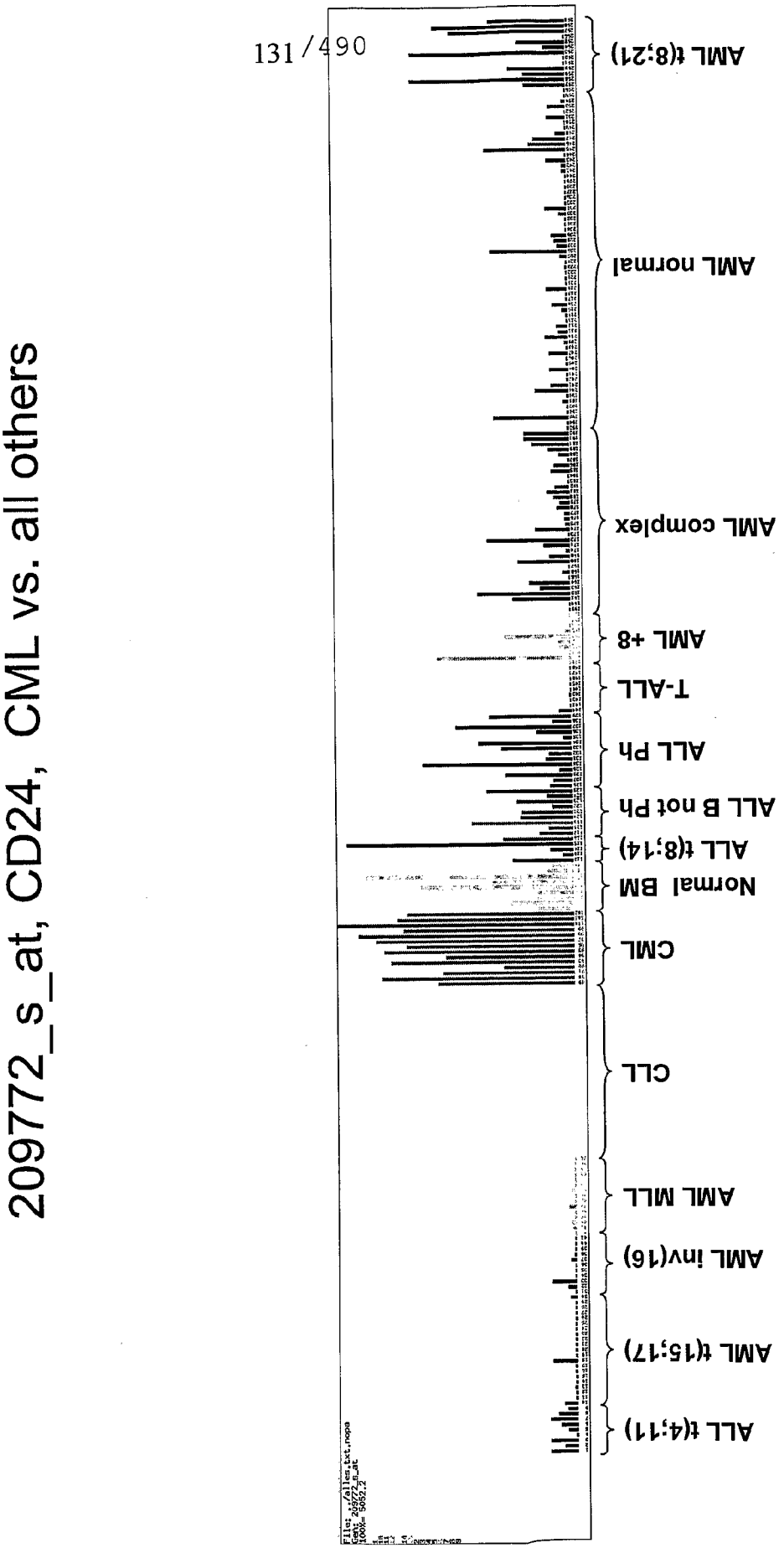

209772_s_at, CD24, CML vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 105

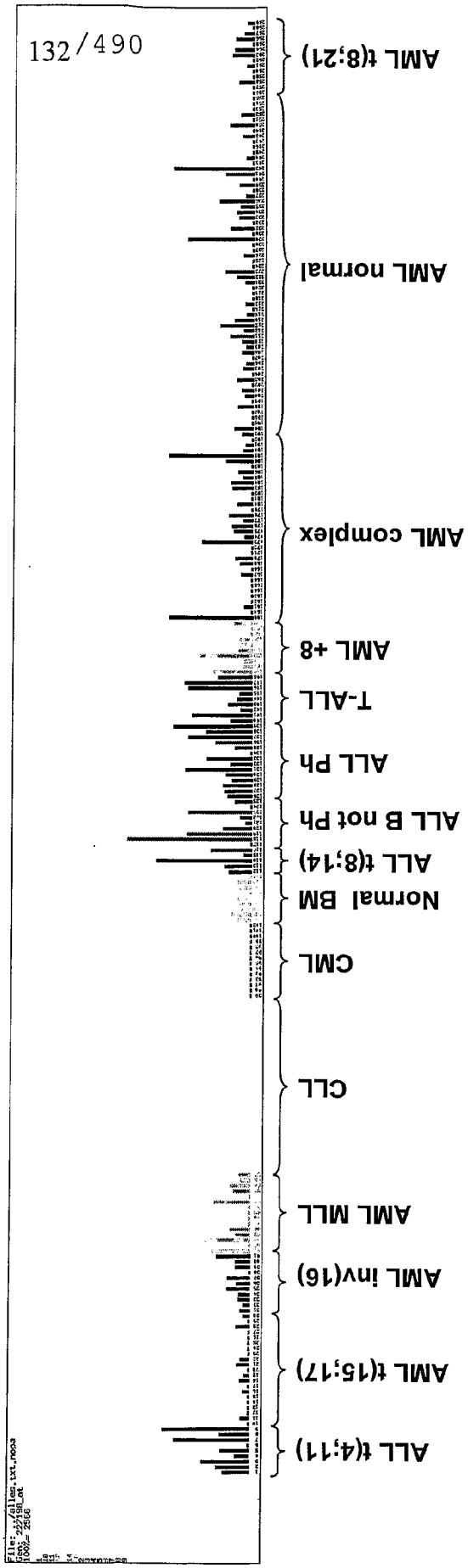

227198_at, CML vs. normal BM
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 106

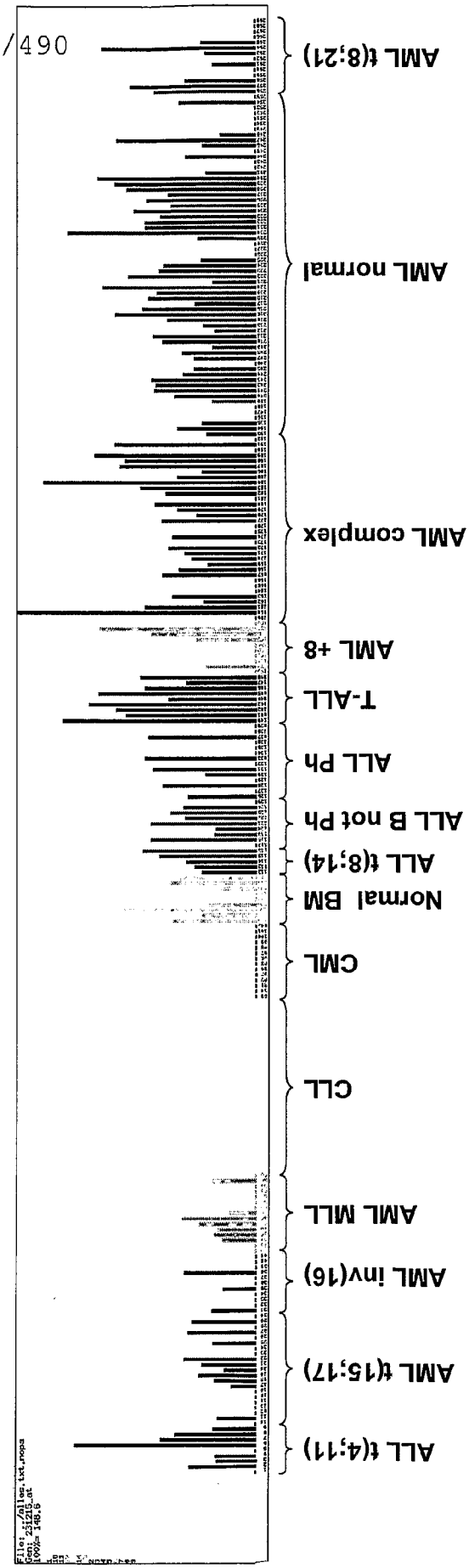

231215_at, CML vs. ALL t(8;14)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 107

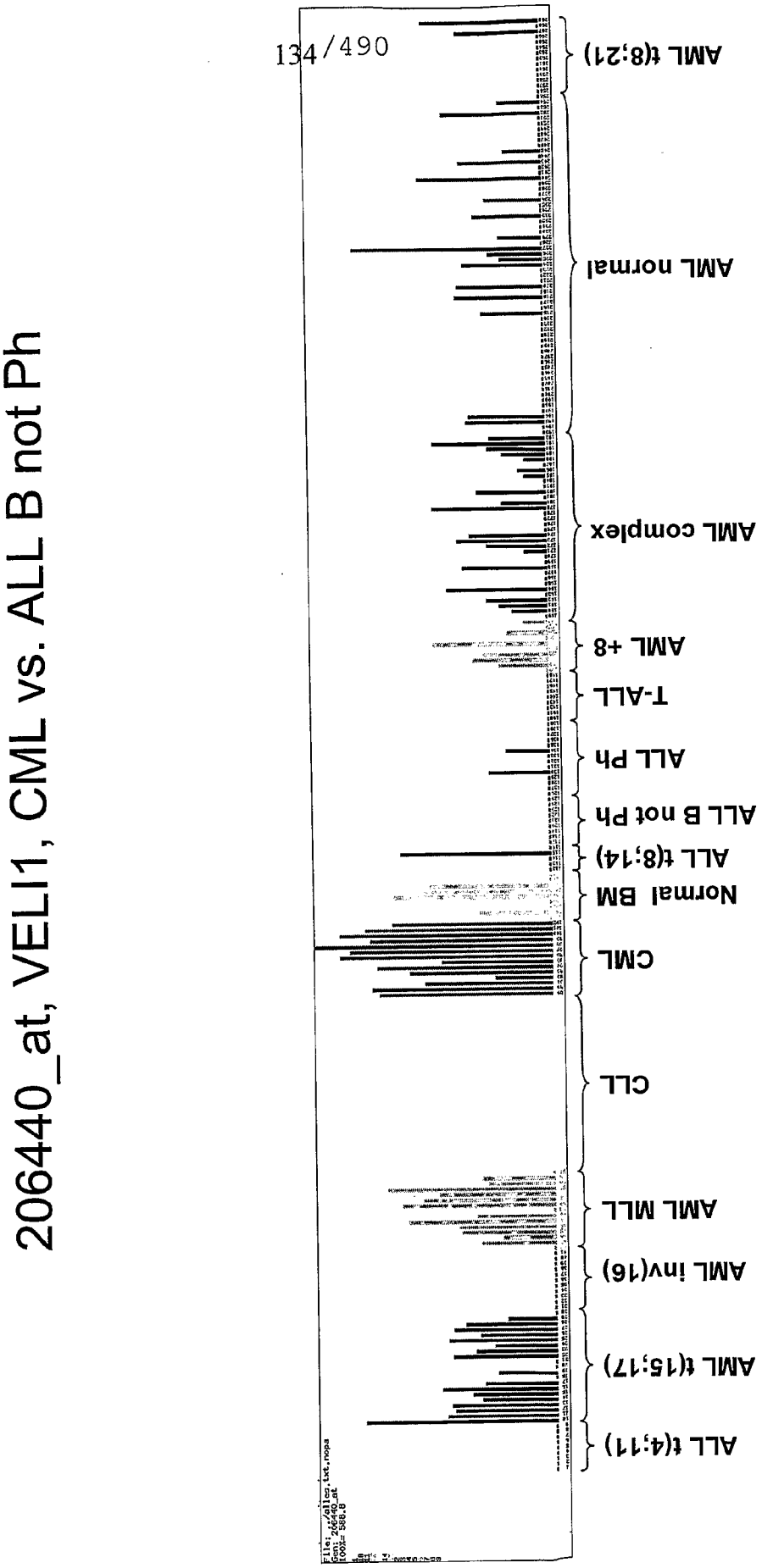

206440_at, VELI1, CML vs. ALL B not Ph
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 108

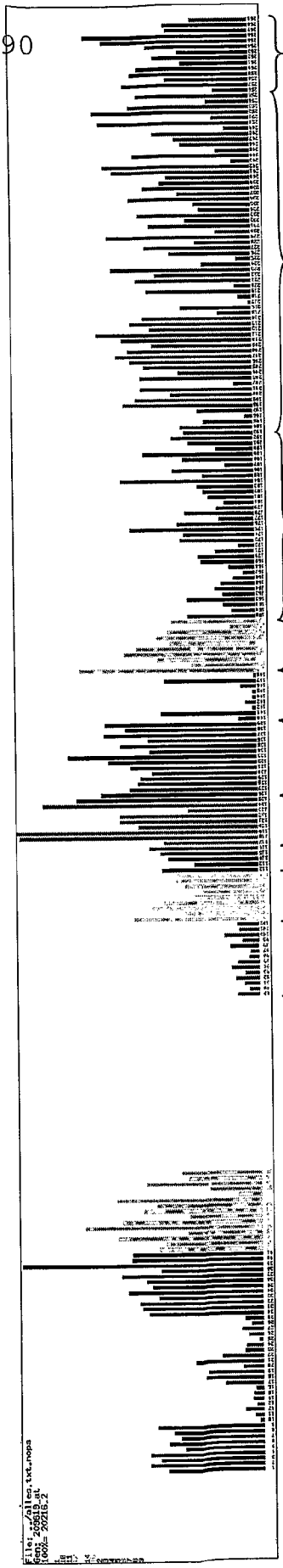

209619_at, CD74, CML vs. ALL Ph
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 109

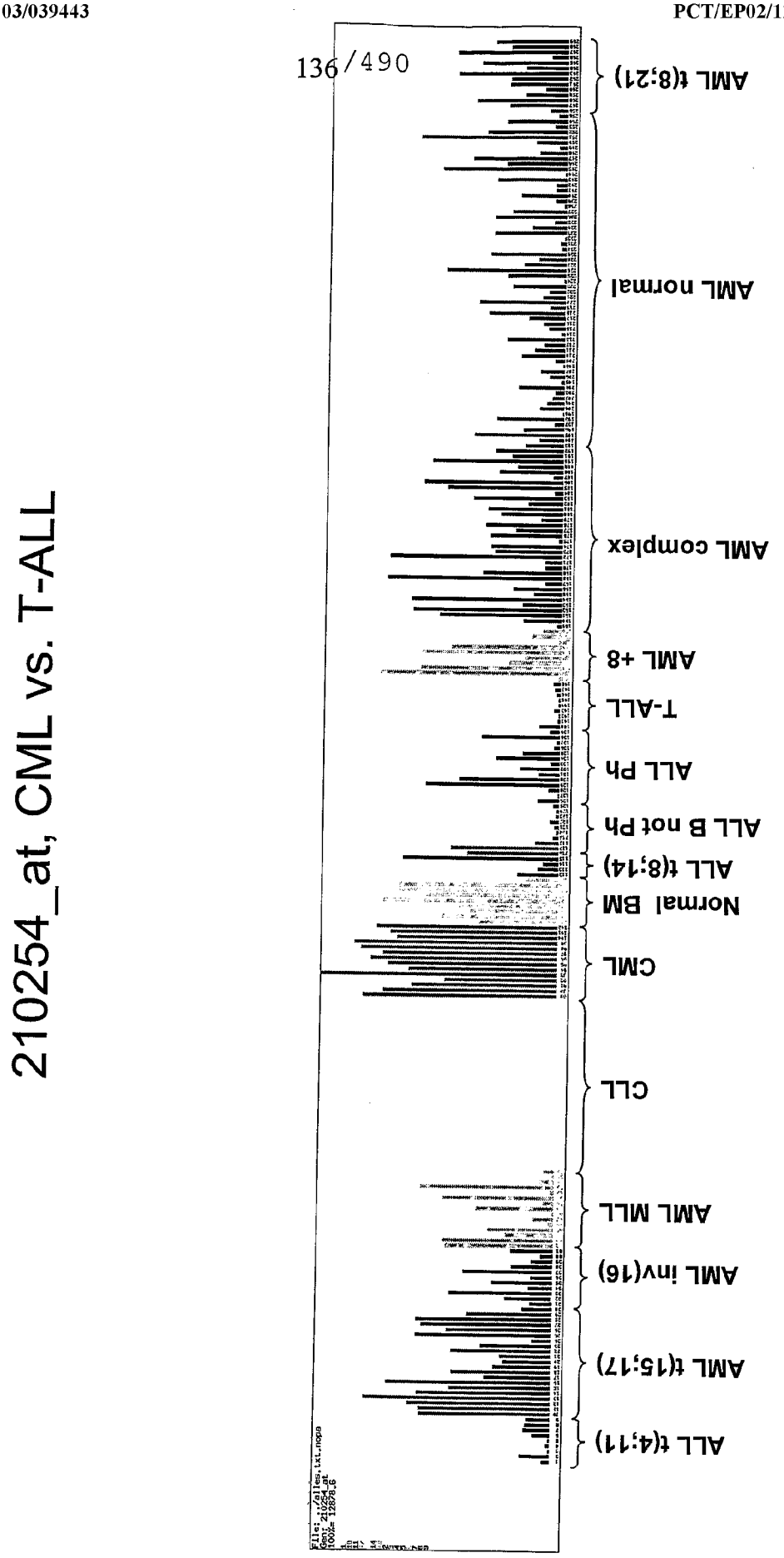

210254_at, CML vs. T-ALL
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 110

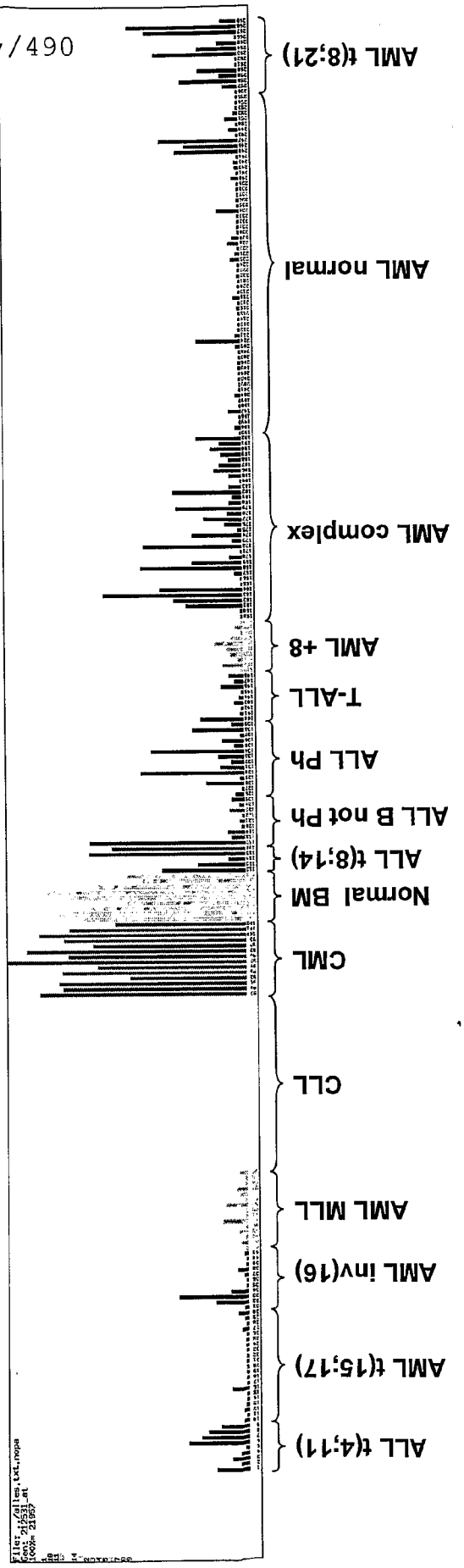

212531_at, LCN2, CML vs. AML +8
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 111

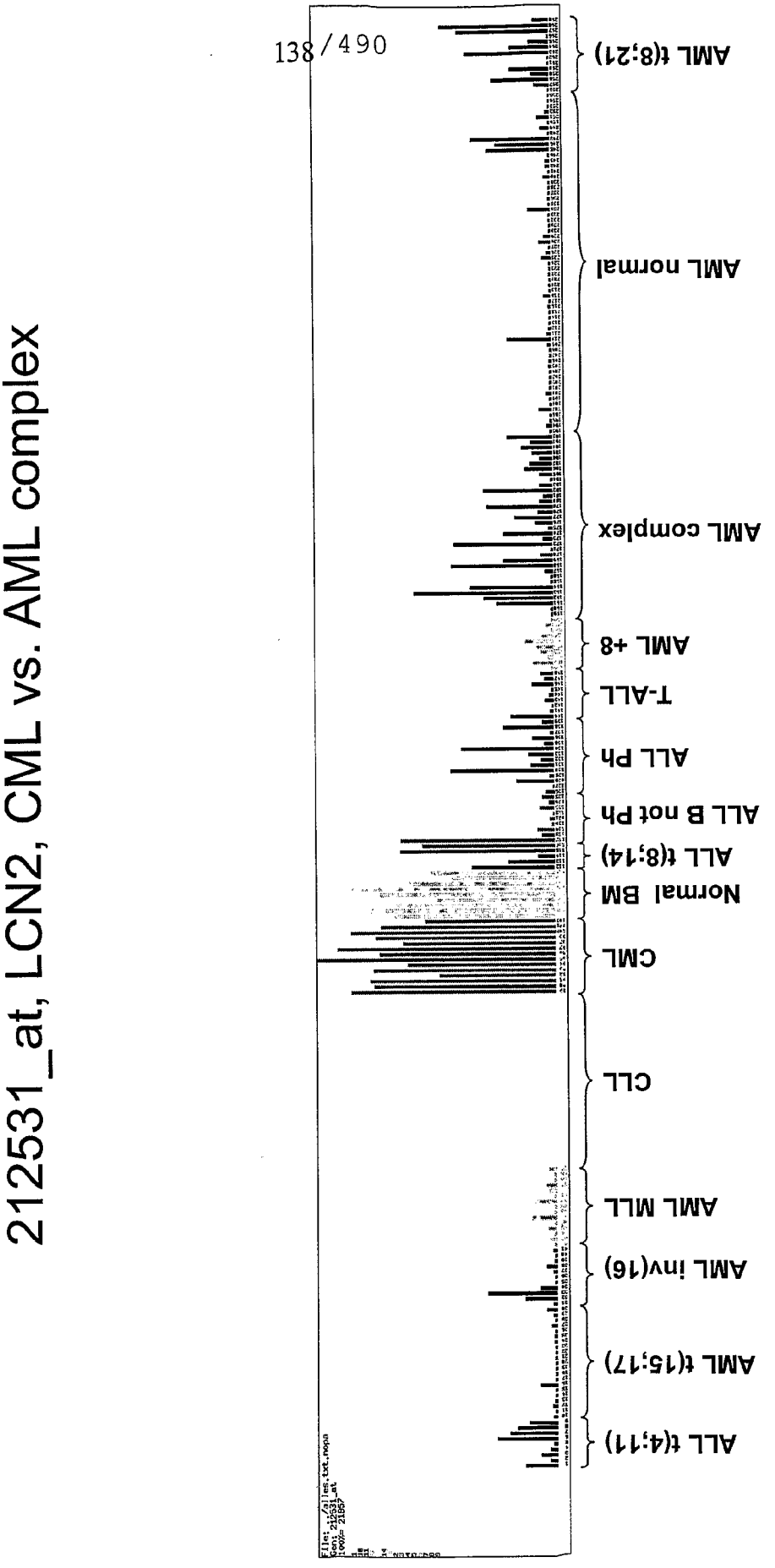

212531_at, LCN2, CML vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 112

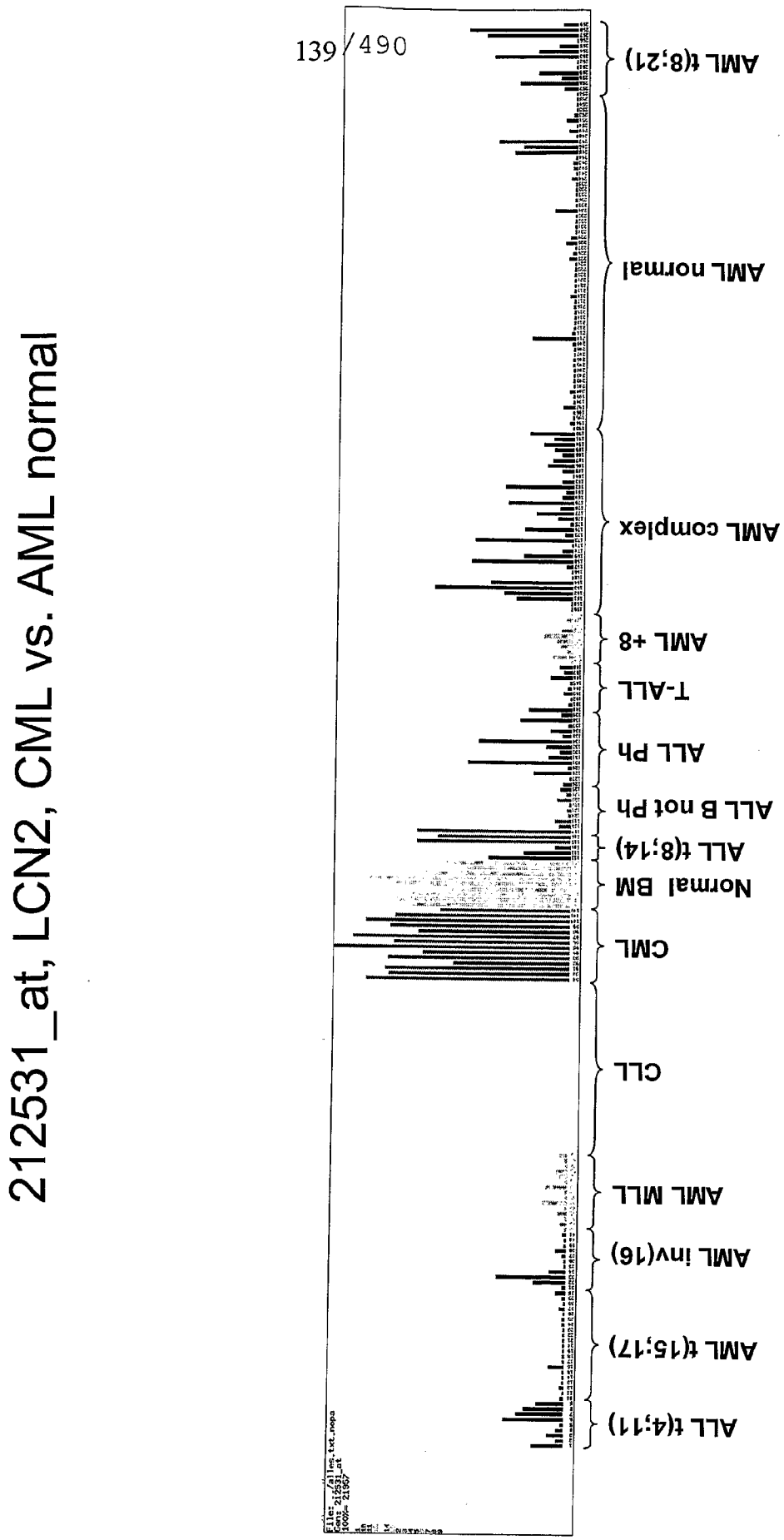

212531_at, LCN2, CML vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 113

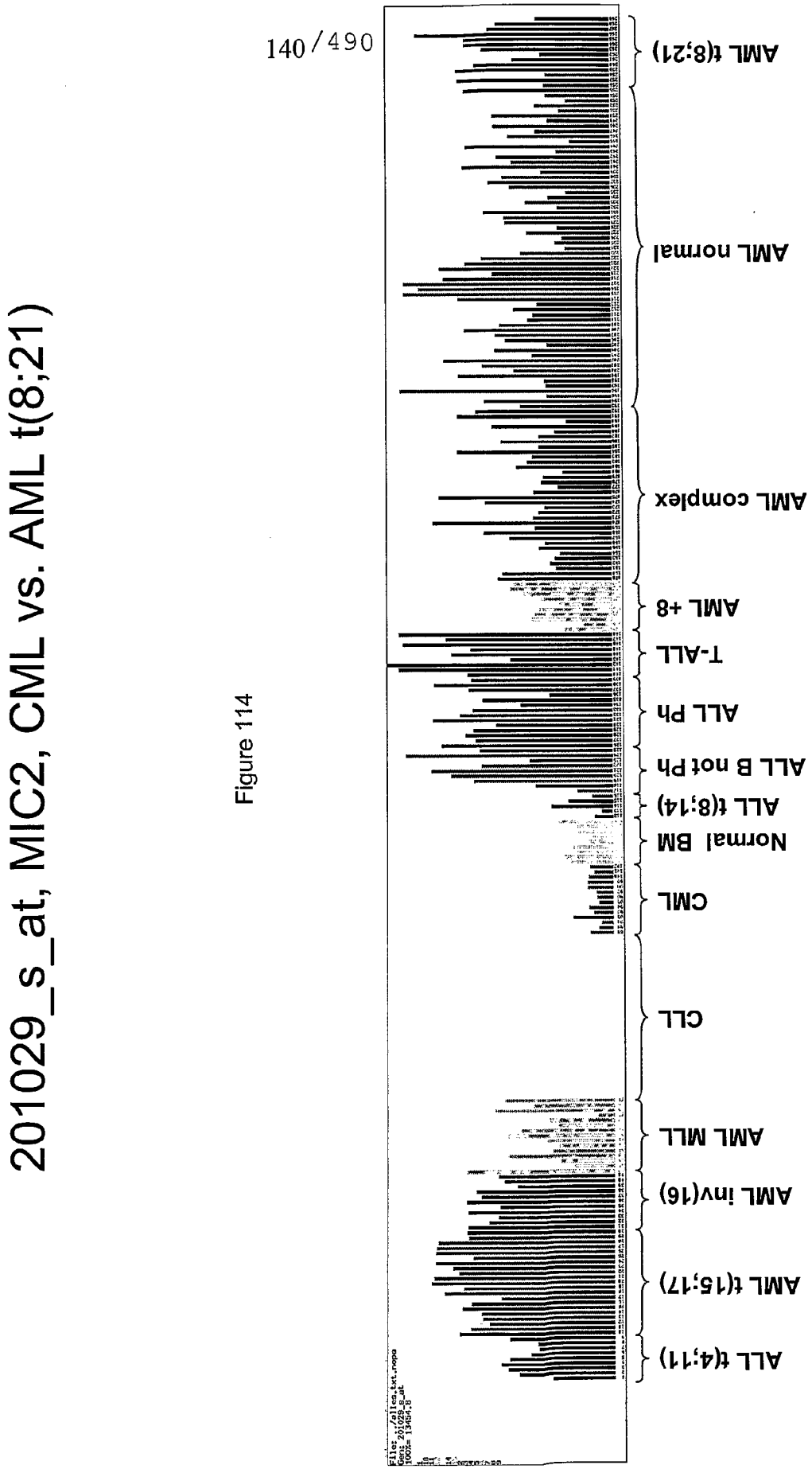

201029_s_at, MIC2, CML vs. AML t(8;21)
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 114

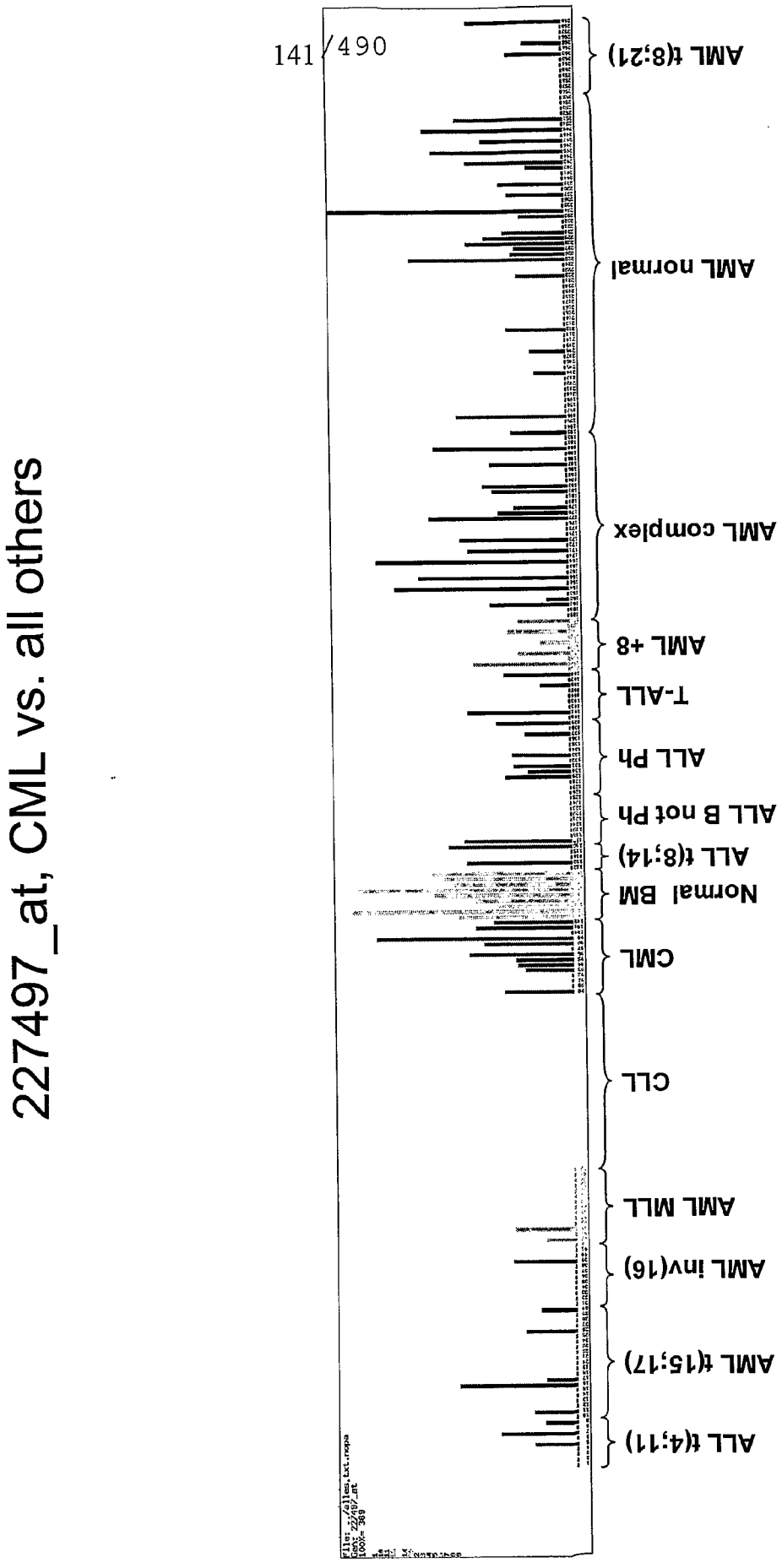

227497_at, CML vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 115

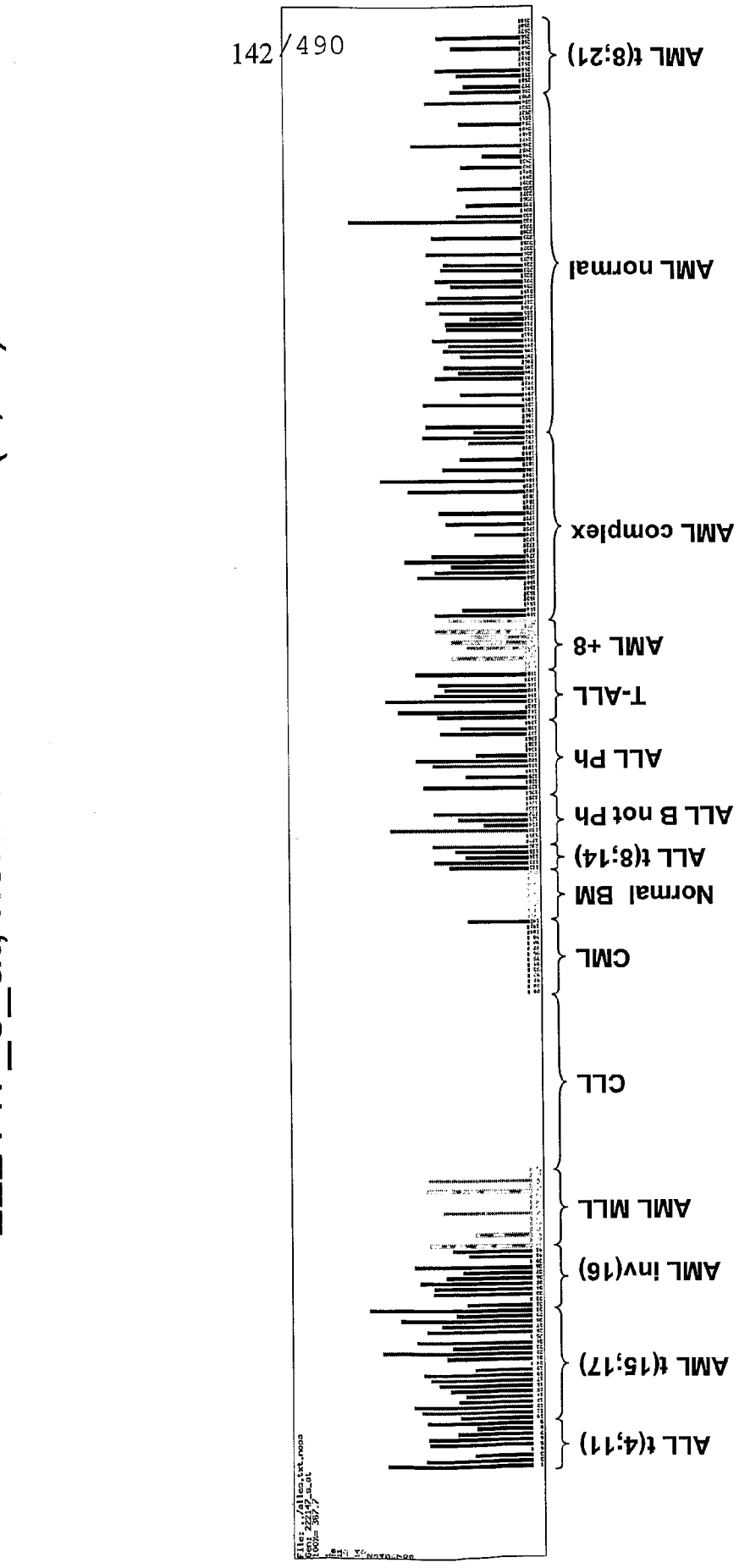

222147_s_at, normal BM vs. ALL t(8;14)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 116

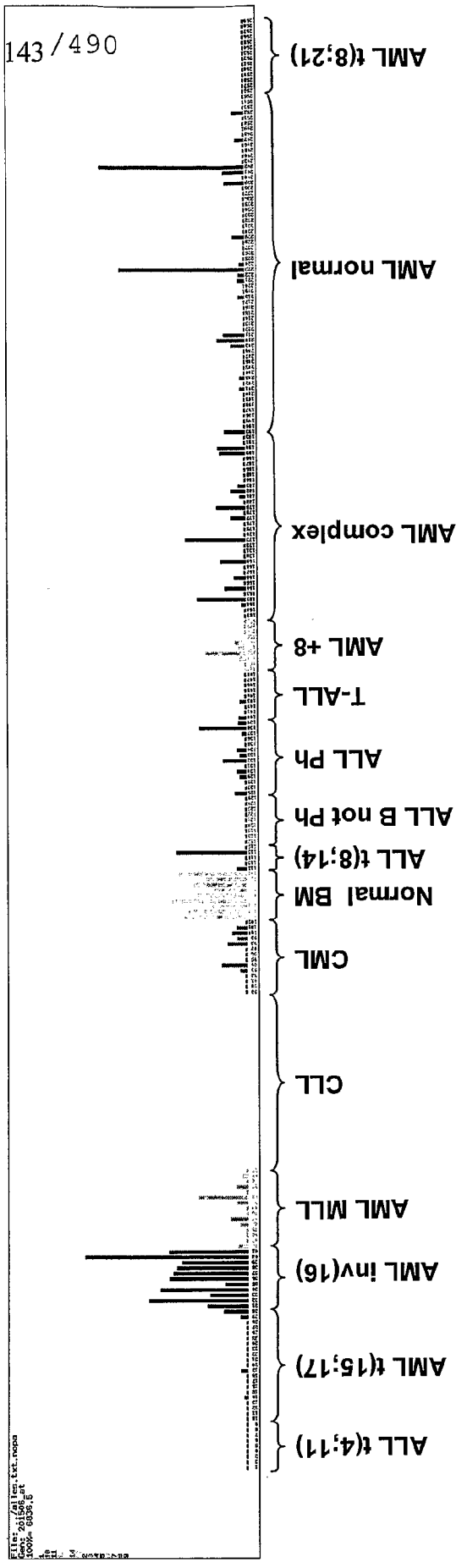

201506_at, TGFBI, normal BM vs. ALL B not Ph
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 117

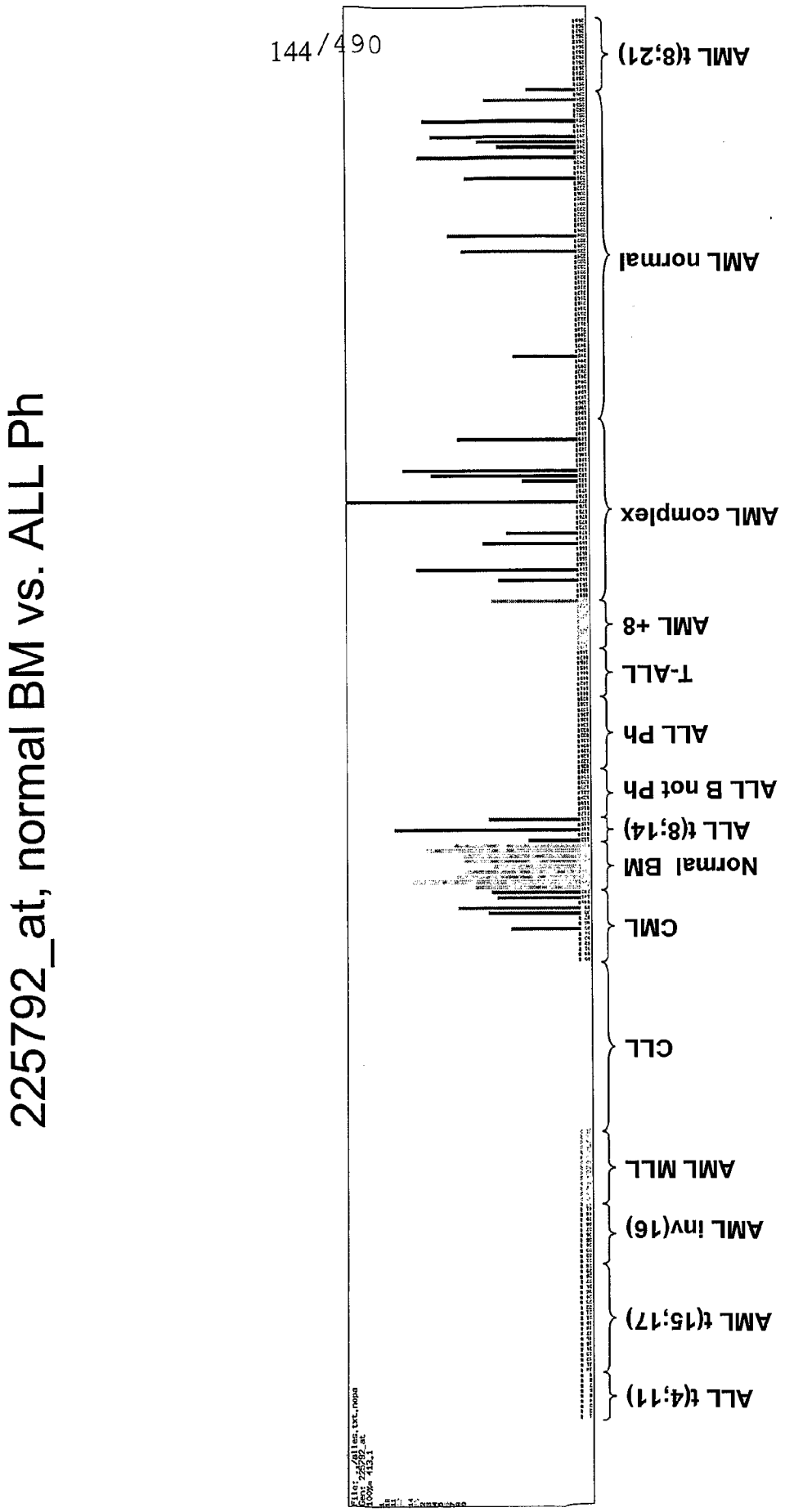

225792_at, normal BM vs. ALL Ph
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 118

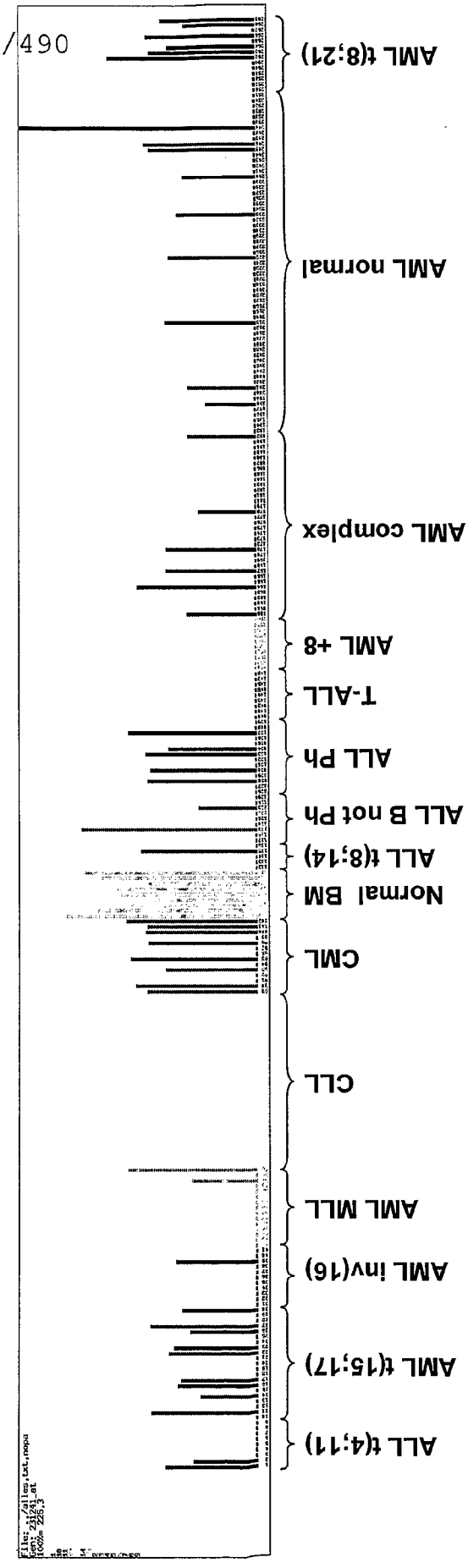

231241_at, normal BM vs. T-ALL
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 119

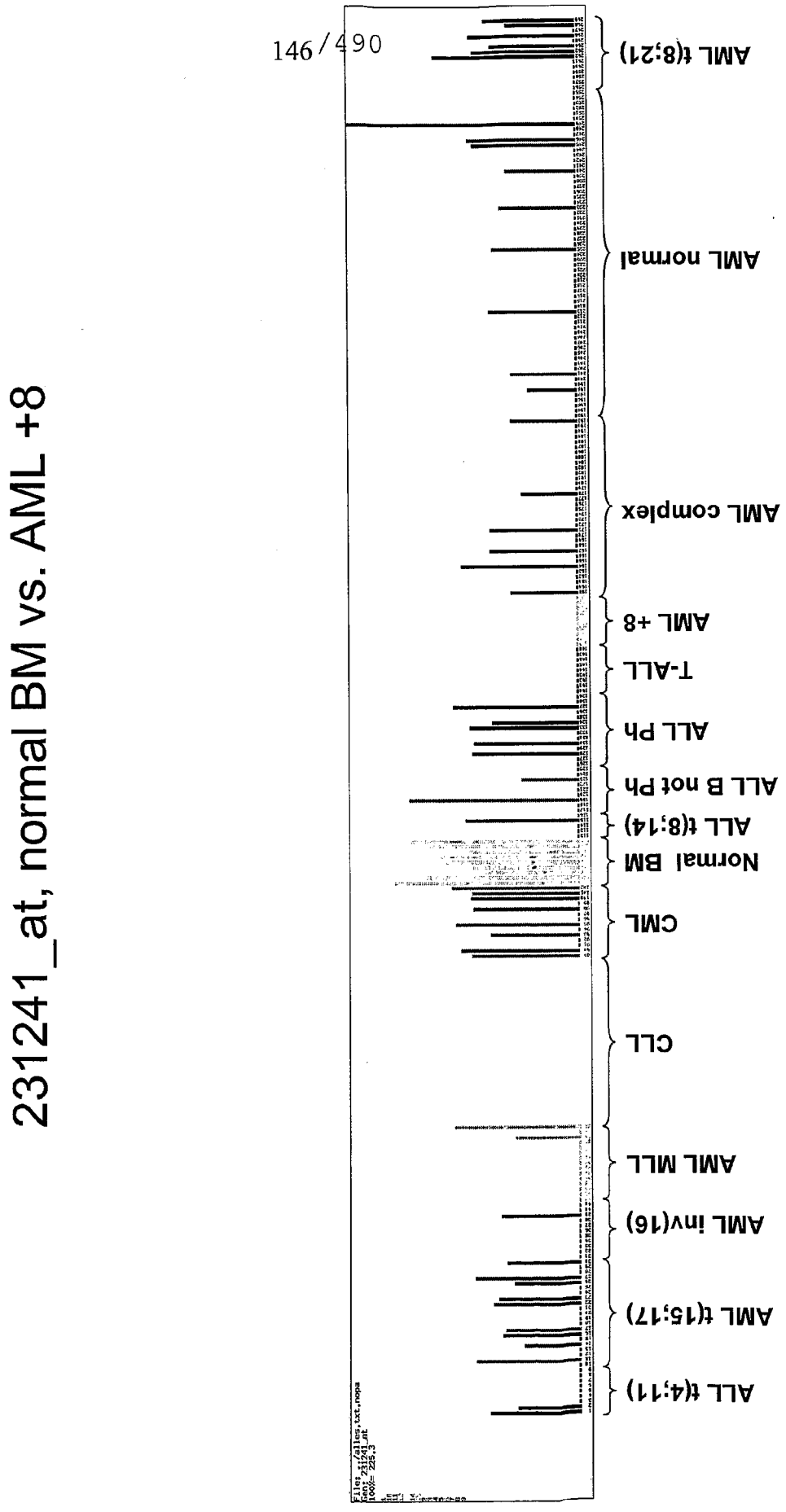

231241_at, normal BM vs. AML +8
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 120

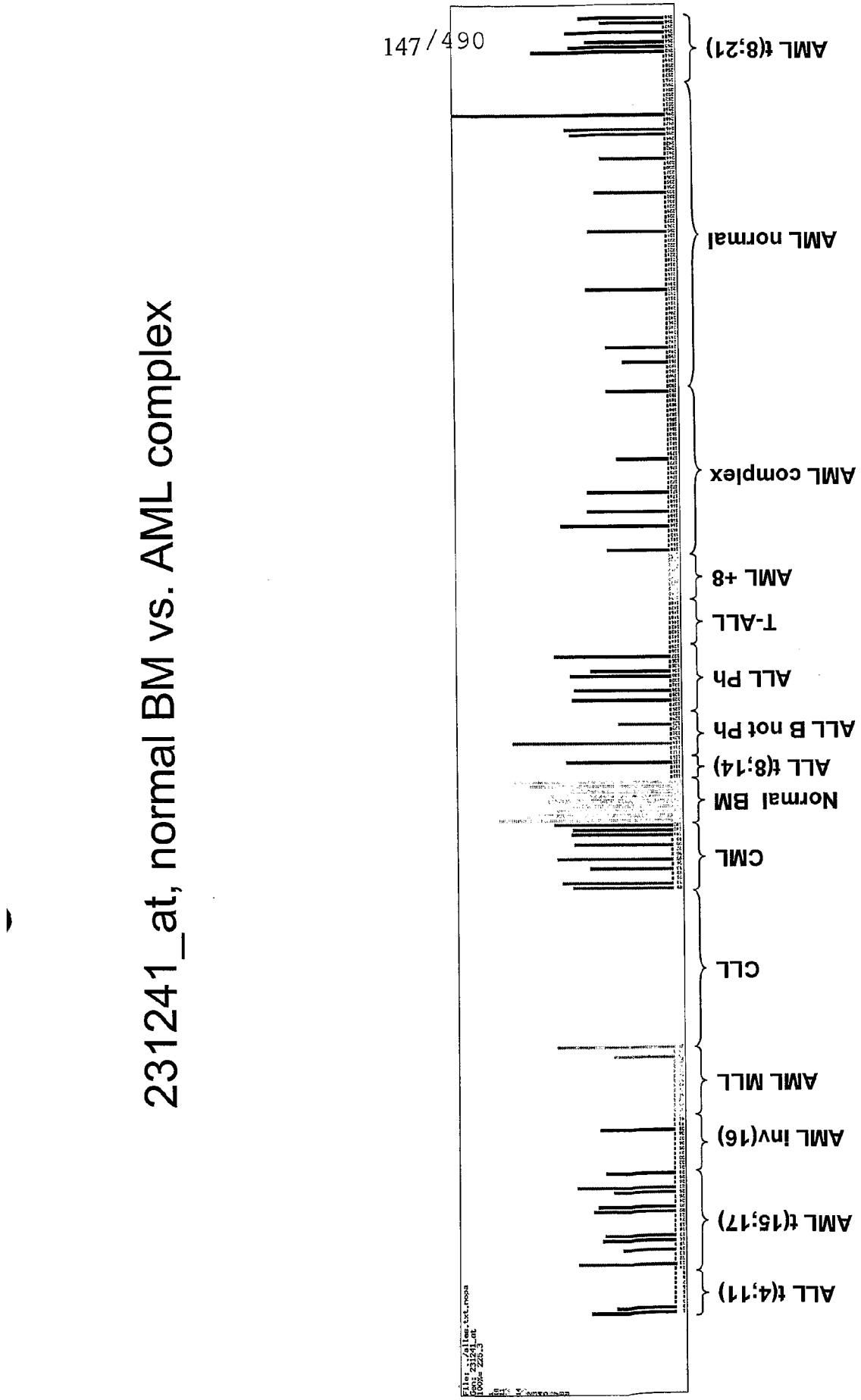

231241_at, normal BM vs. AML complex
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 121

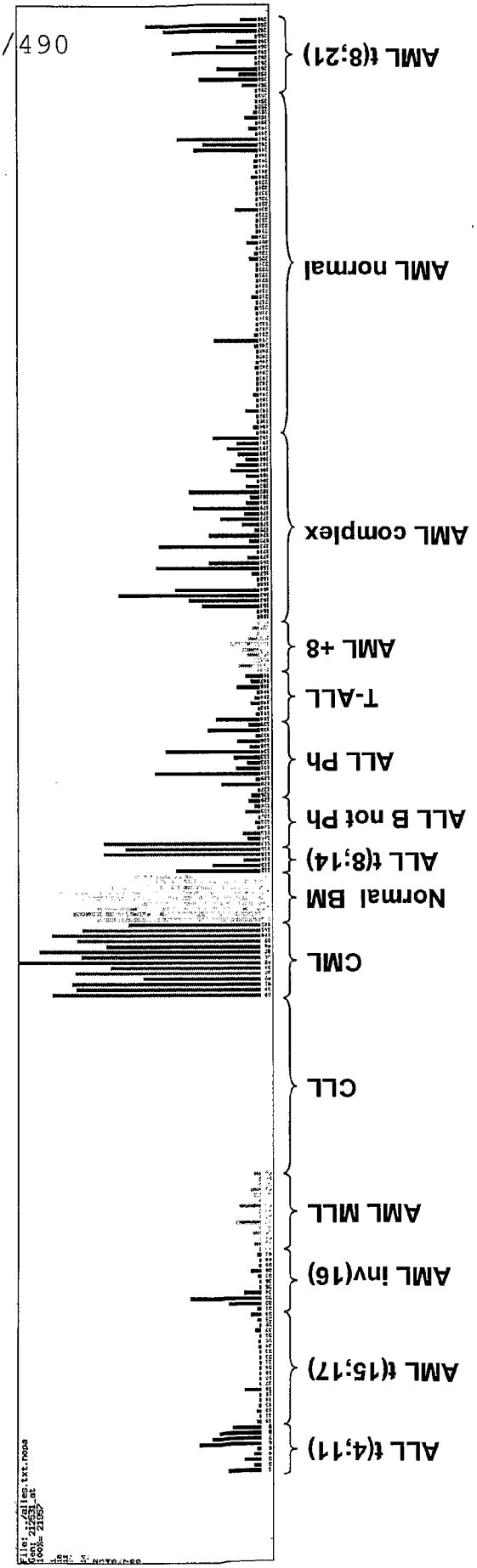

212531_at, LCN2, normal BM vs. AML normal
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 122

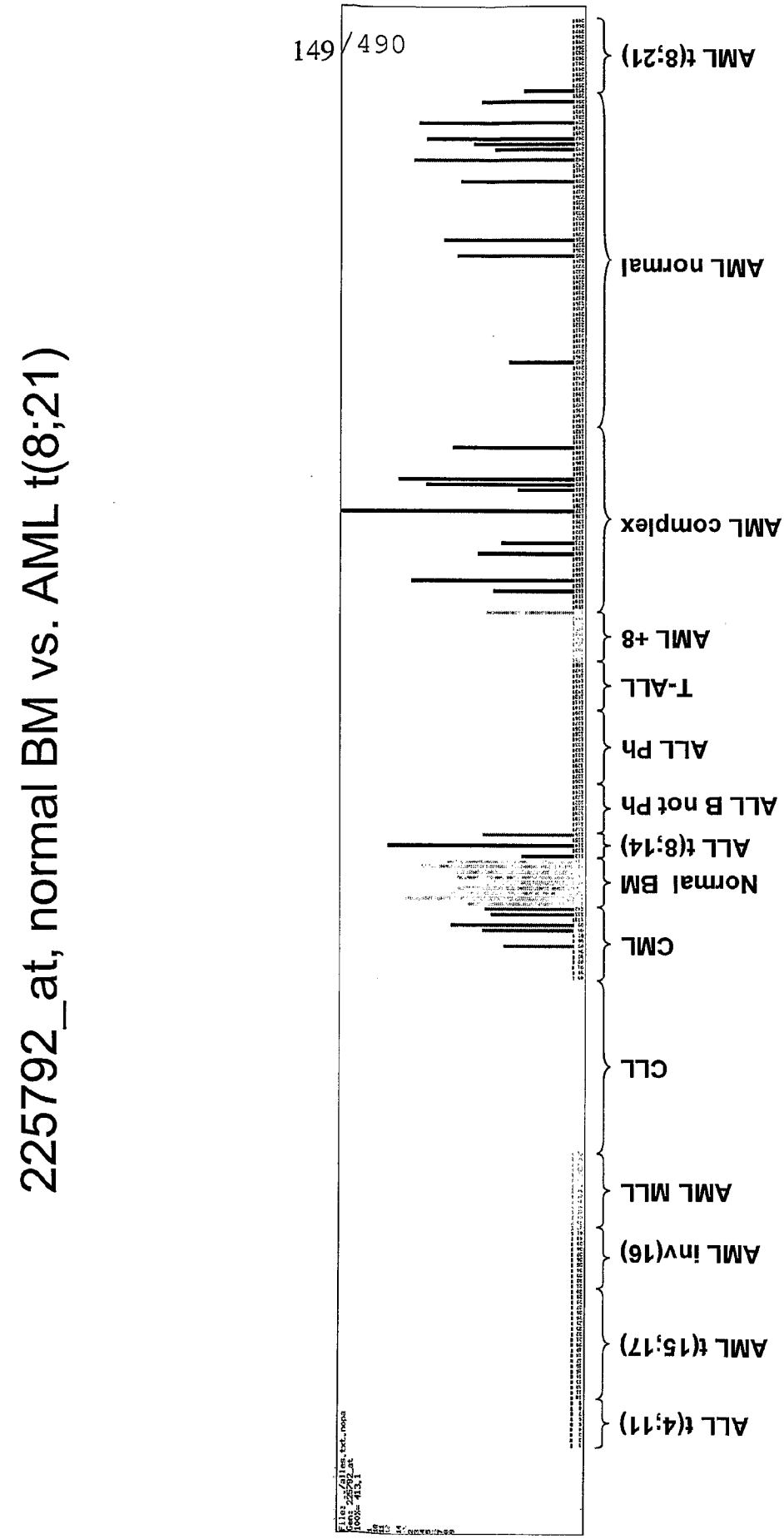

225792_at, normal BM vs. AML t(8;21)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 123

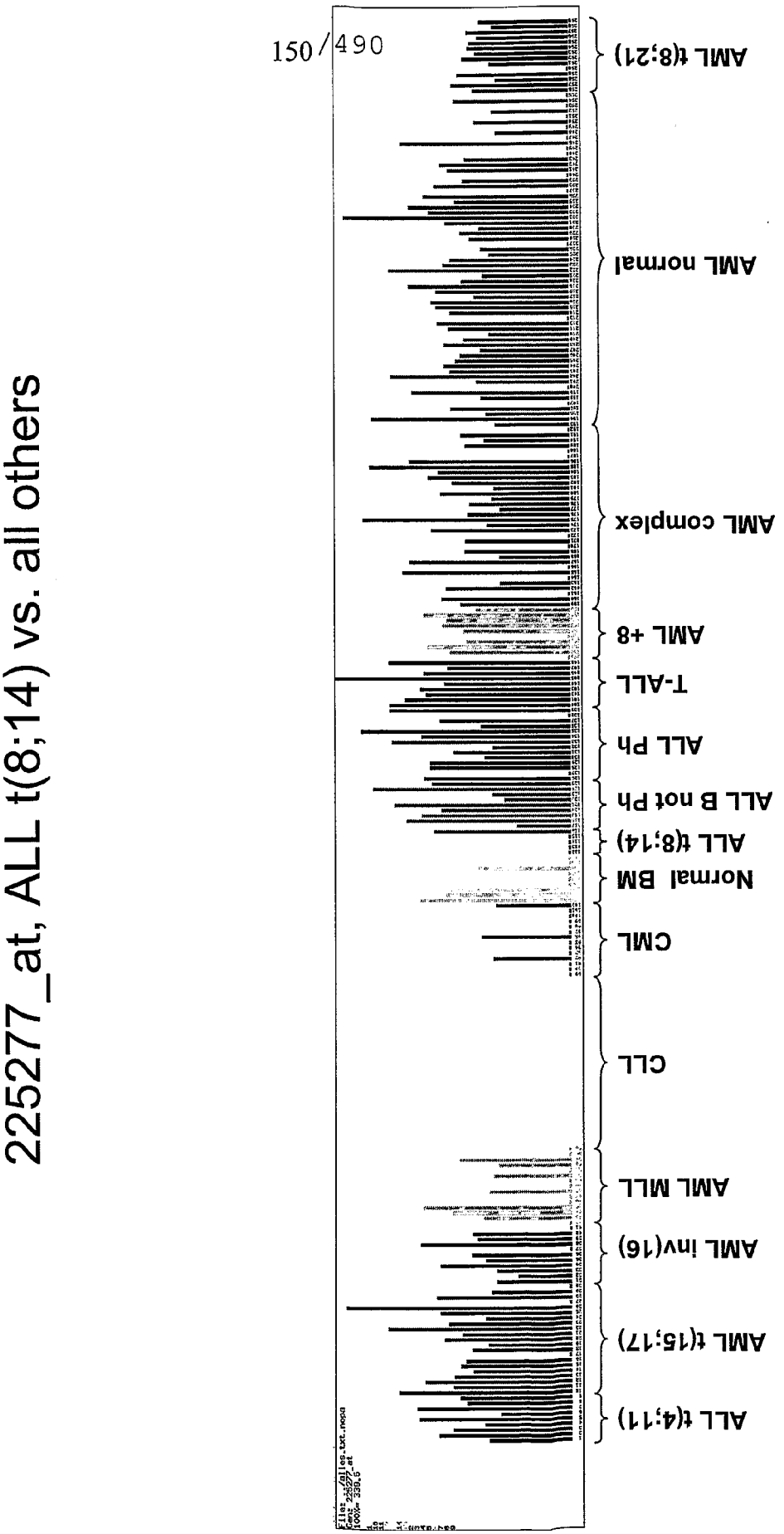

225277_at, ALL t(8;14) vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 124

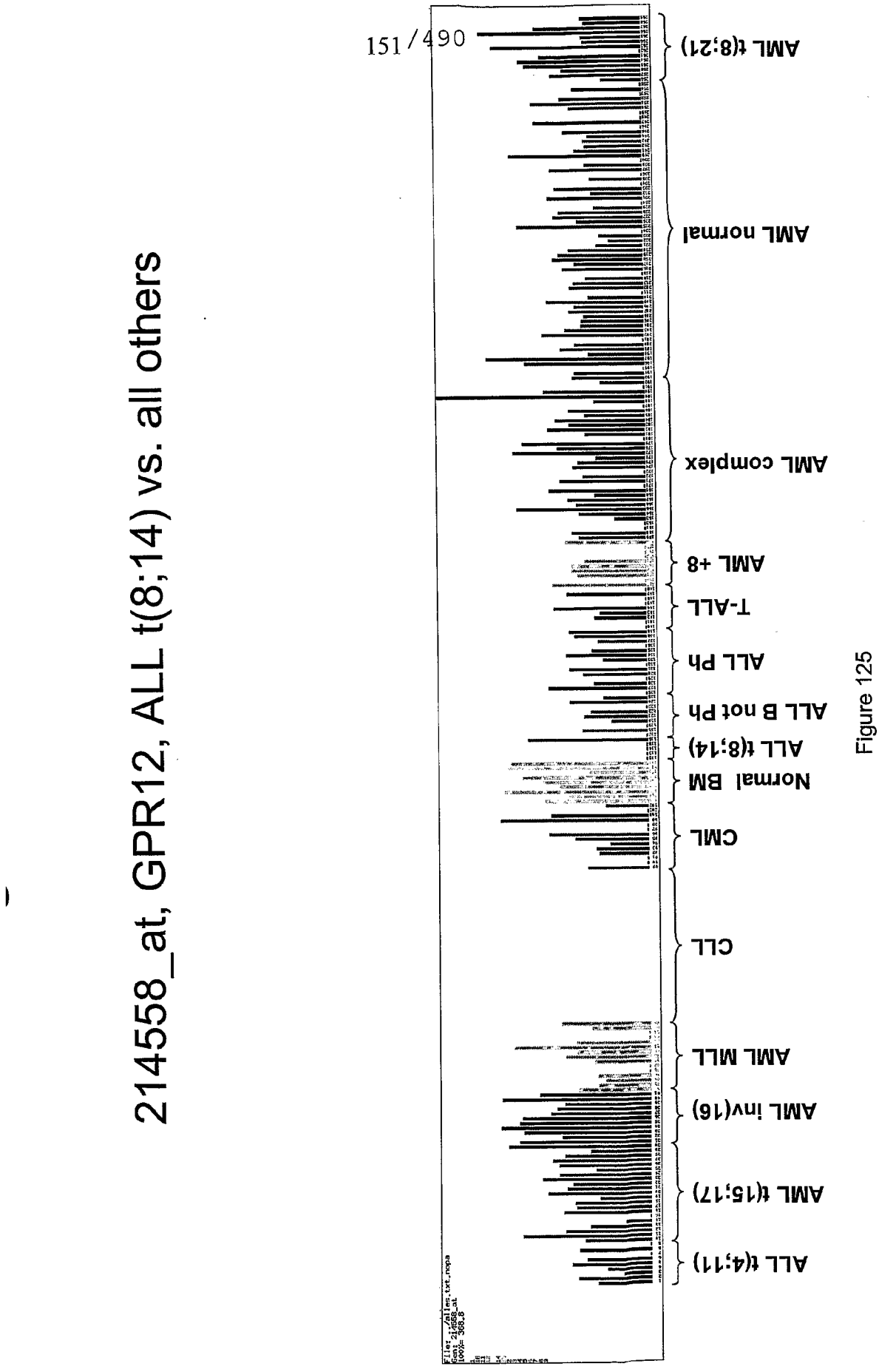

214558_at, GPR12, ALL t(8;14) vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 125

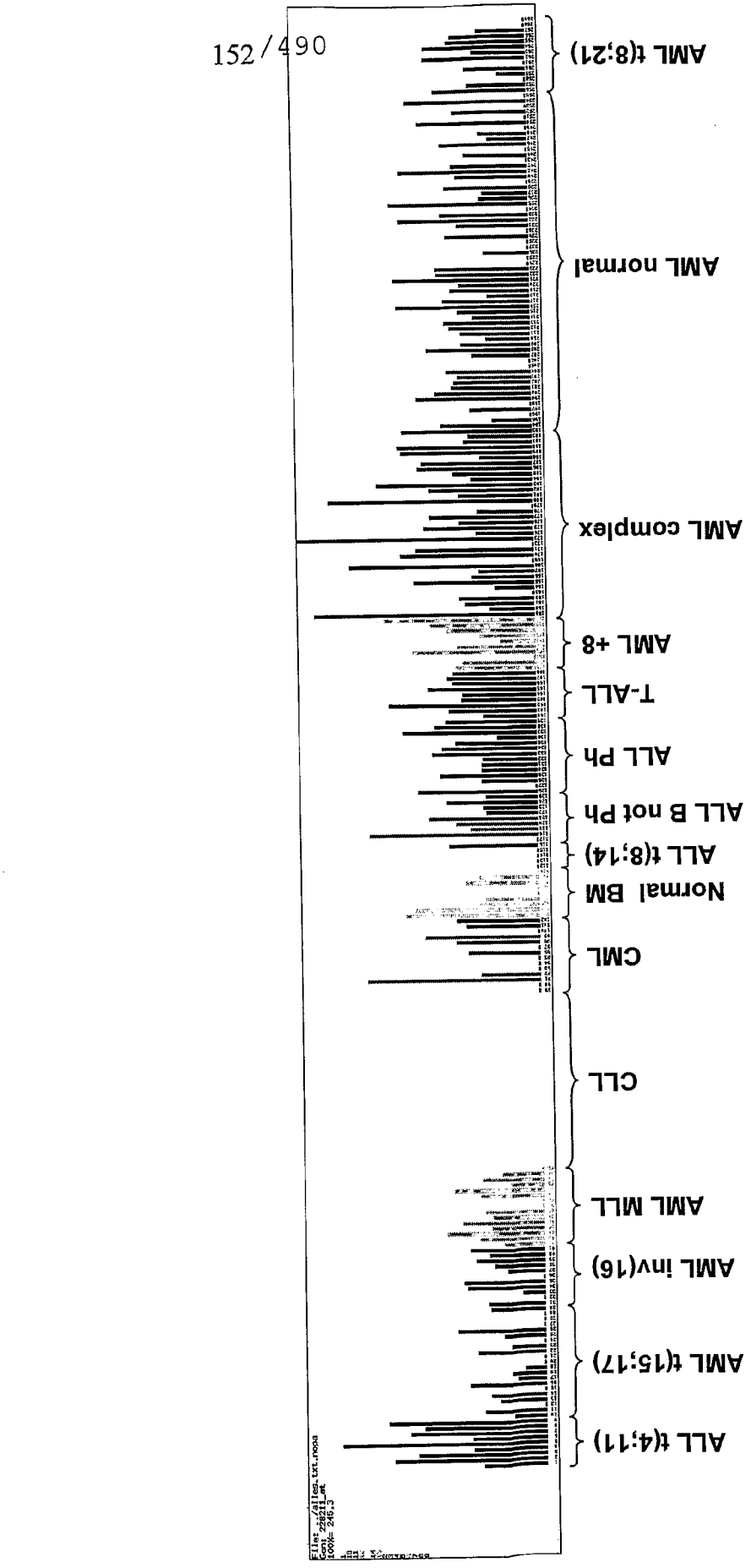

228211_at, ALL t(8;14) vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
AML t(4;11)

Figure 126

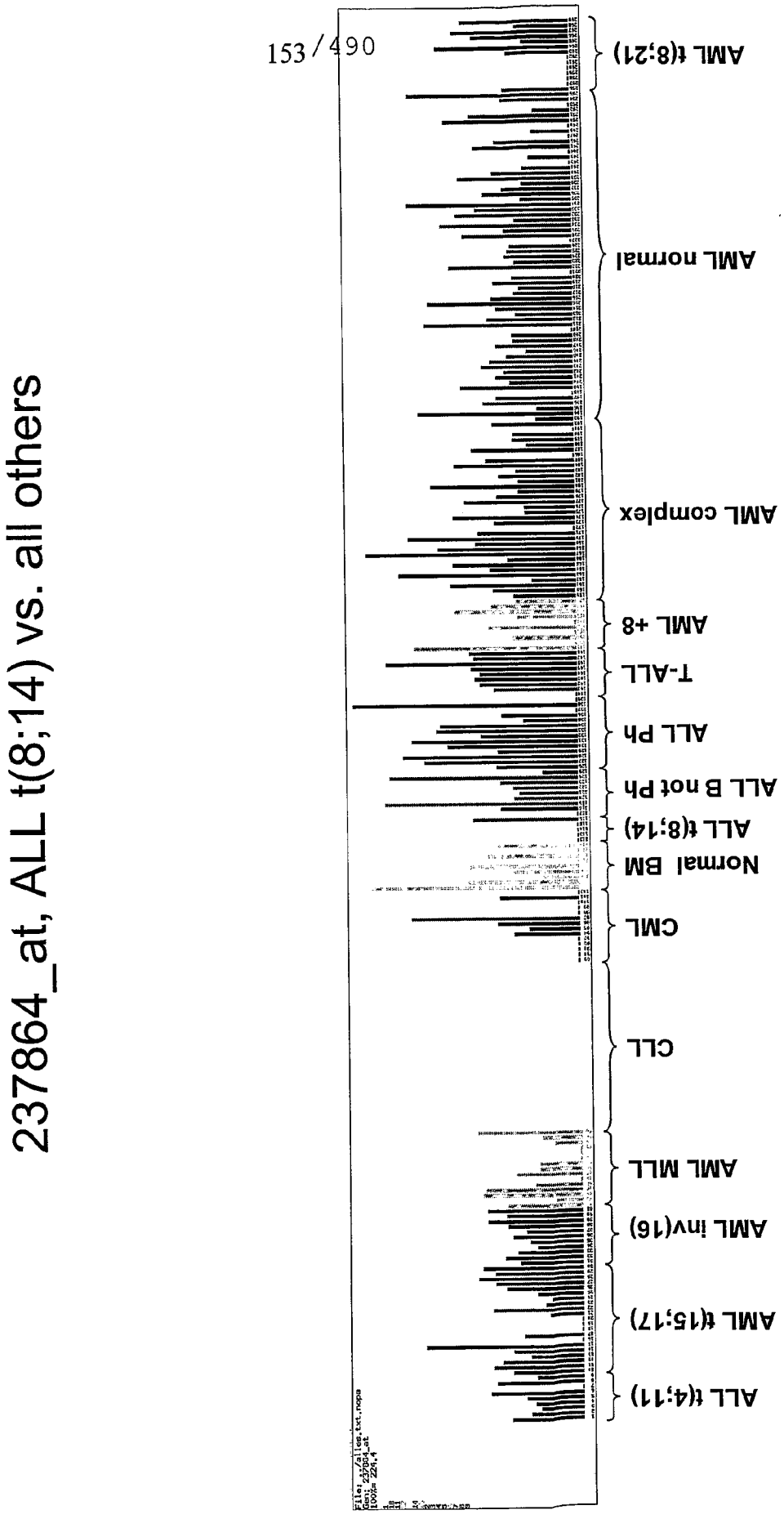

237864_at, ALL t(8;14) vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 127

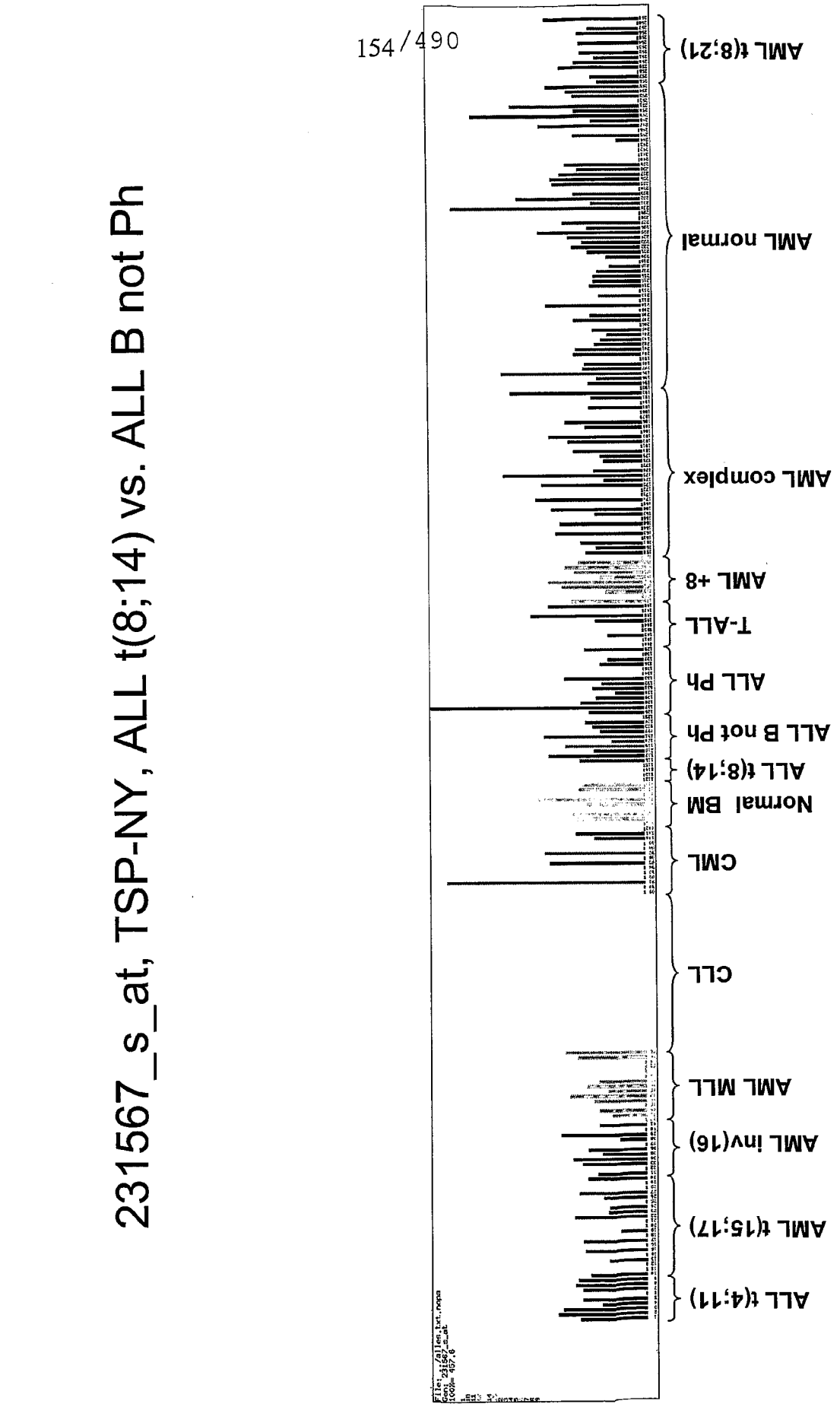

231567_s_at, TSP-NY, ALL t(8;14) vs. ALL B not Ph
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 128

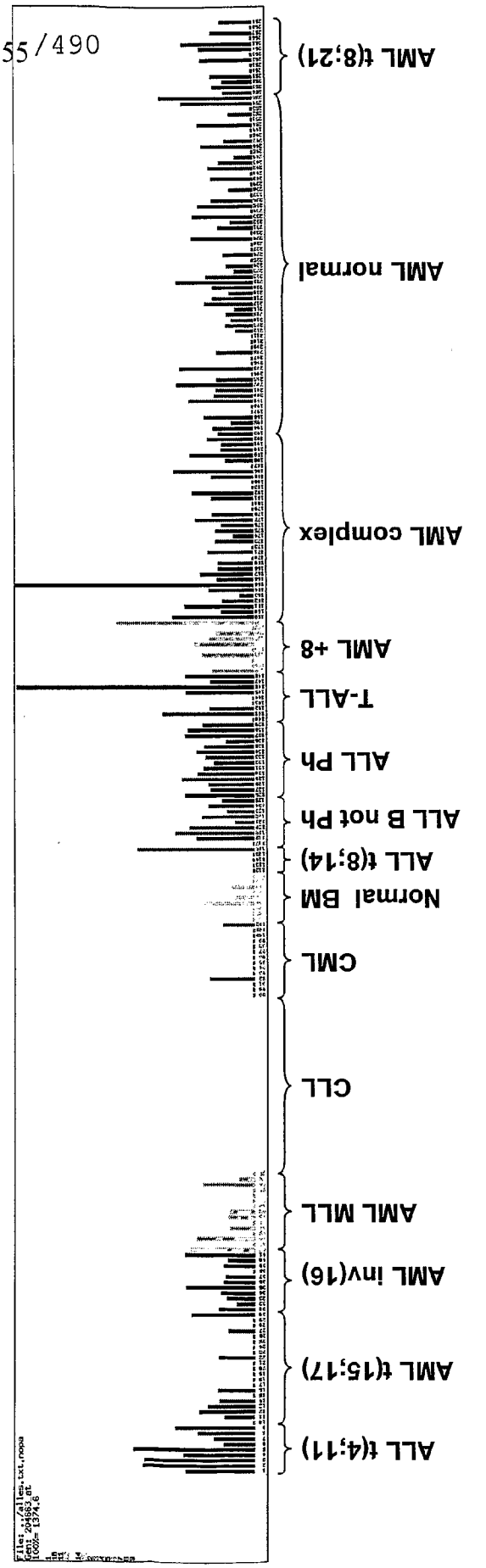

204663_at, ME3, ALL t(8;14) vs. ALL Ph
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 129

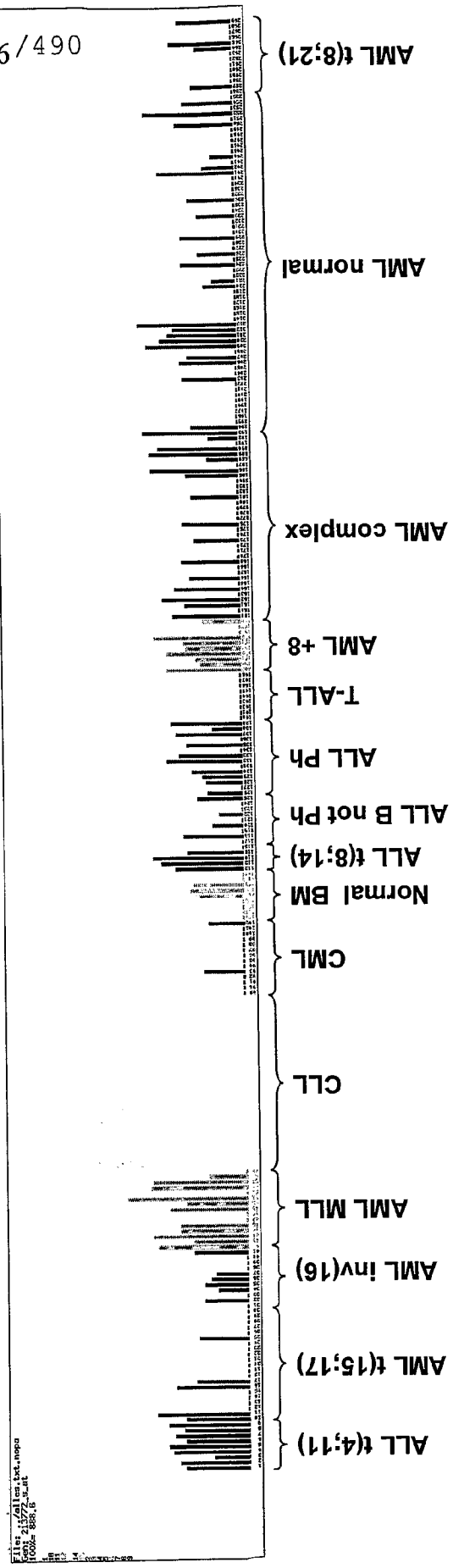

213772_s_at, GGA2, ALL t(8;14) vs. T-ALL
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 130

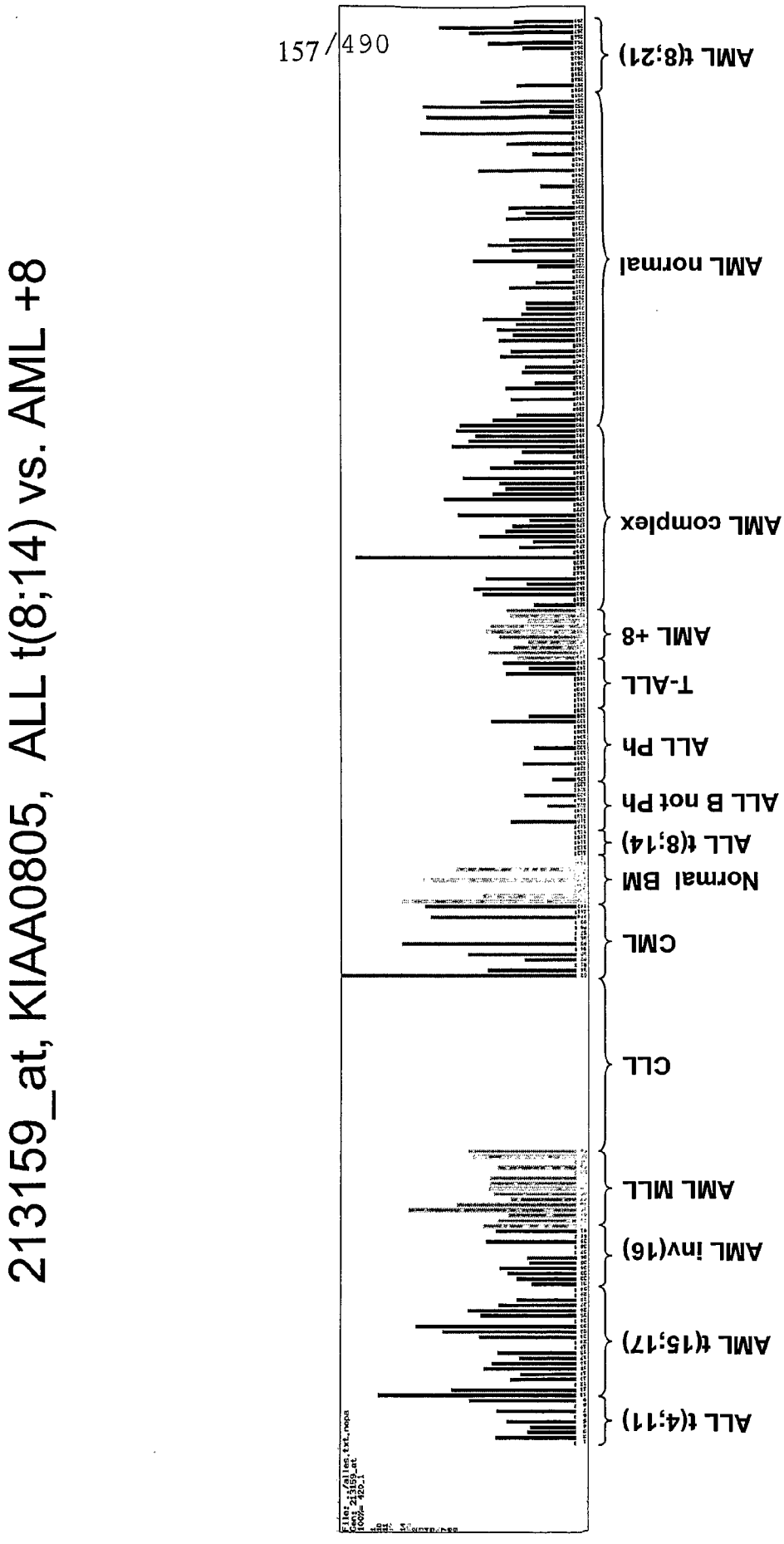

213159_at, KIAA0805, ALL t(8;14) vs. AML +8
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 131

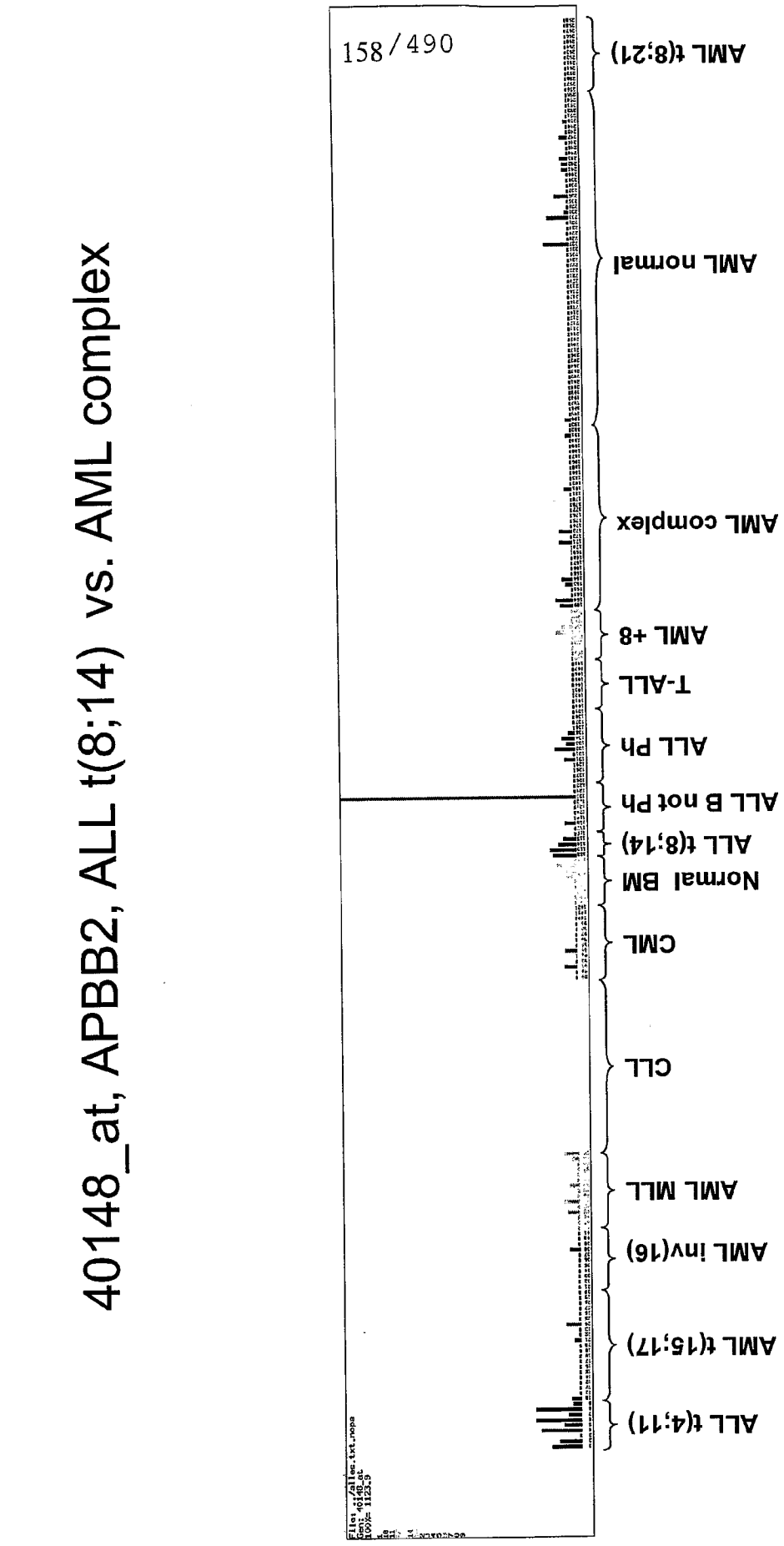

40148_at, APBB2, ALL t(8;14) vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 132

212293_at, KIAA0630, ALL t(8;14) vs. AML complex

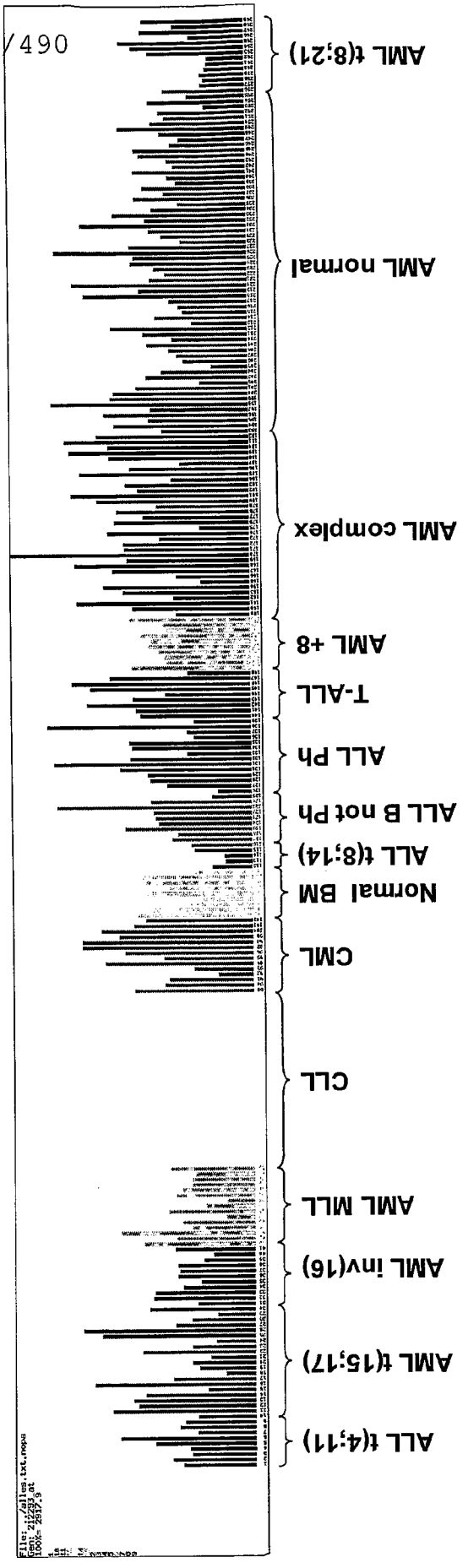


Figure 133

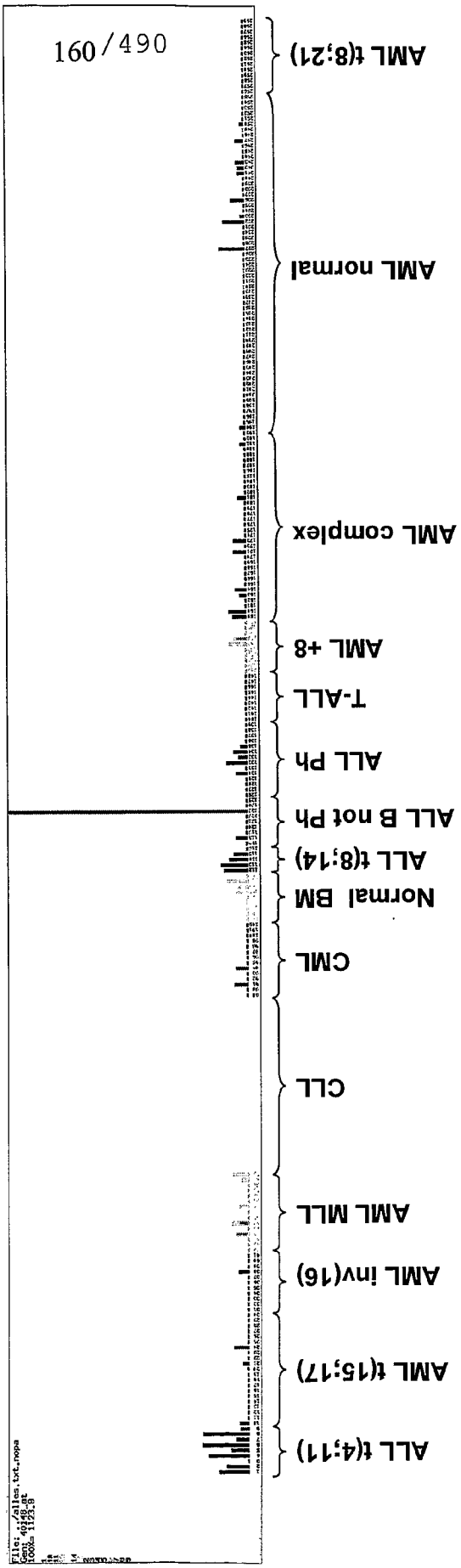

40148_at, APBB2, ALL t(8;14) vs. AML normal
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 134

WO03039443 file://E:/WO03039443.com1

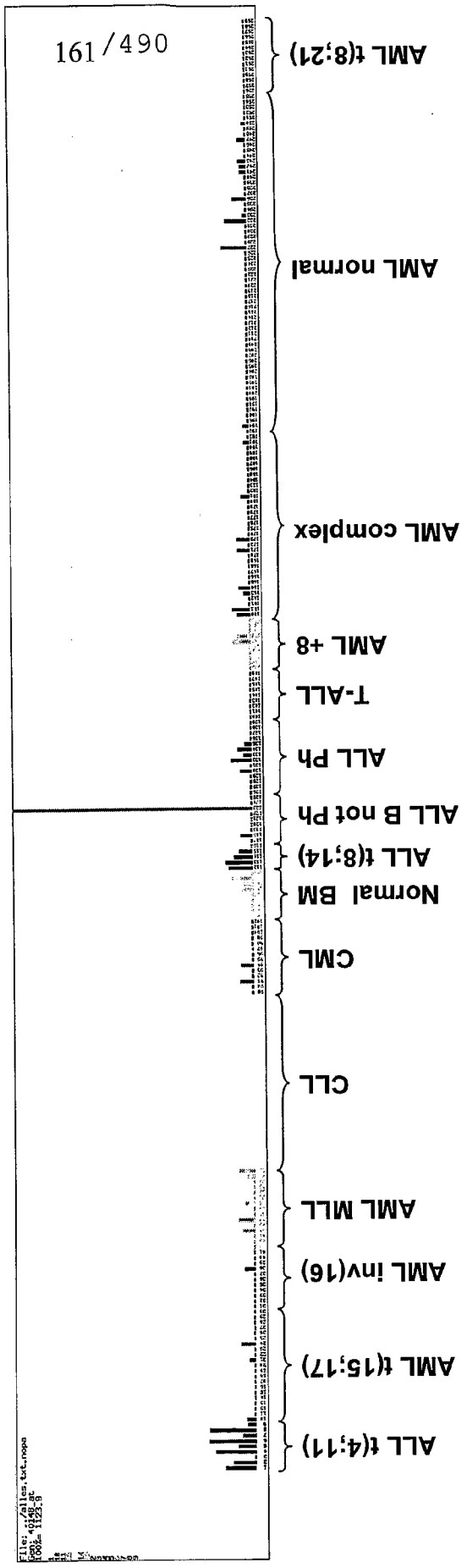


Figure 135

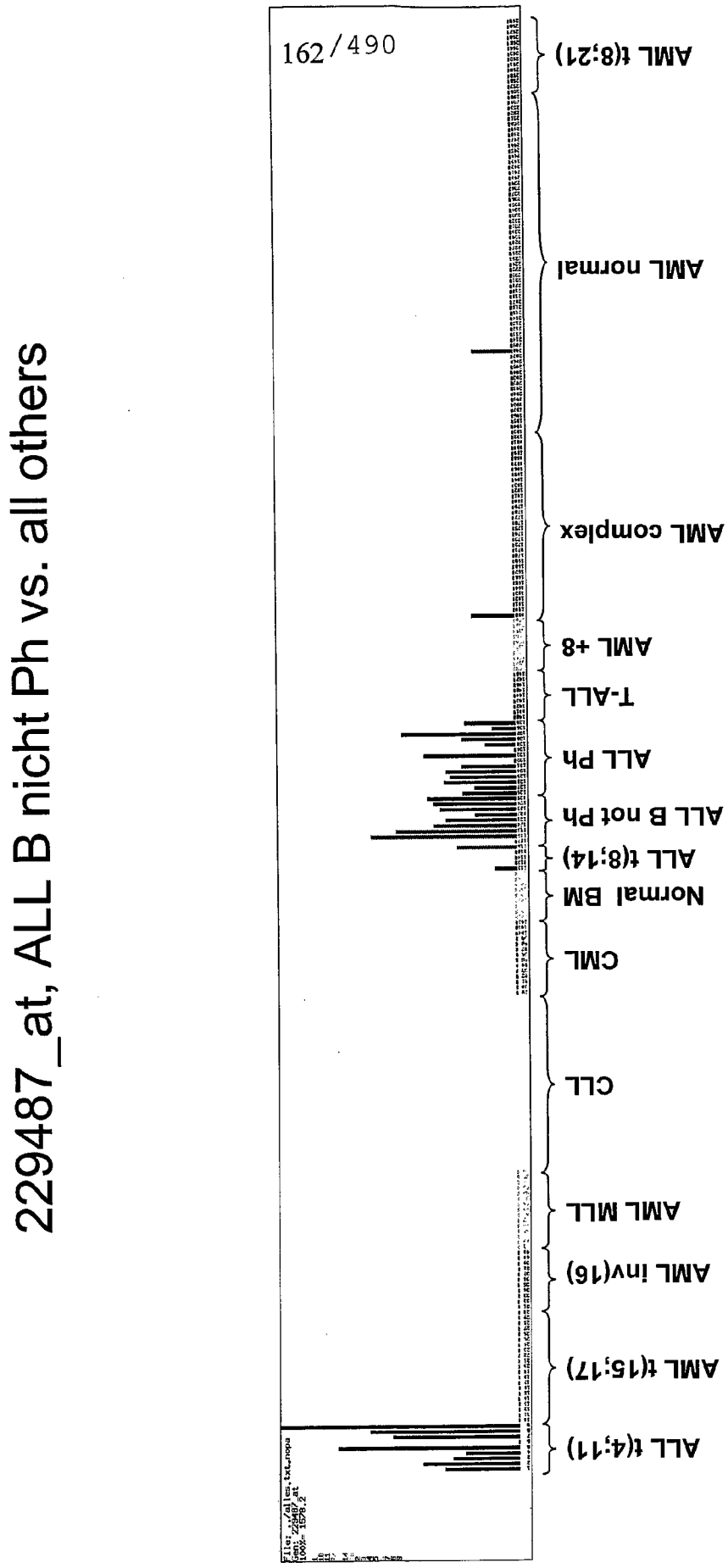

229487_at, ALL B nicht Ph vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 136

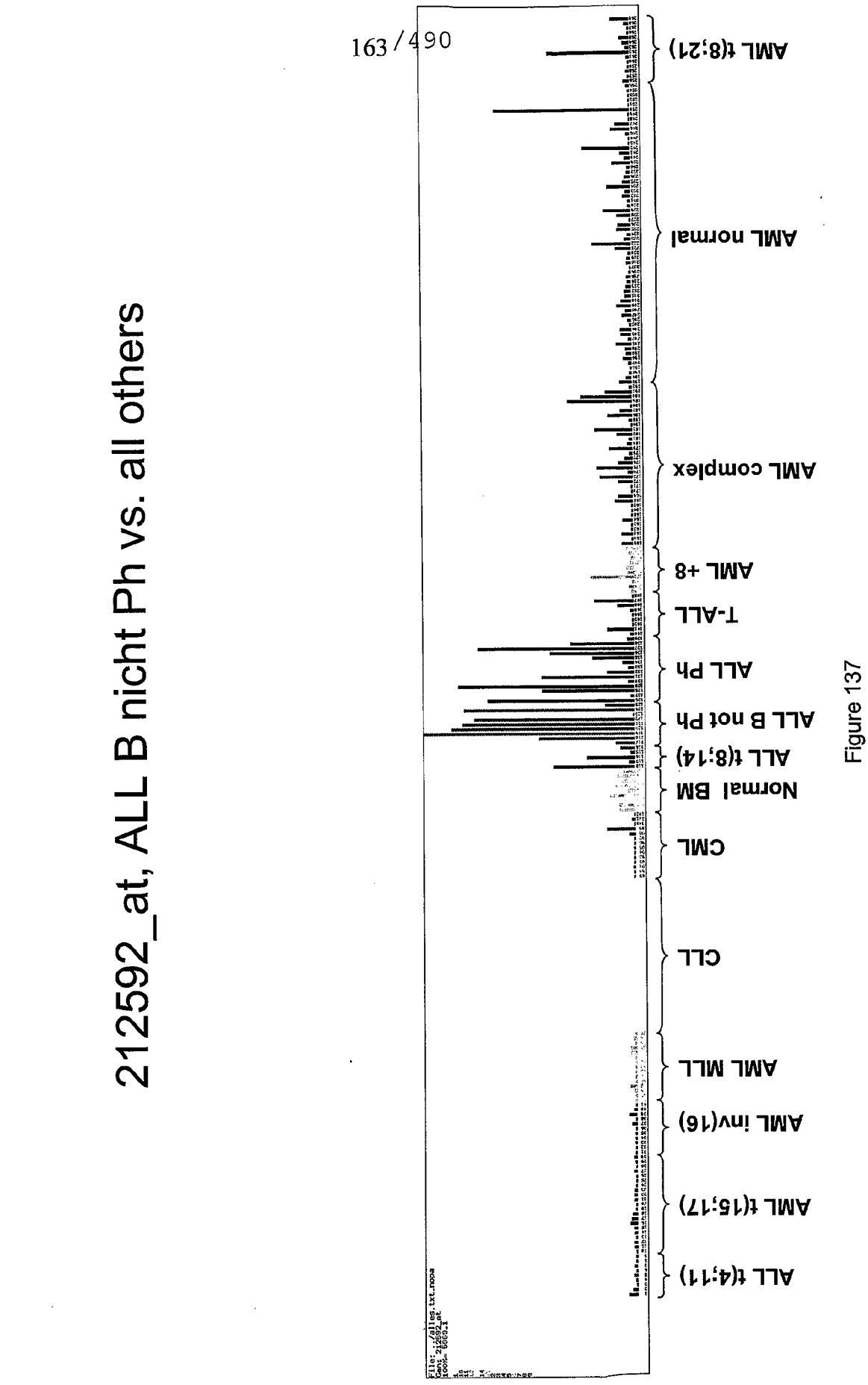

212592_at, ALL B nicht Ph vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 137

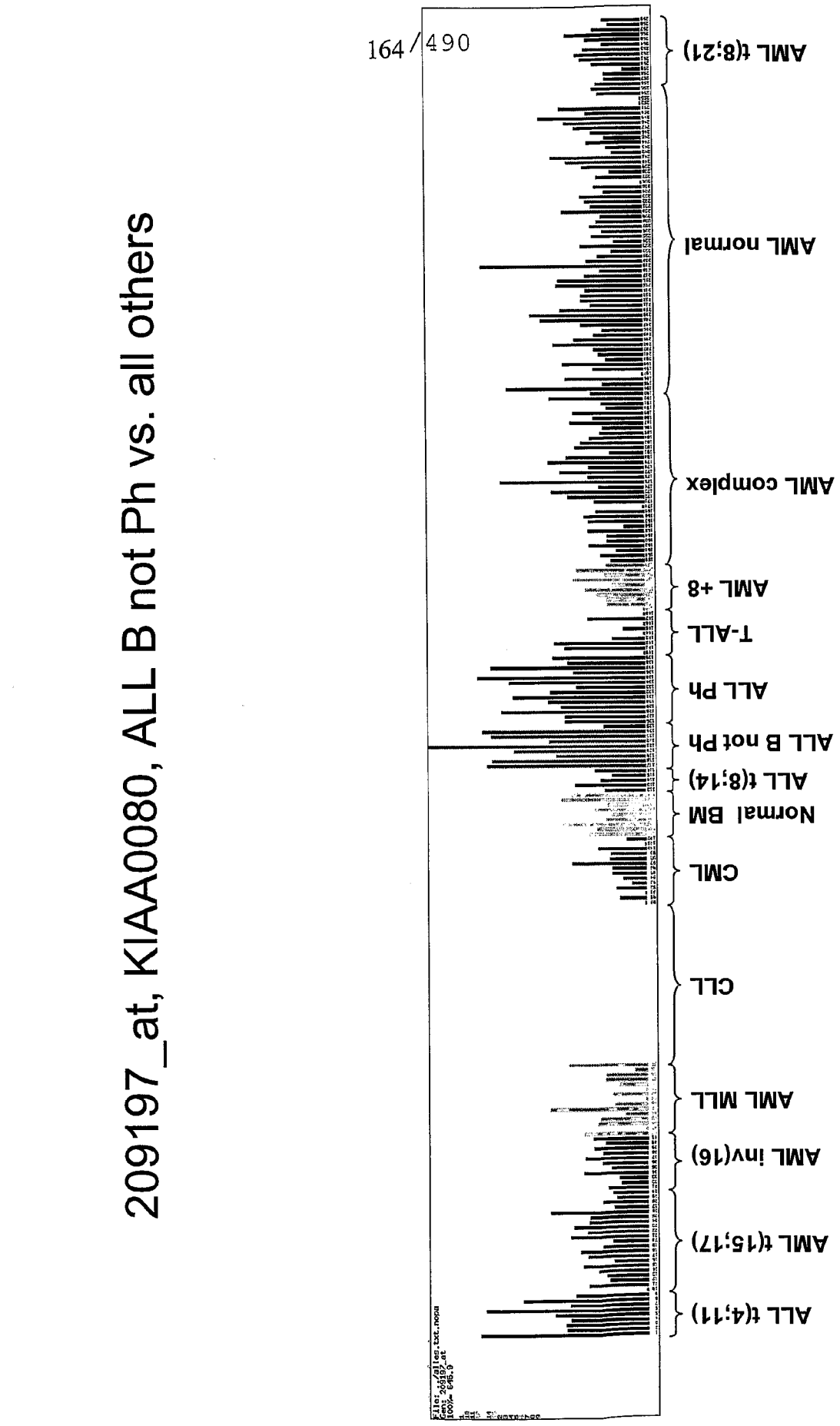

209197_at, KIAA0080, ALL B not Ph vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 138

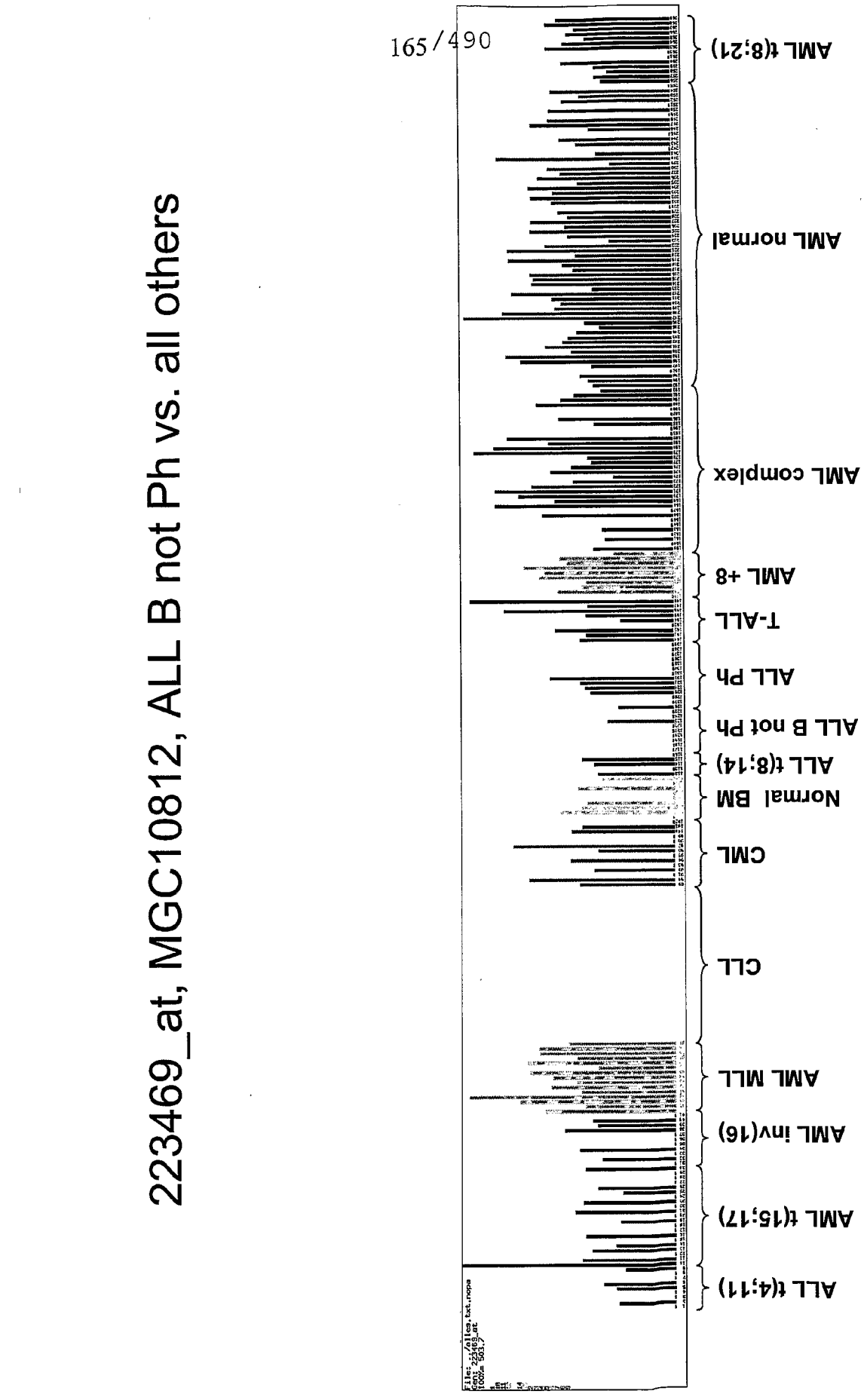

223469_at, MGC10812, ALL B not Ph vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 139

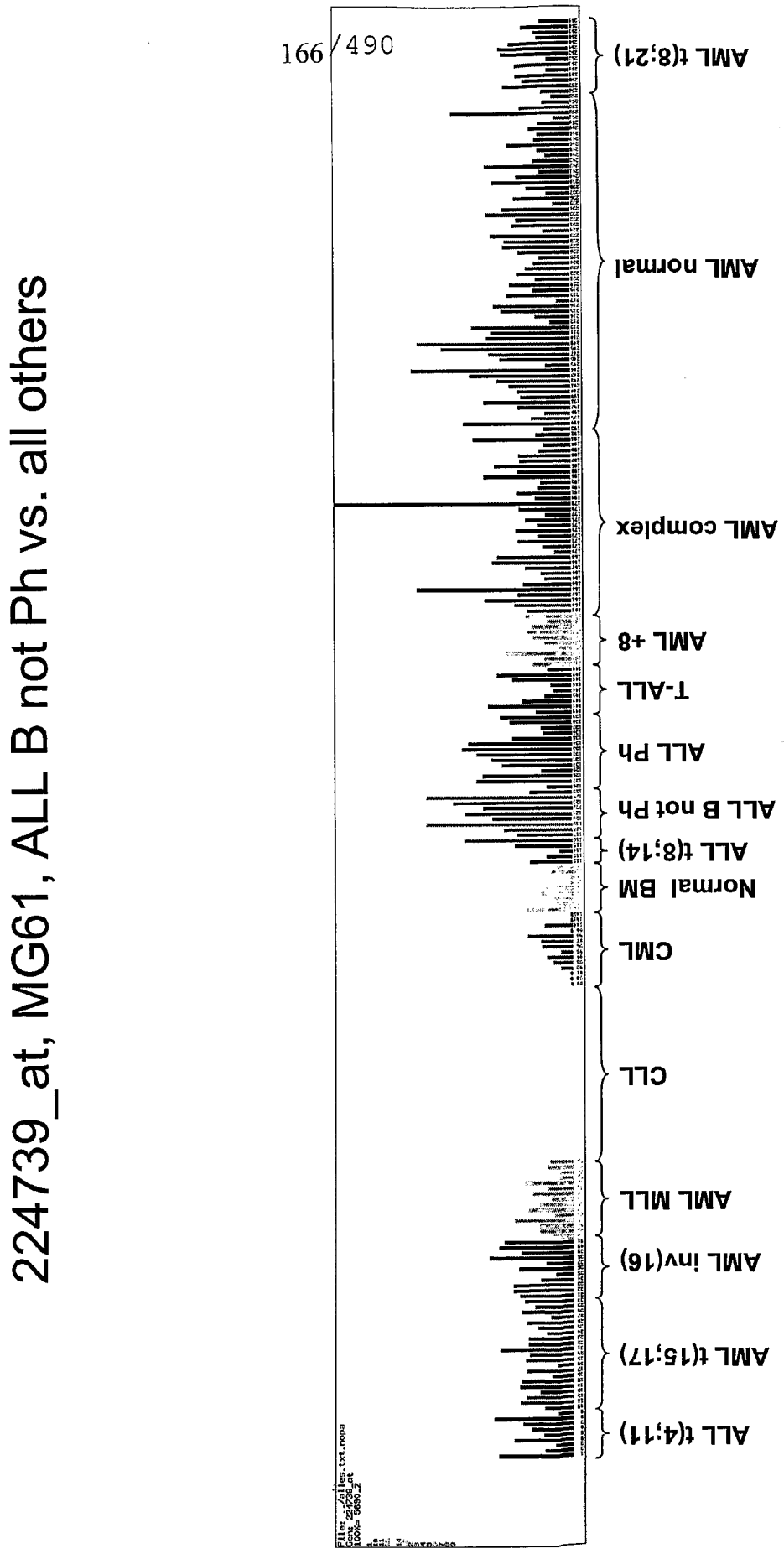

224739_at, MG61, ALL B not Ph vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 140

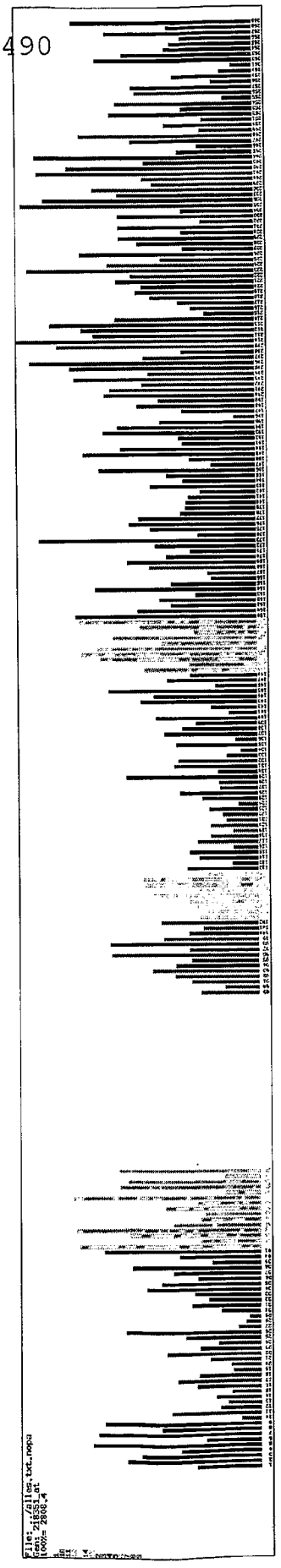

218351_at, FLJ20502, ALL B not Ph vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 141

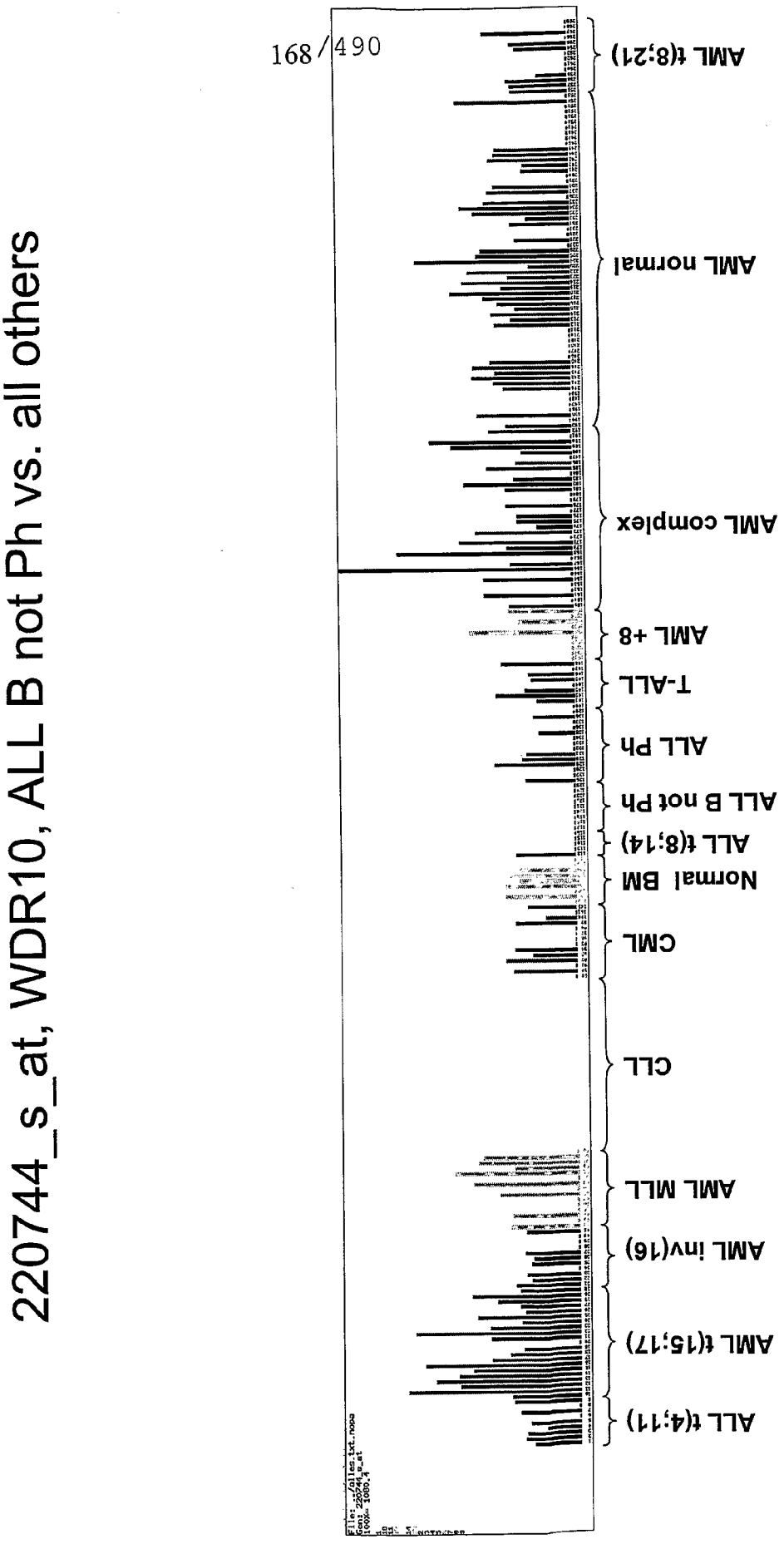

220744_s_at, WDR10, ALL B not Ph vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 142

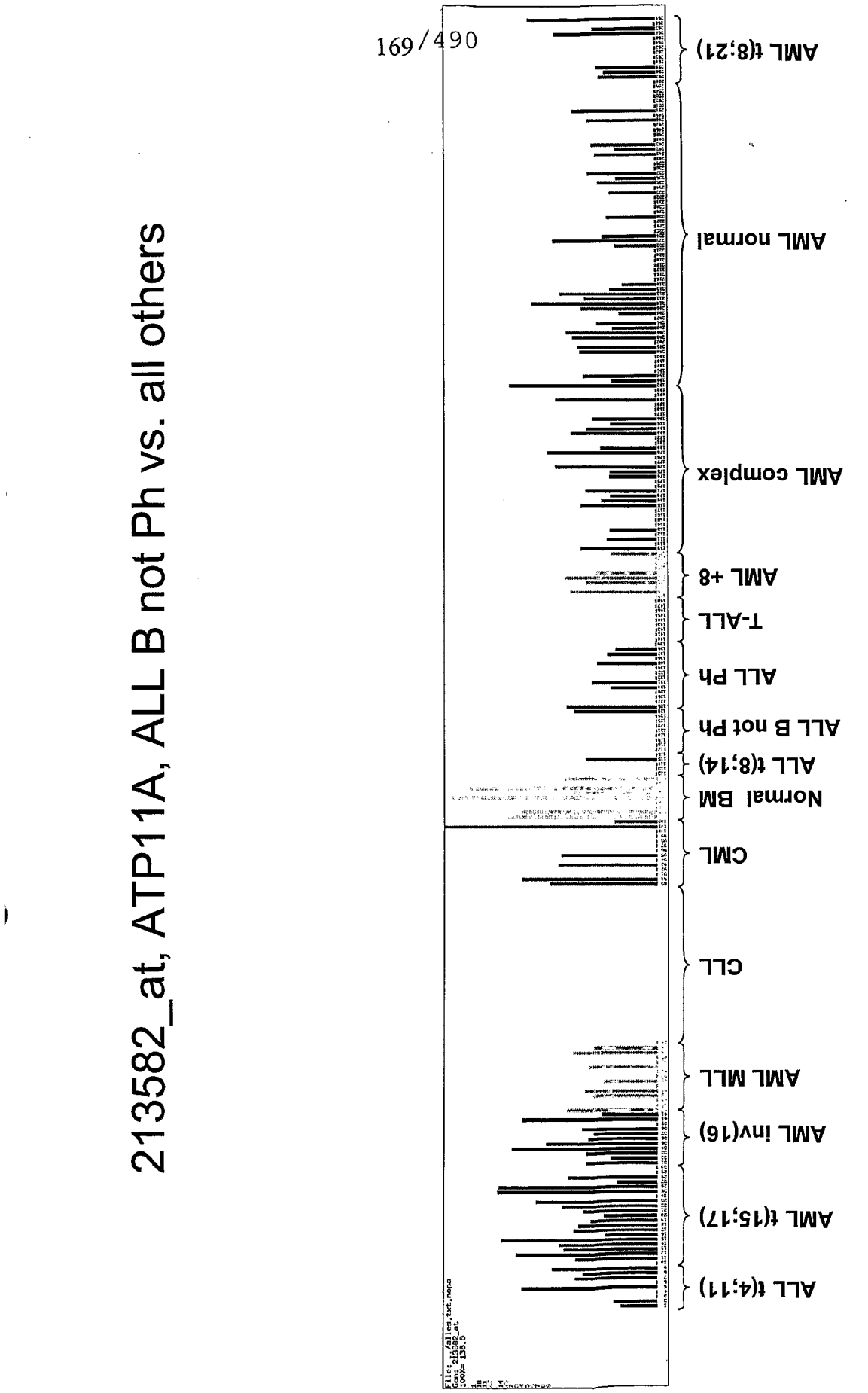

213582_at, ATP11A, ALL B not Ph vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 143

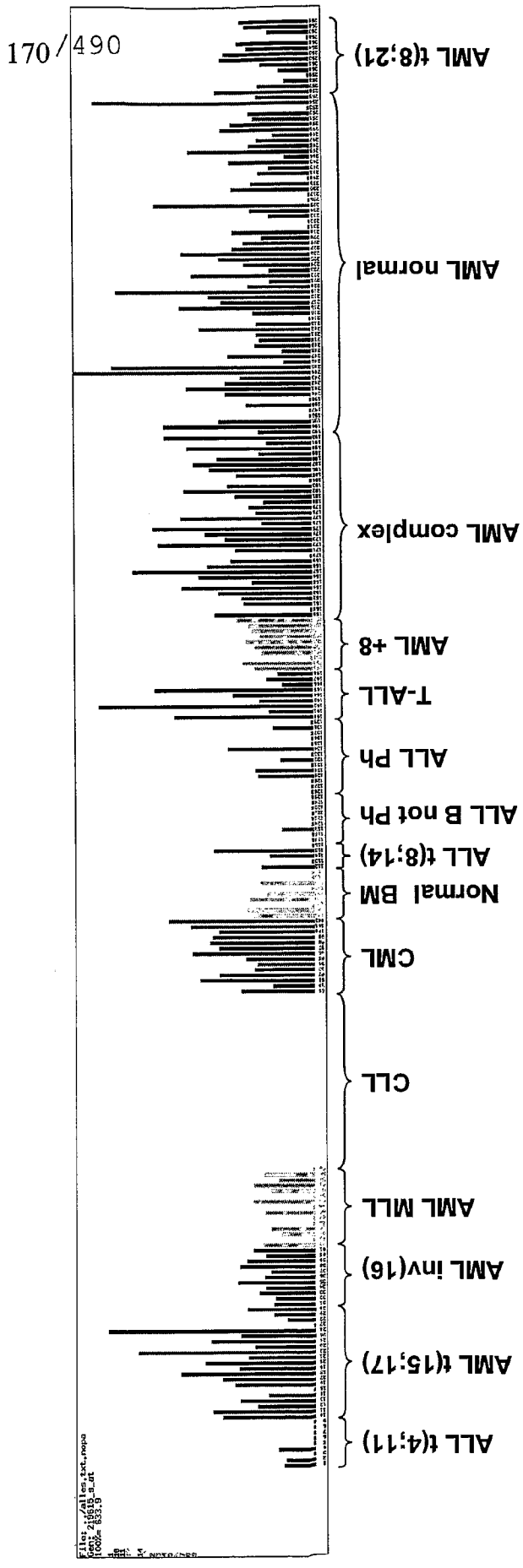

219615_s_at, KCNK5, ALL B not Ph vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 144

202123_s_at, ABL1, ALL B not Ph vs. ALL Ph

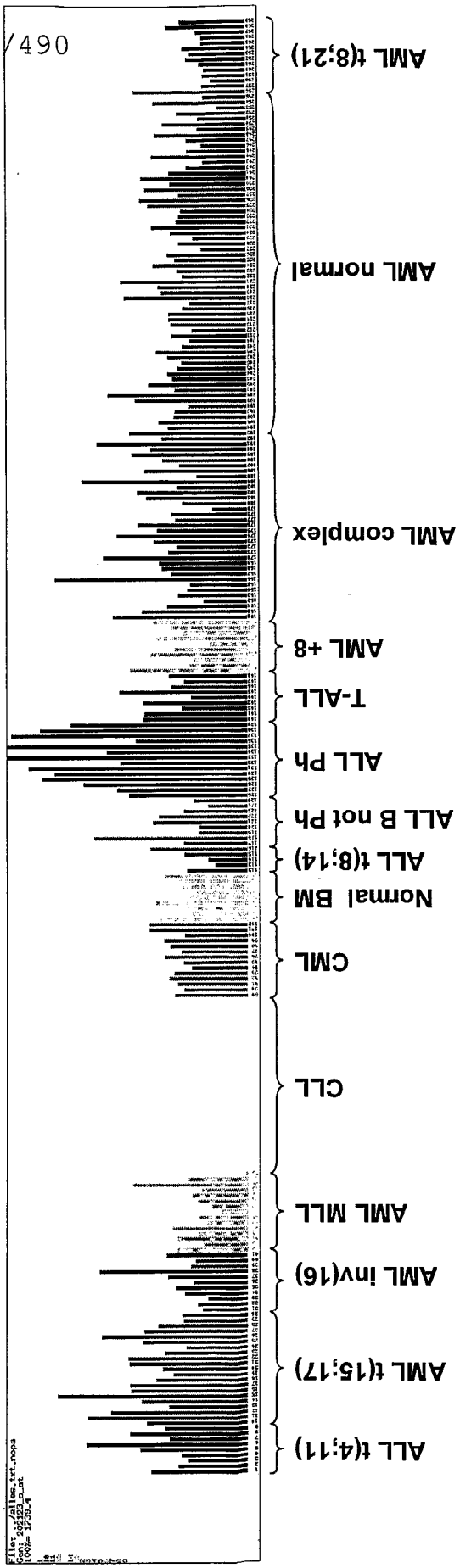


Figure 145

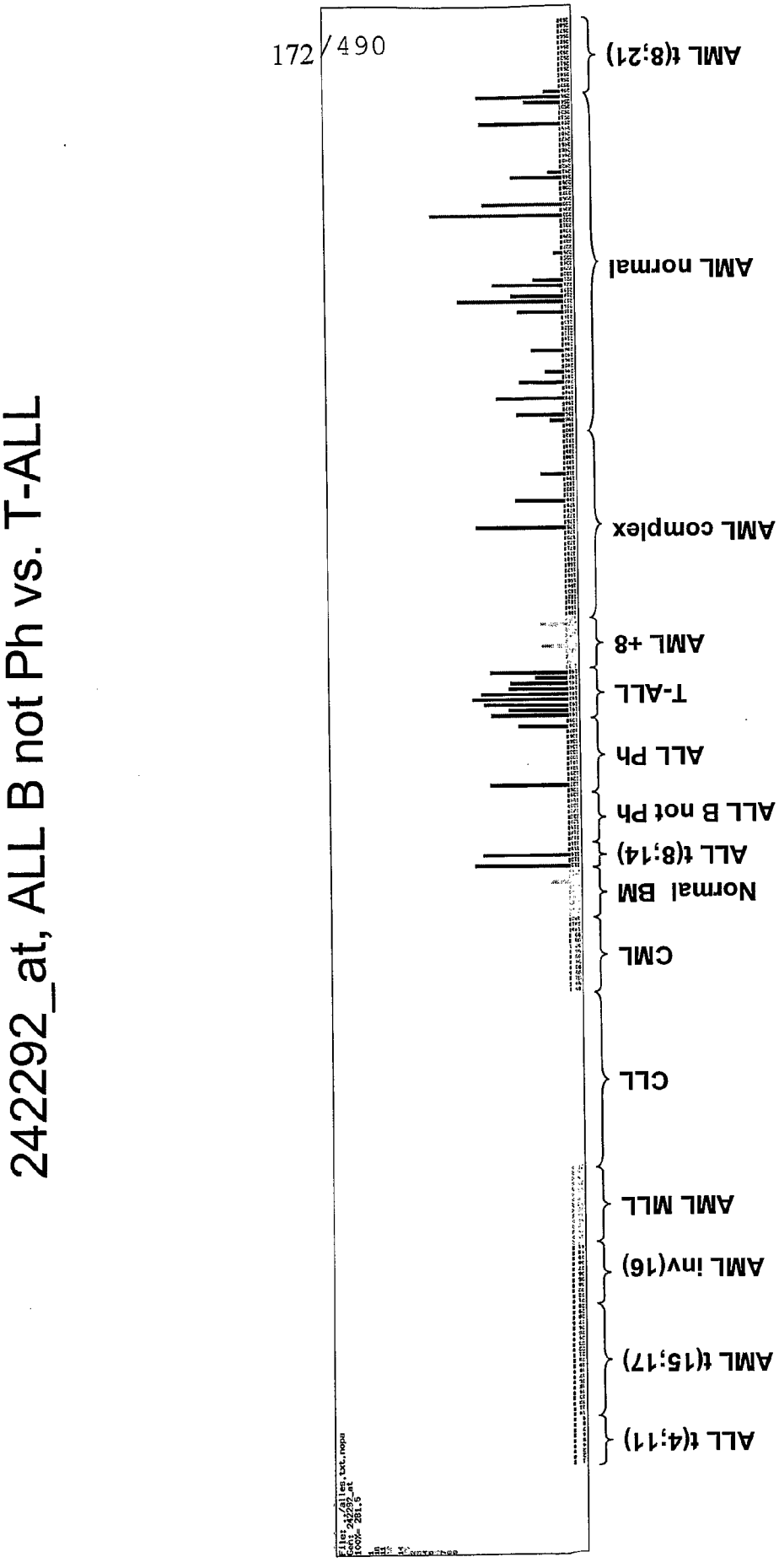

242292_at, ALL B not Ph vs. T-ALL
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 146

208248_x_at, APLP2, ALL B not Ph vs. AML +8

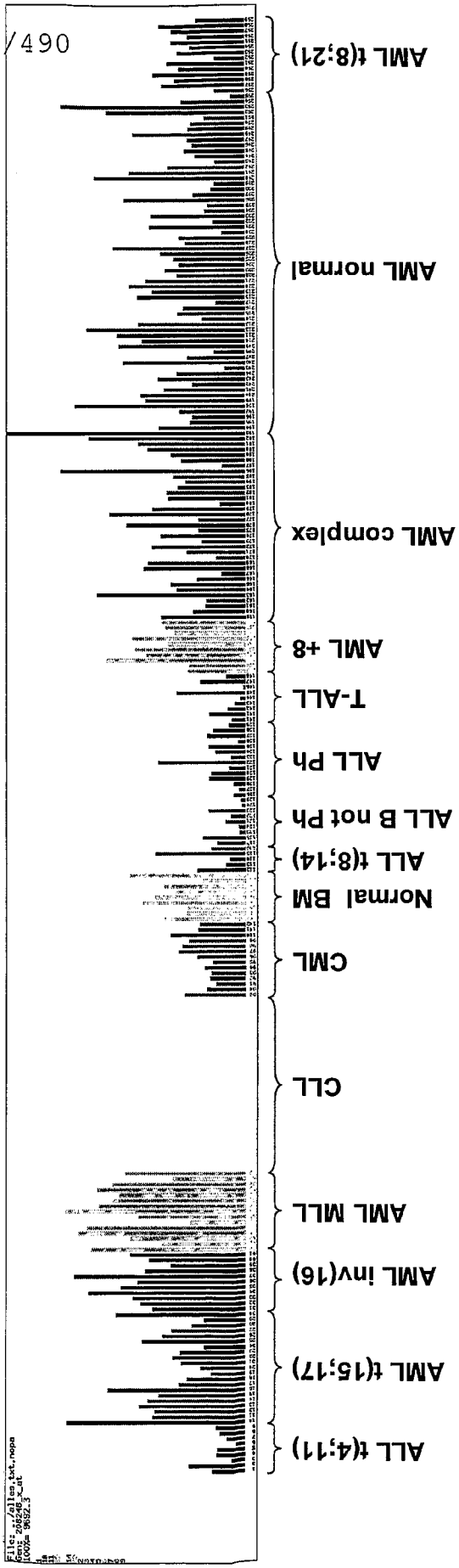


Figure 147

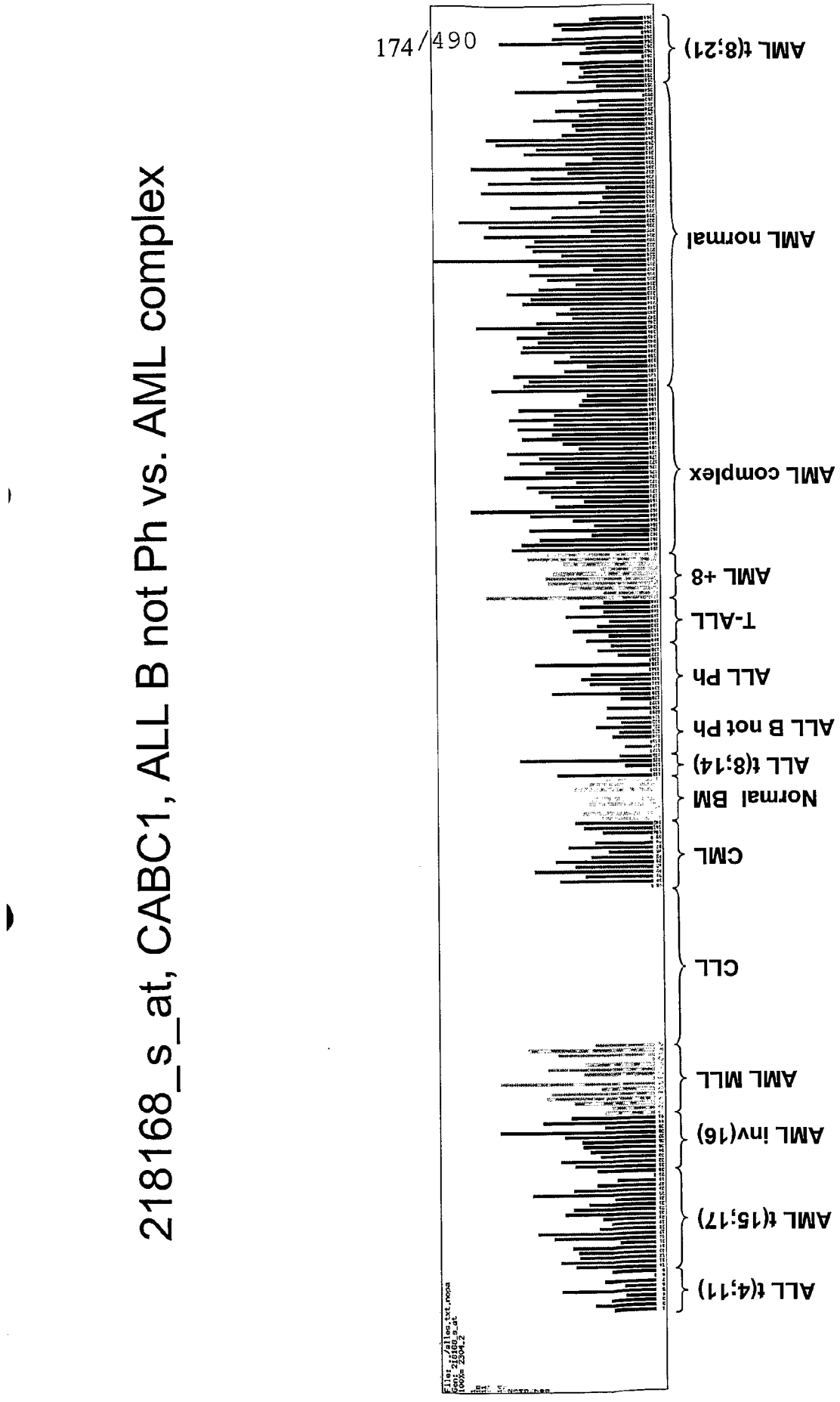

218168_s_at, CABC1, ALL B not Ph vs. AML complex
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 148

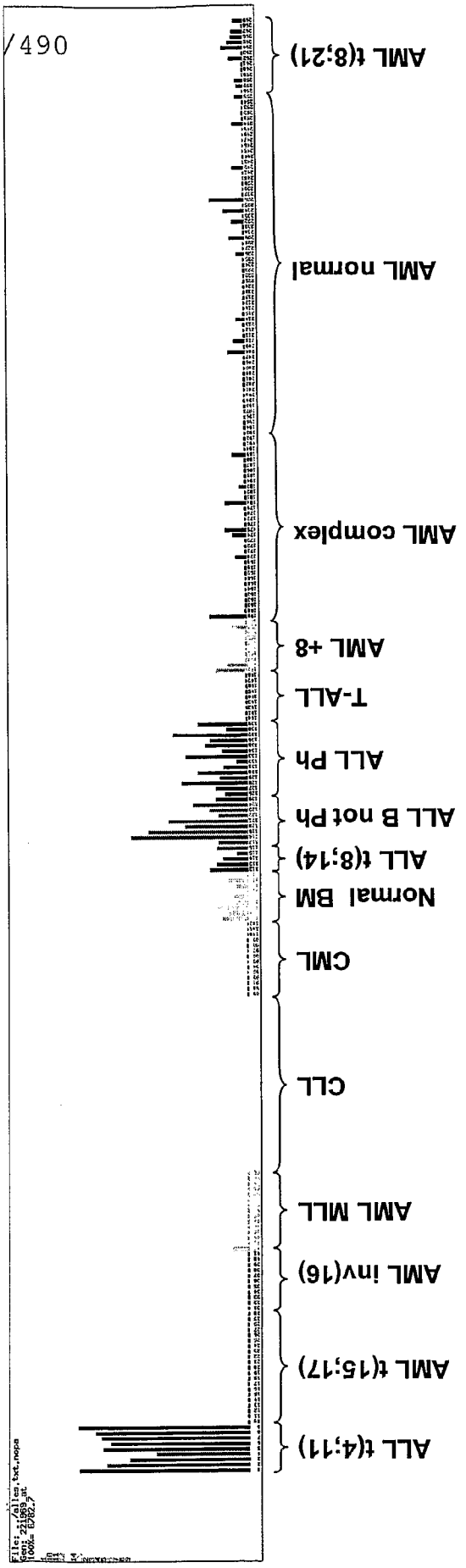

221969_at, PAX5, ALL B not Ph vs. AML normal
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 149

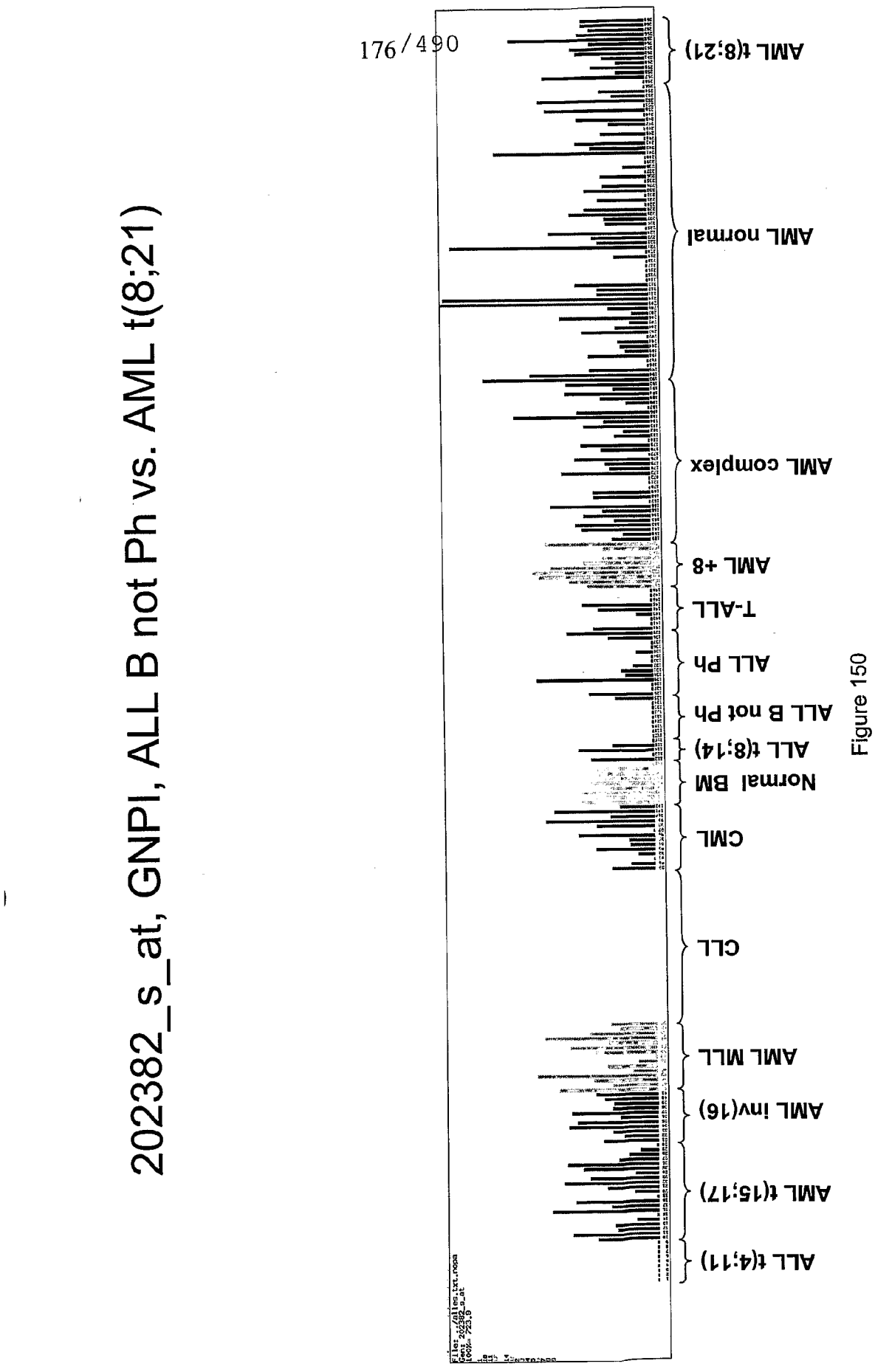

202382_s_at, GNPI, ALL B not Ph vs. AML t(8;21)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 150

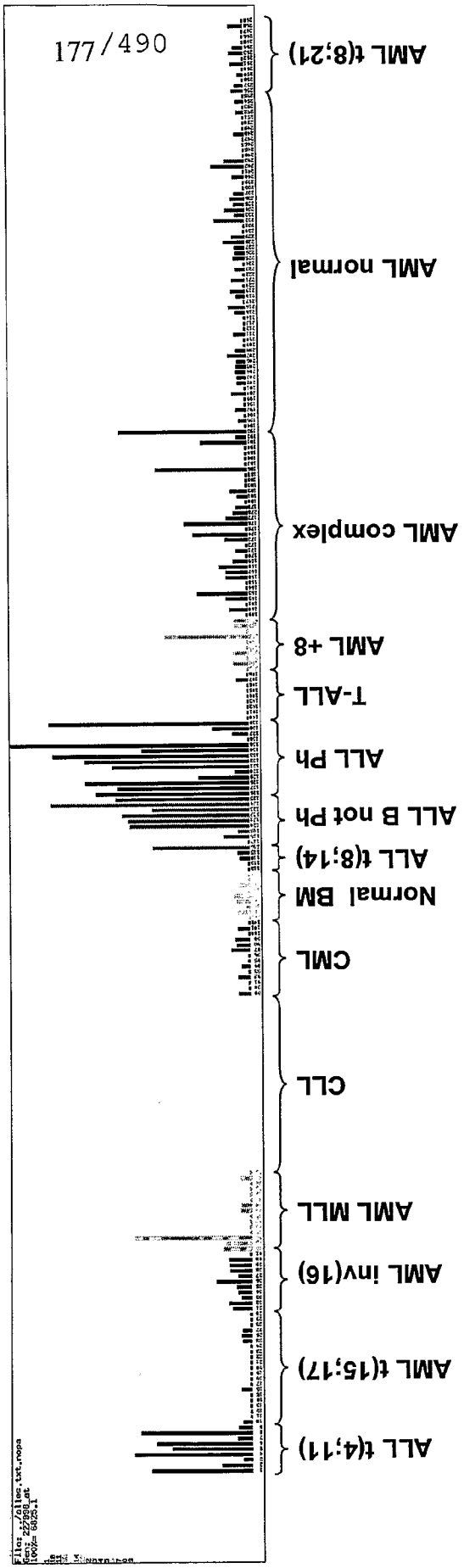

227998_at, MGC17528, ALL Ph vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 151

221969_at, PAX5, ALL Ph vs. T-ALL

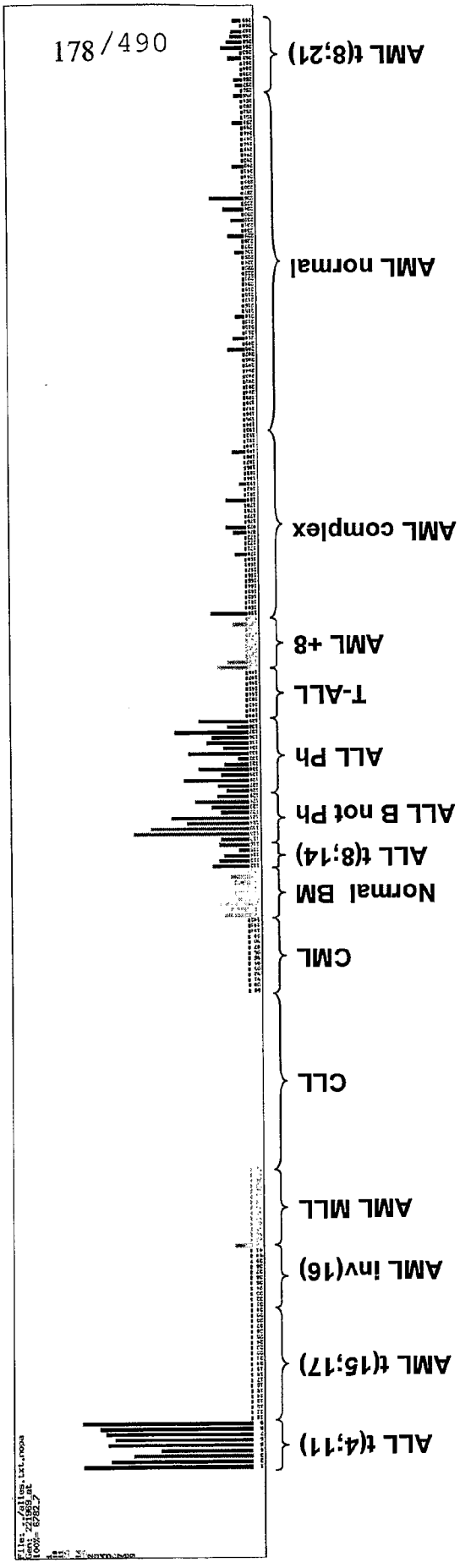


Figure 152

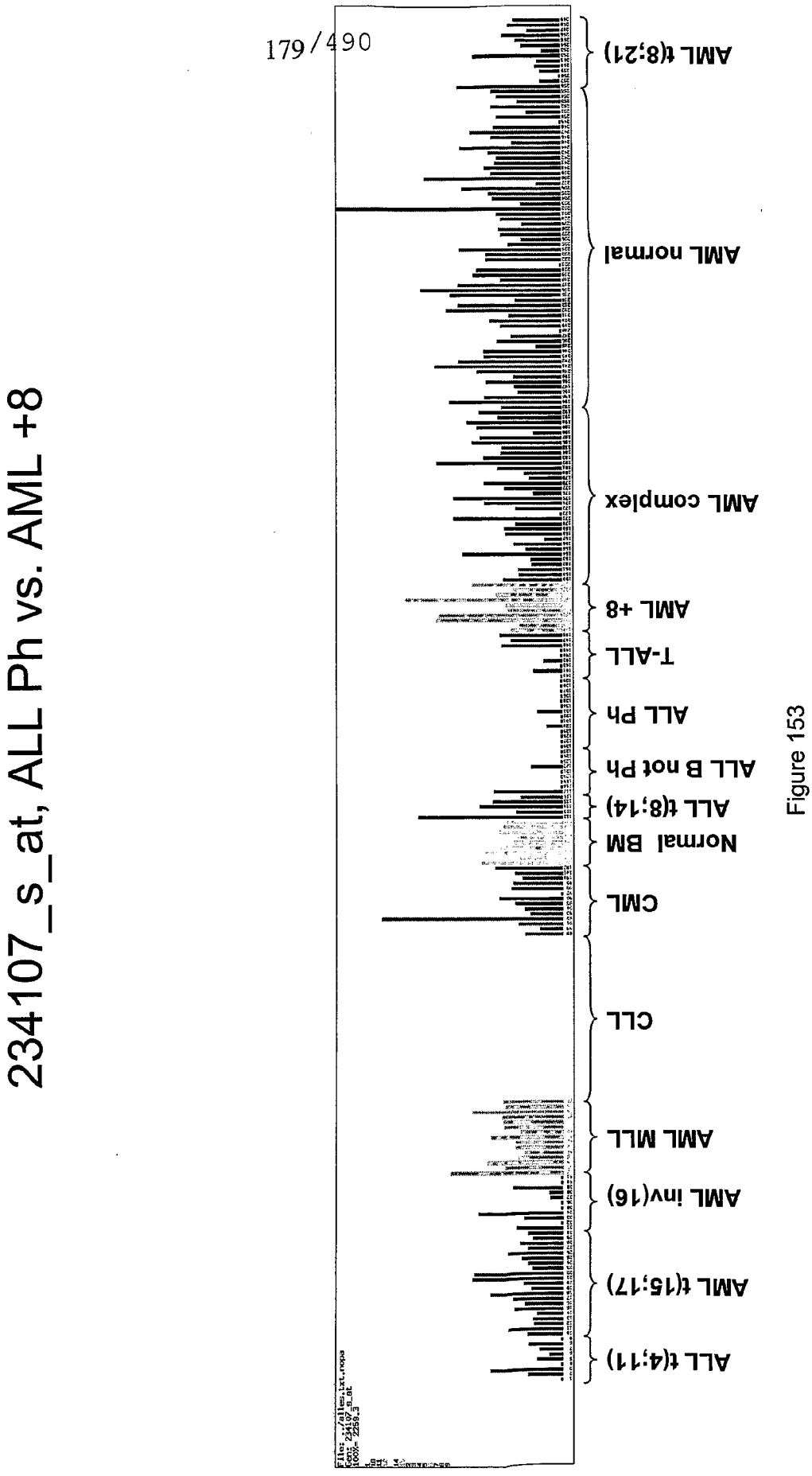

234107_s_at, ALL Ph vs. AML +8
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 153

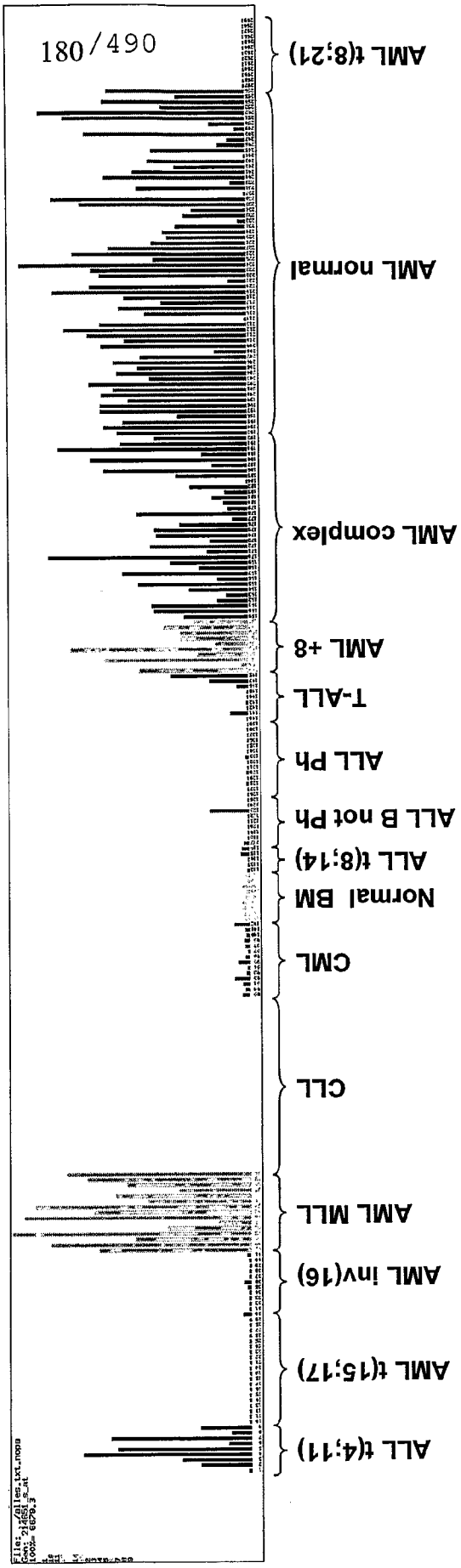

214641_s_at, HOXA9, ALL Ph vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 154

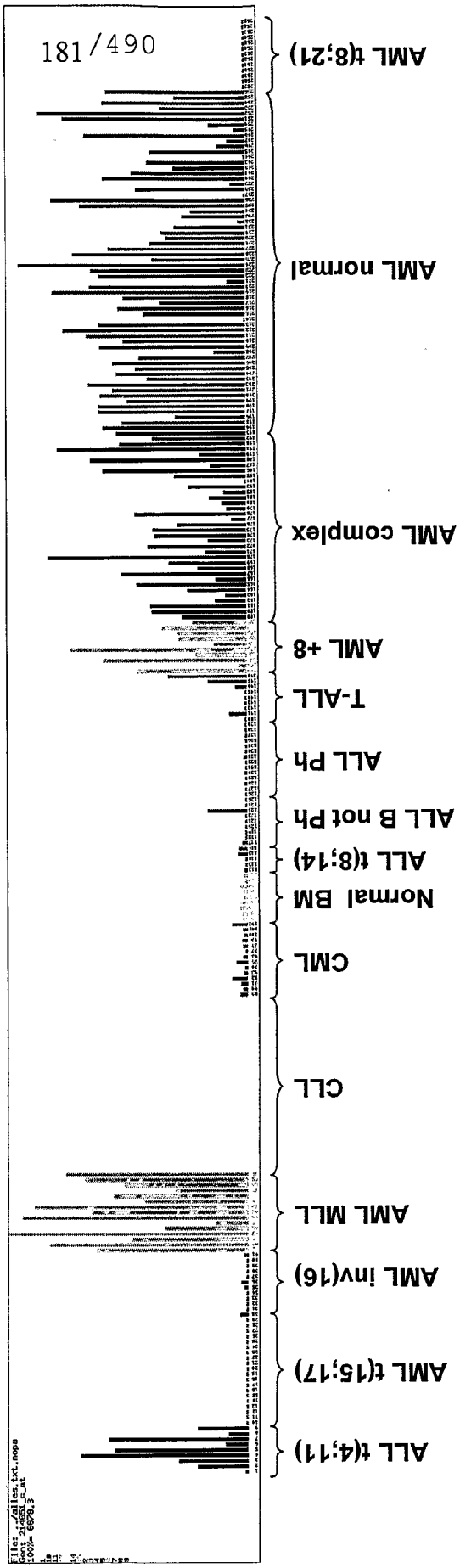

214641_s_at, HOXA9, ALL Ph vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 155

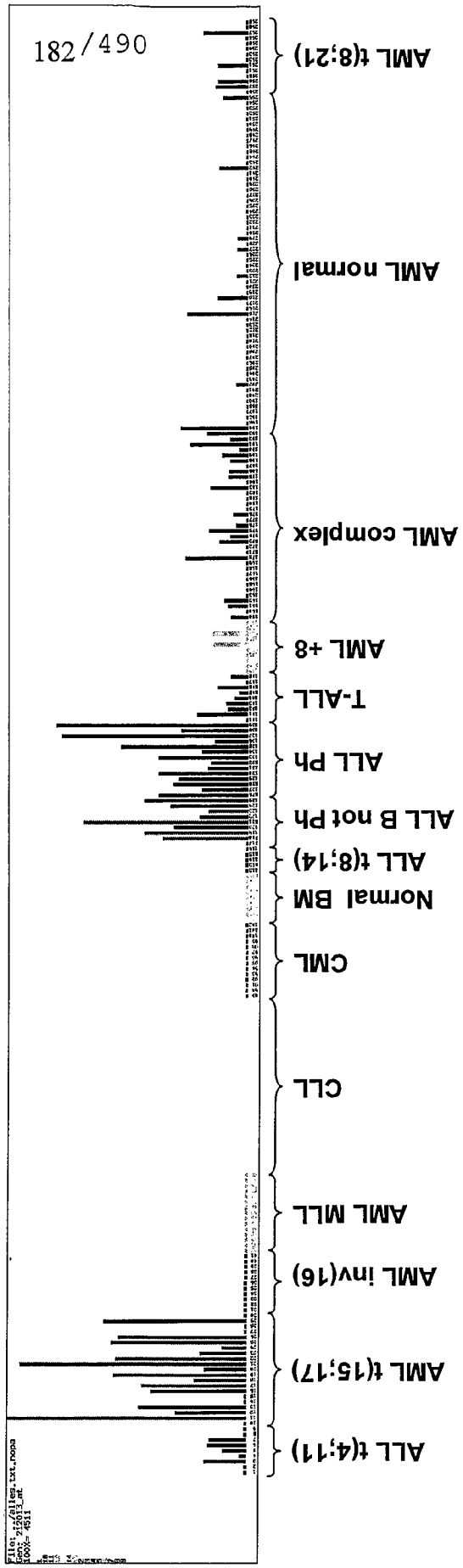

212013_at, D2S448, ALL Ph vs. AML normal
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 156

228827_at, ALL Ph vs. AML t(8;21)

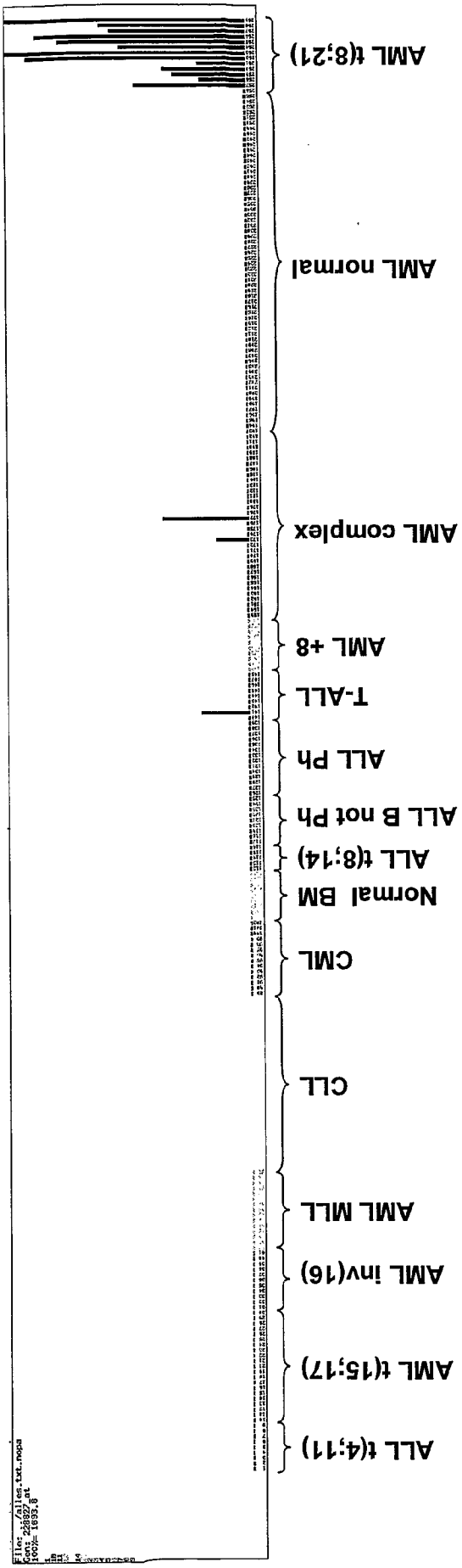


Figure 157

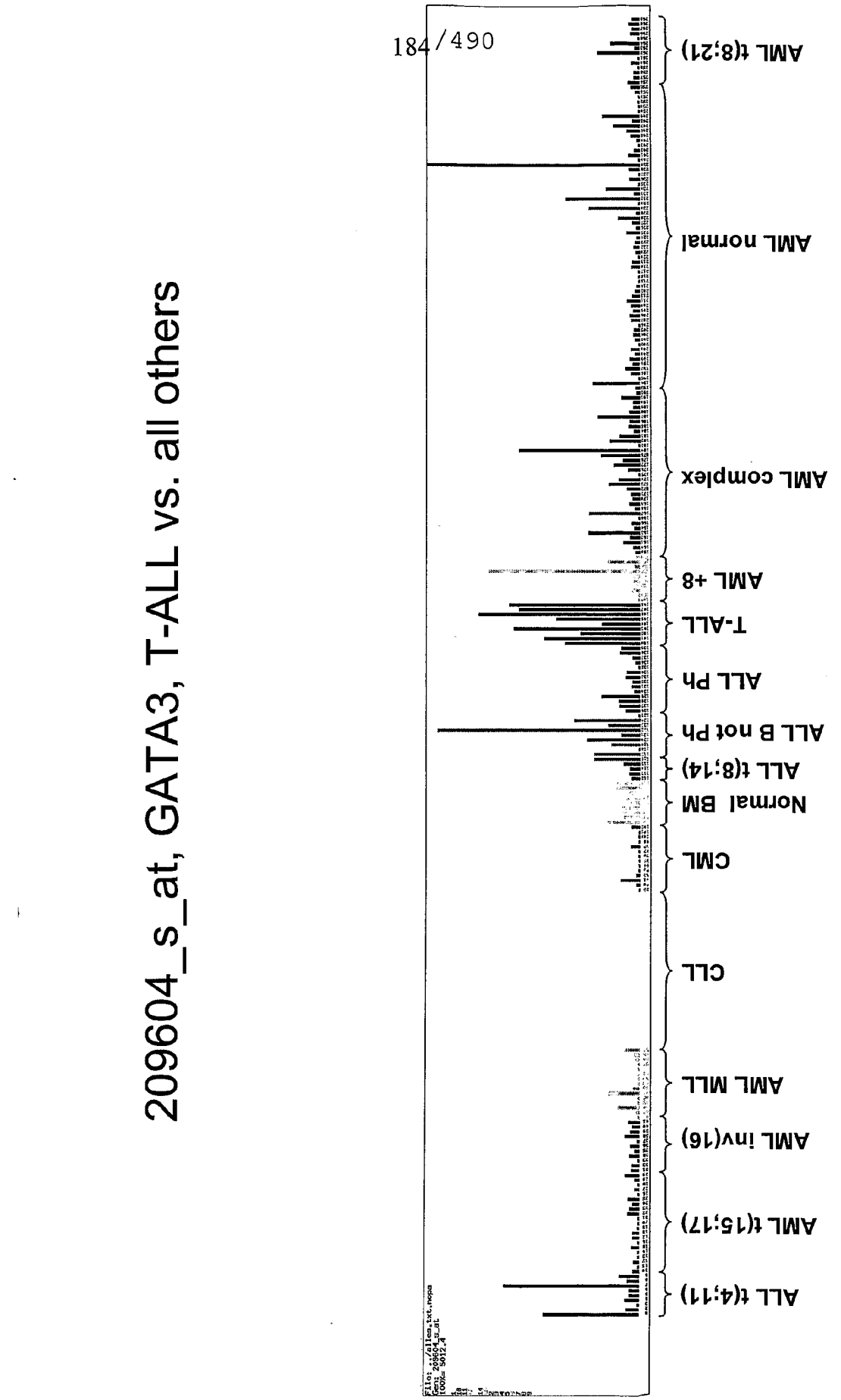

209604_s_at, GATA3, T-ALL vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 158

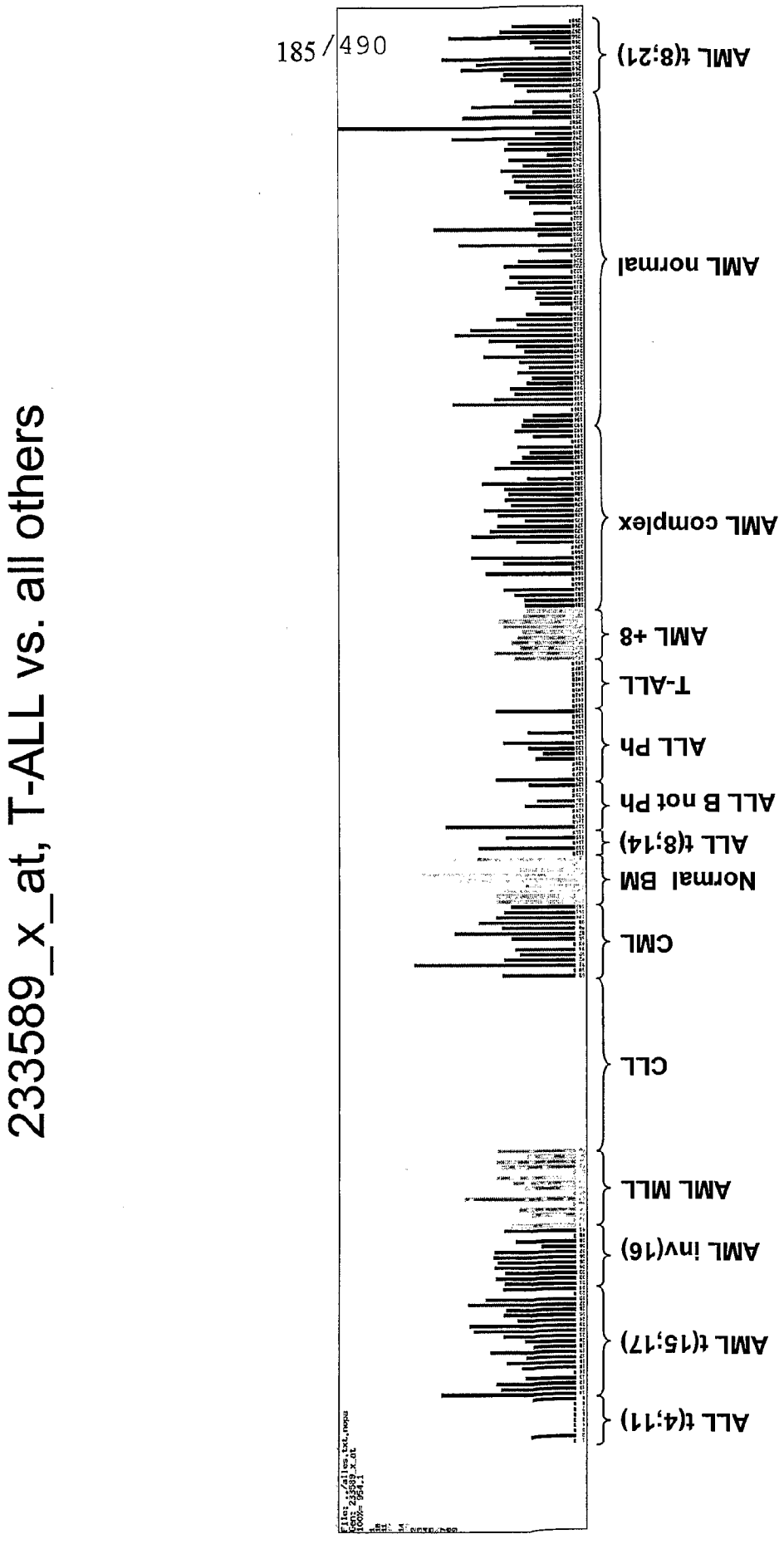

233589_x_at, T-ALL vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 159

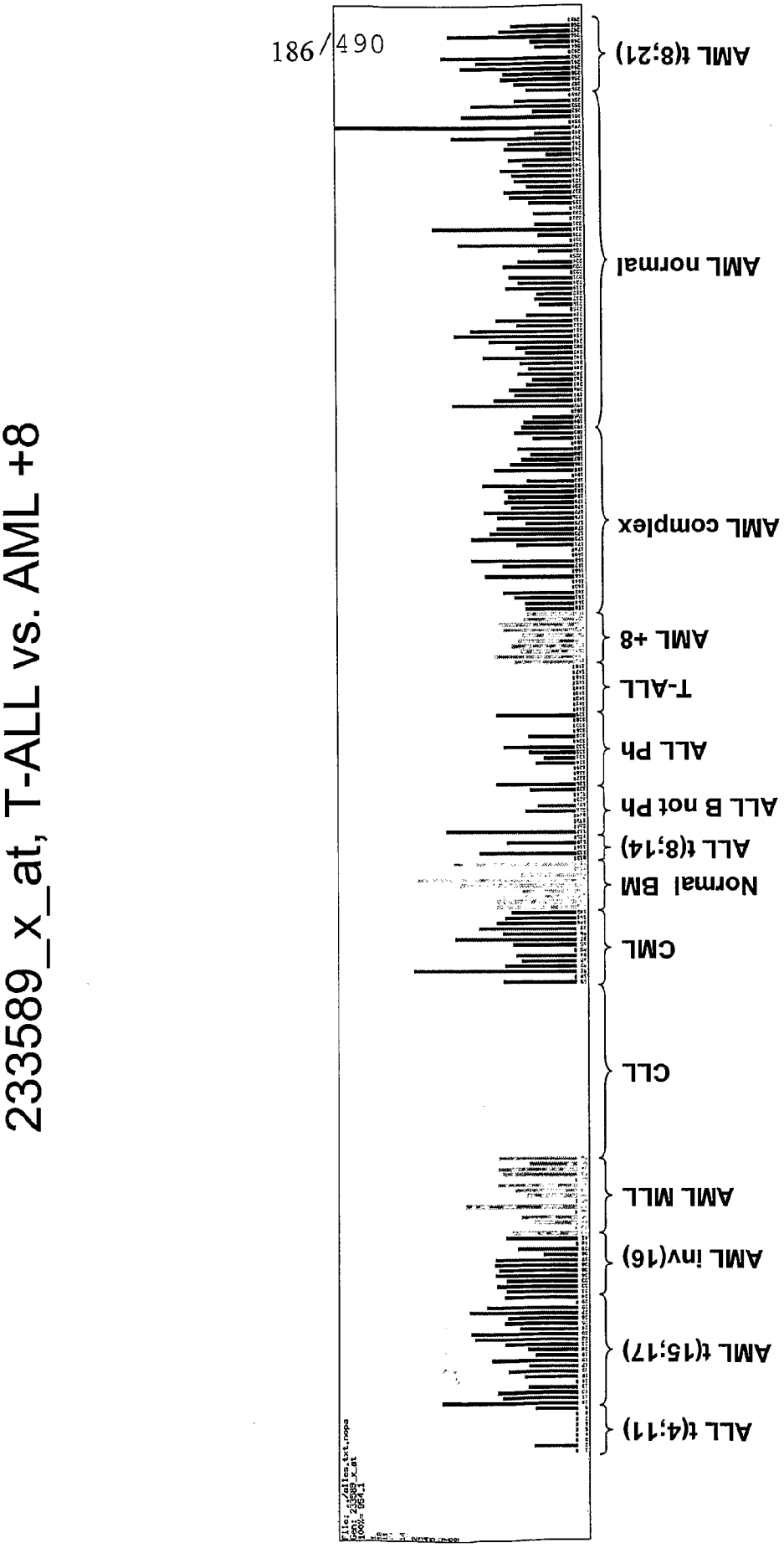

233589_x_at, T-ALL vs. AML +8
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 160

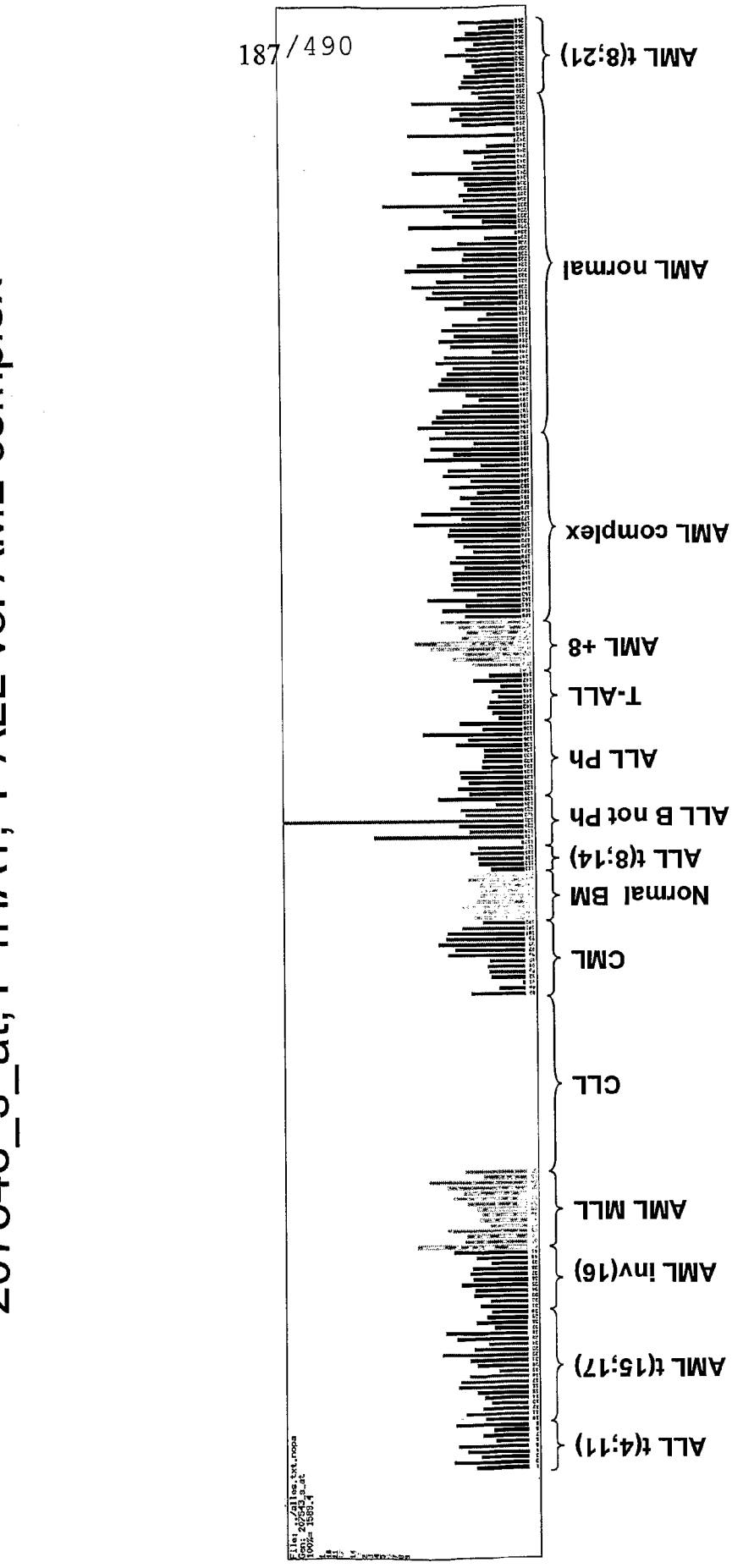

207543_s_at, P4HA1, T-ALL vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 161

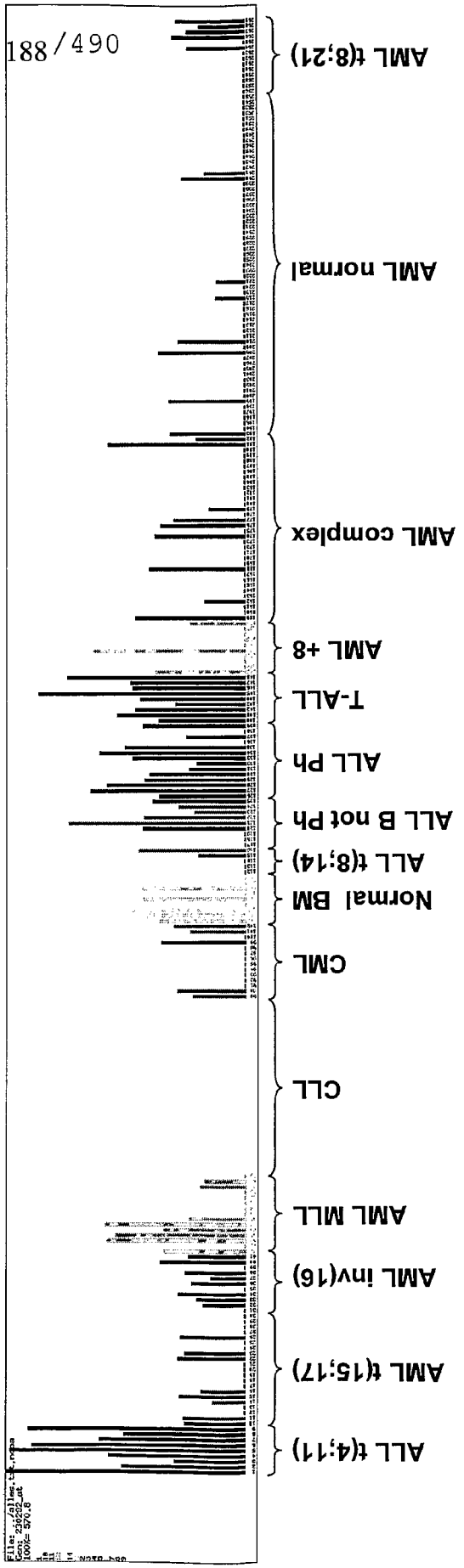

230292_at, T-ALL vs. AML normal
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 162

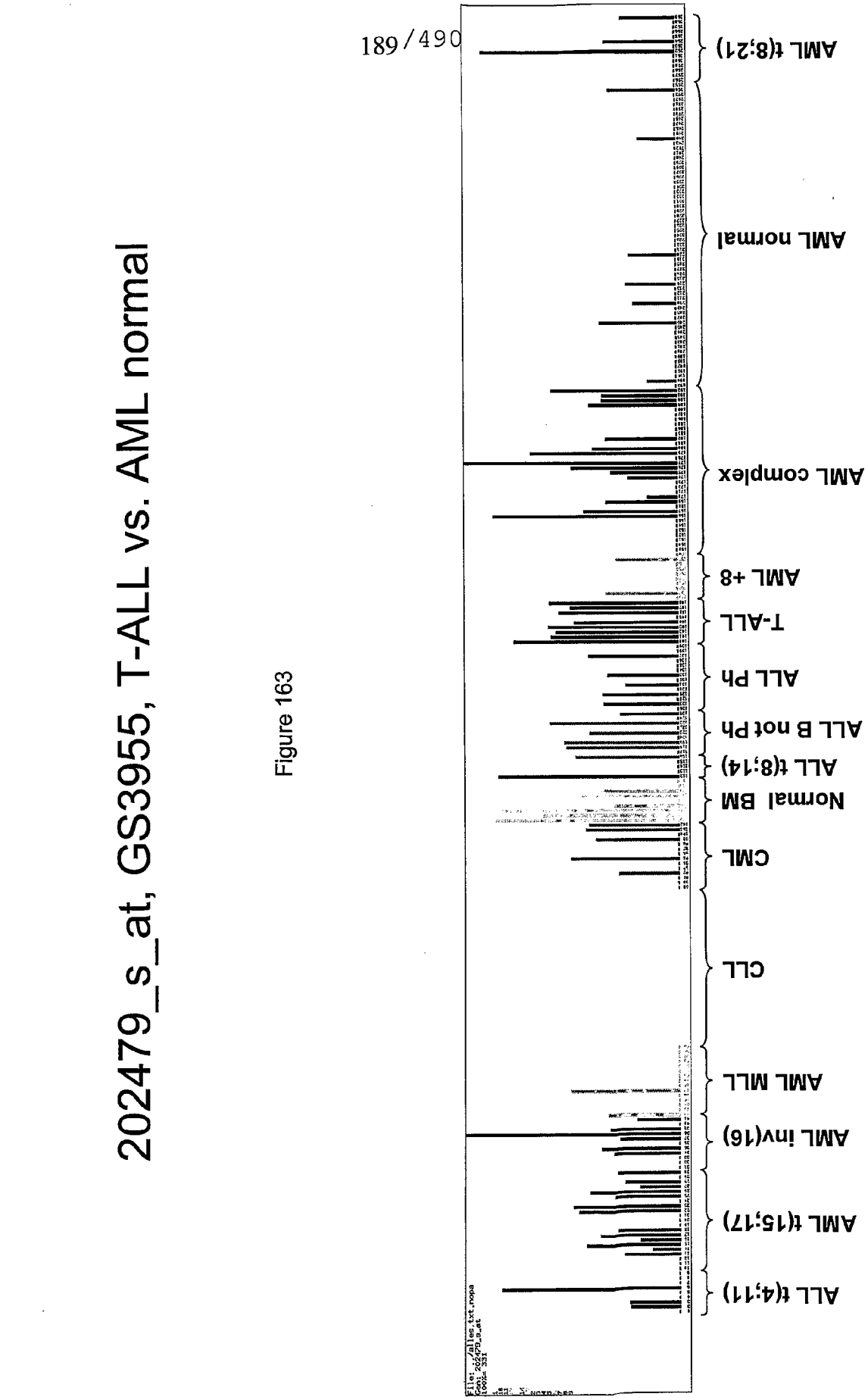

202479_s_at, GS3955, T-ALL vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 163

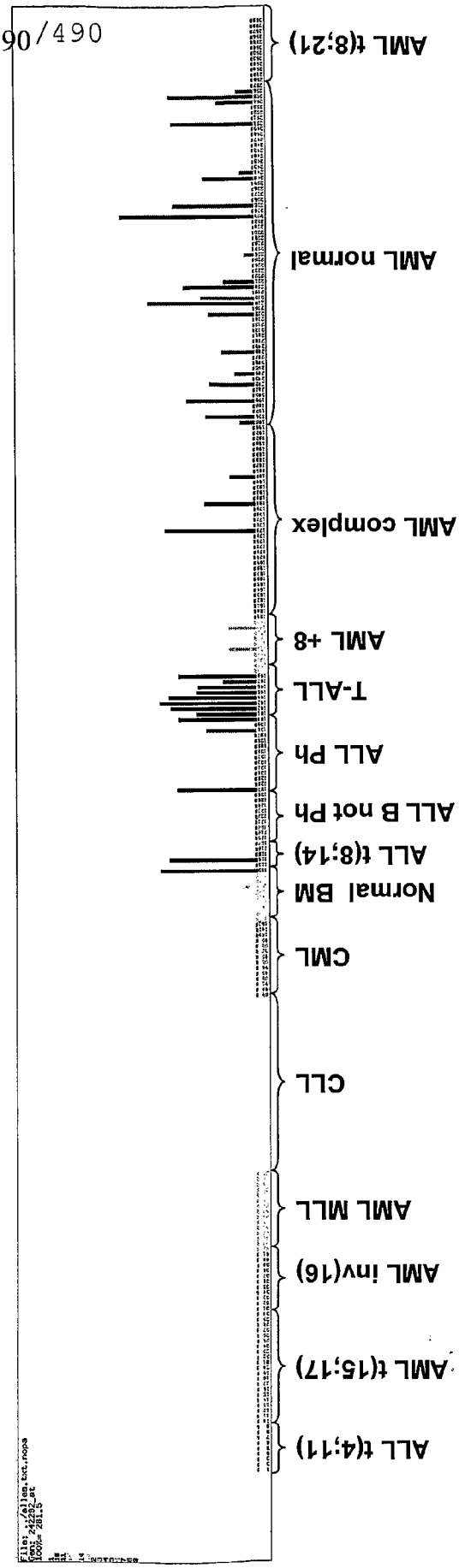

242292_at, T-ALL vs. AML t(8;21)
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 164

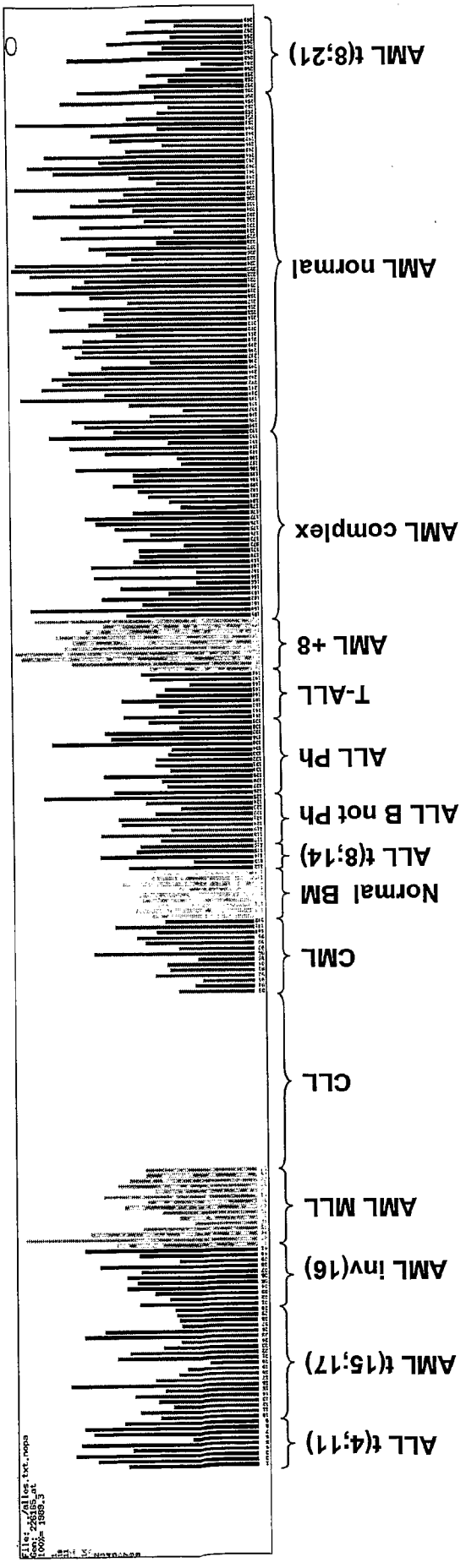

226165_at, E2F5, AML +8 vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 165

212586_at, ARTS-1, AML +8 vs. AML complex

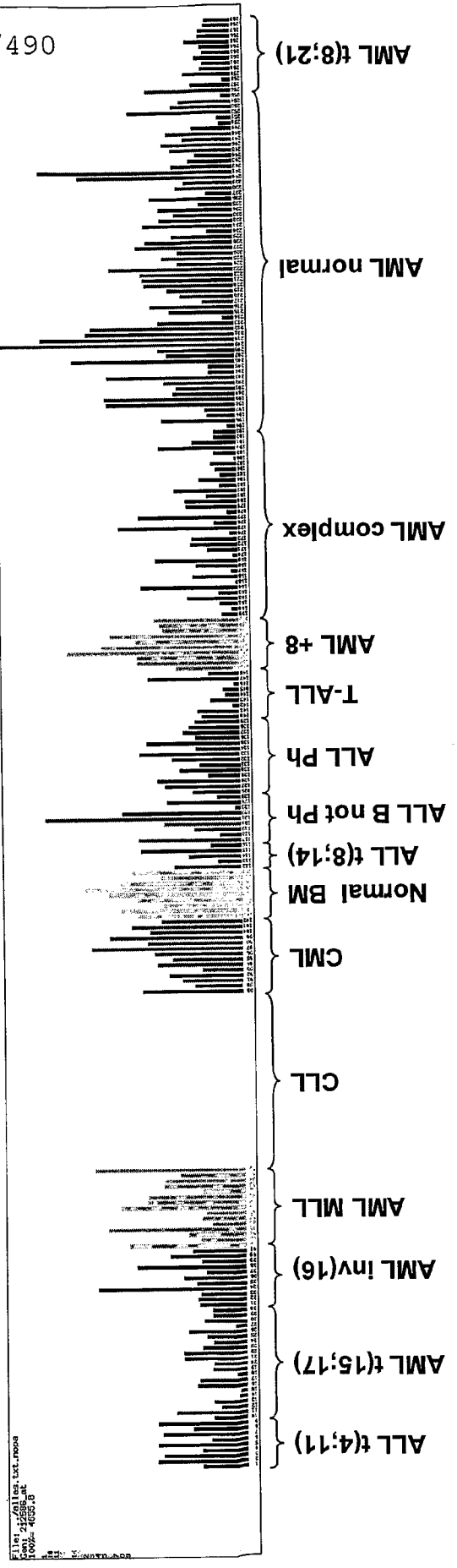


Figure 166

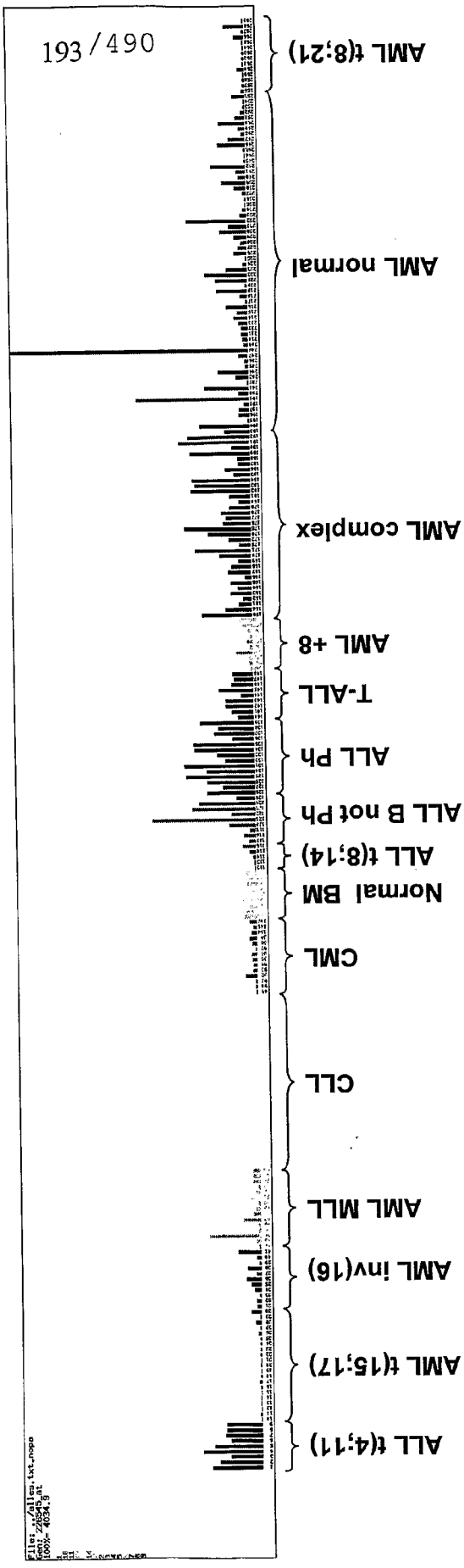

226545_at, AML +8 vs. AML complex
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 167

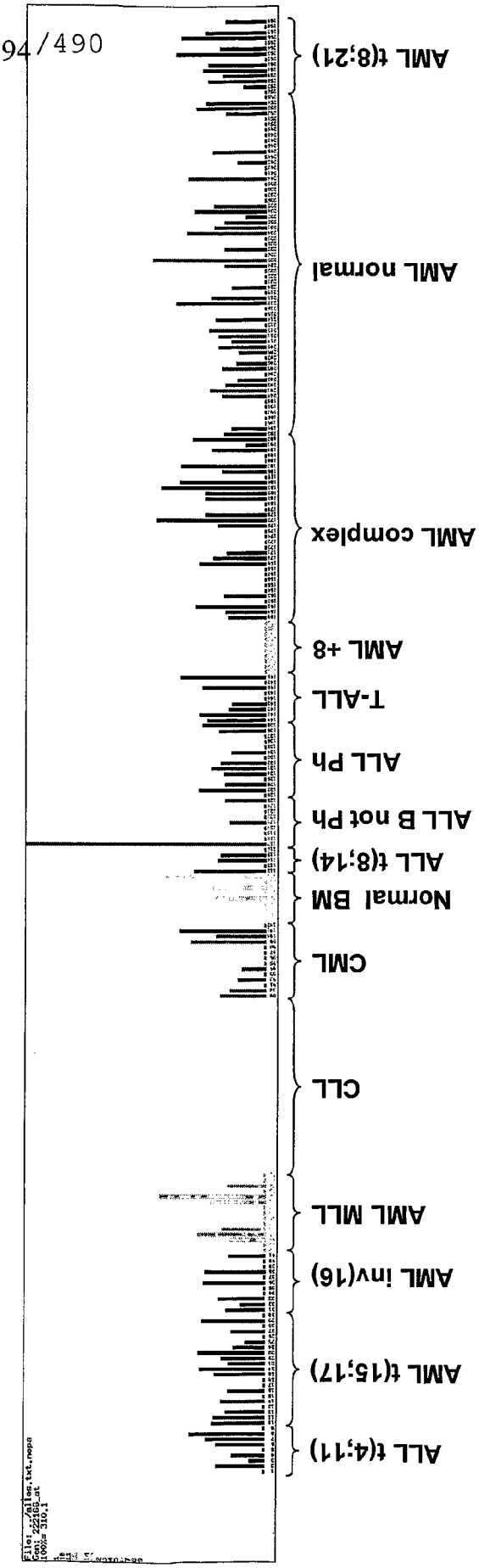

222166_at, AML +8 vs. AML complex
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 168

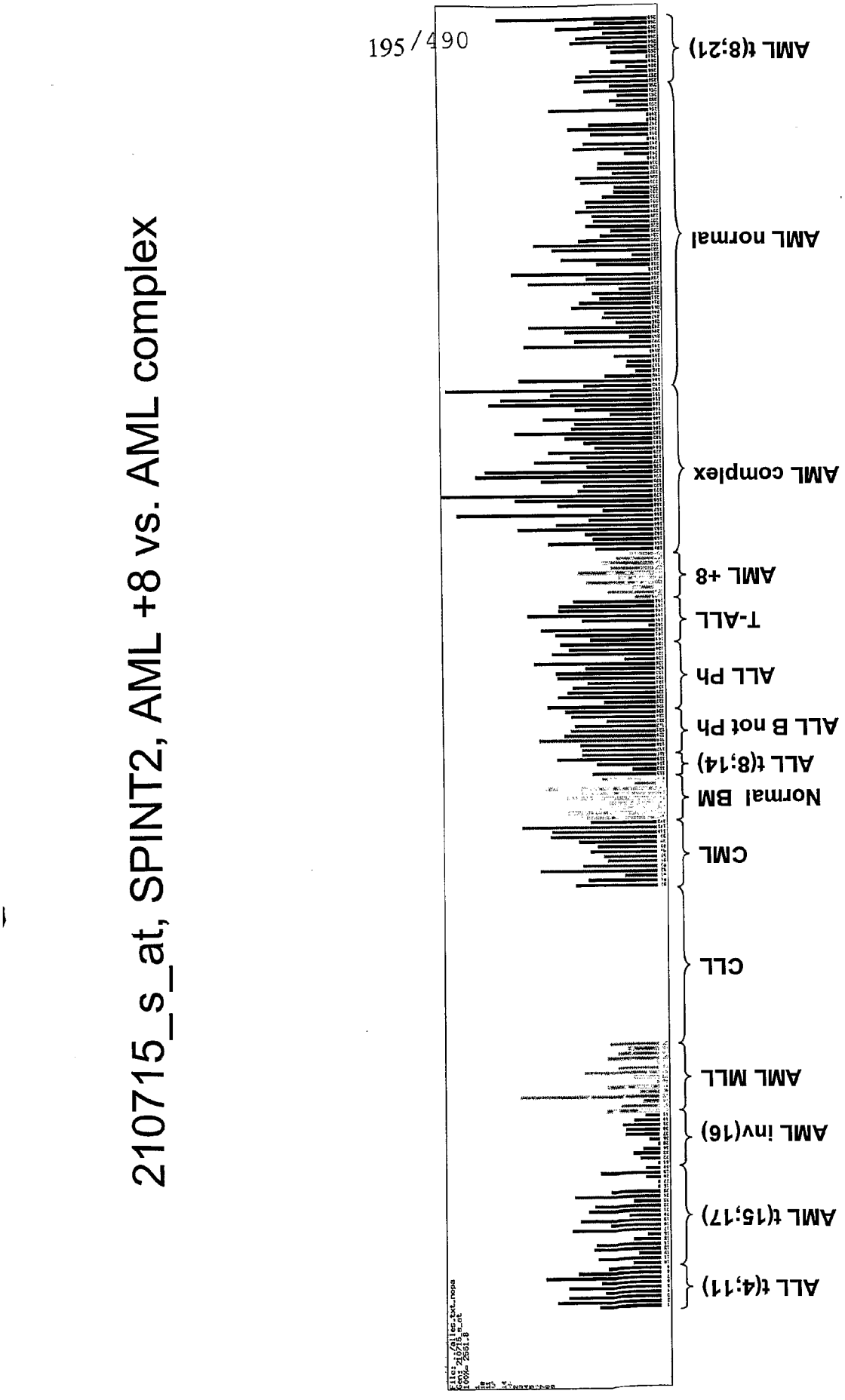

210715_s_at, SPINT2, AML +8 vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 169

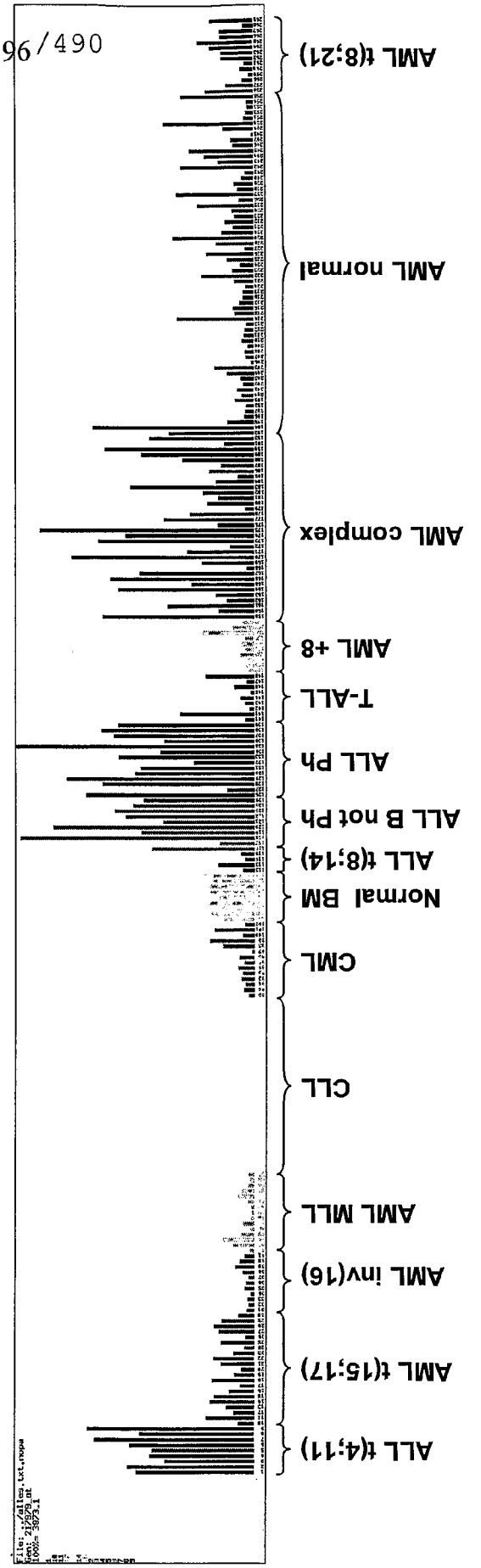

217979_at, NET-6, AML +8 vs. AML complex
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 170

201548_s_at, PLU-1, AML +8 vs. AML complex

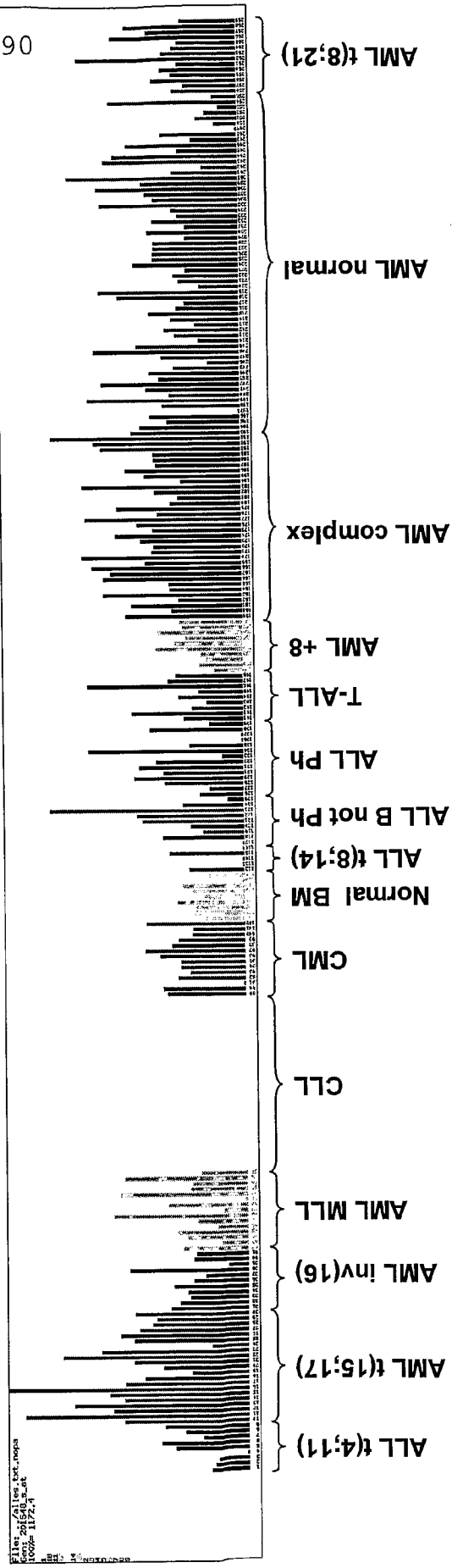


Figure 171

212251_at, AML +8 vs. AML normal

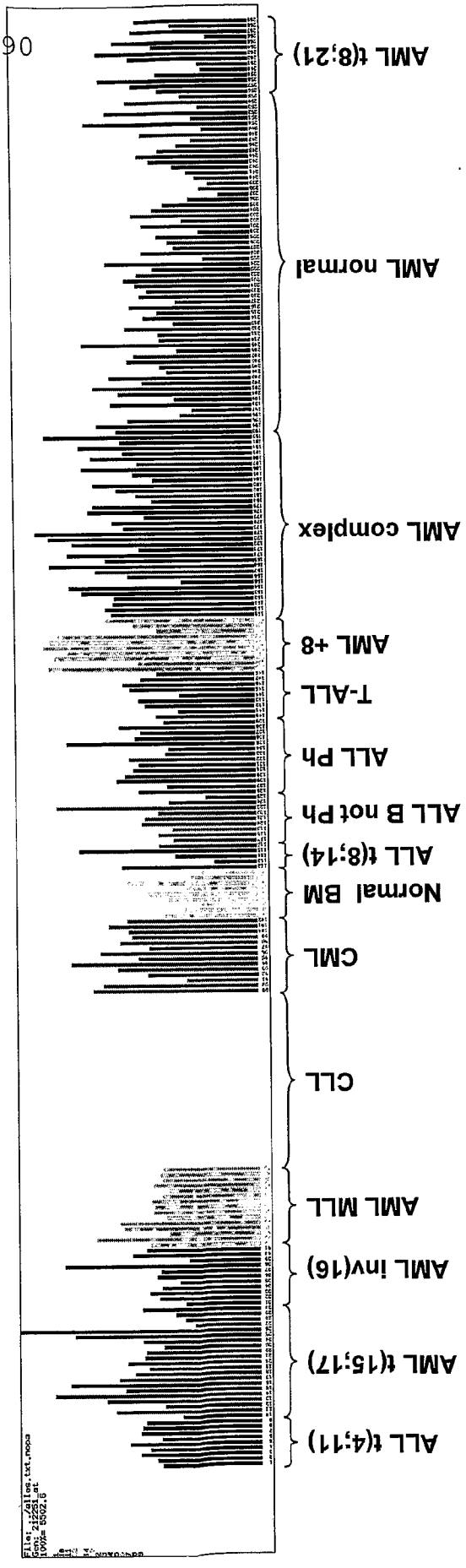


Figure 172

228827_at, AML +8 vs. AML t(8;21)

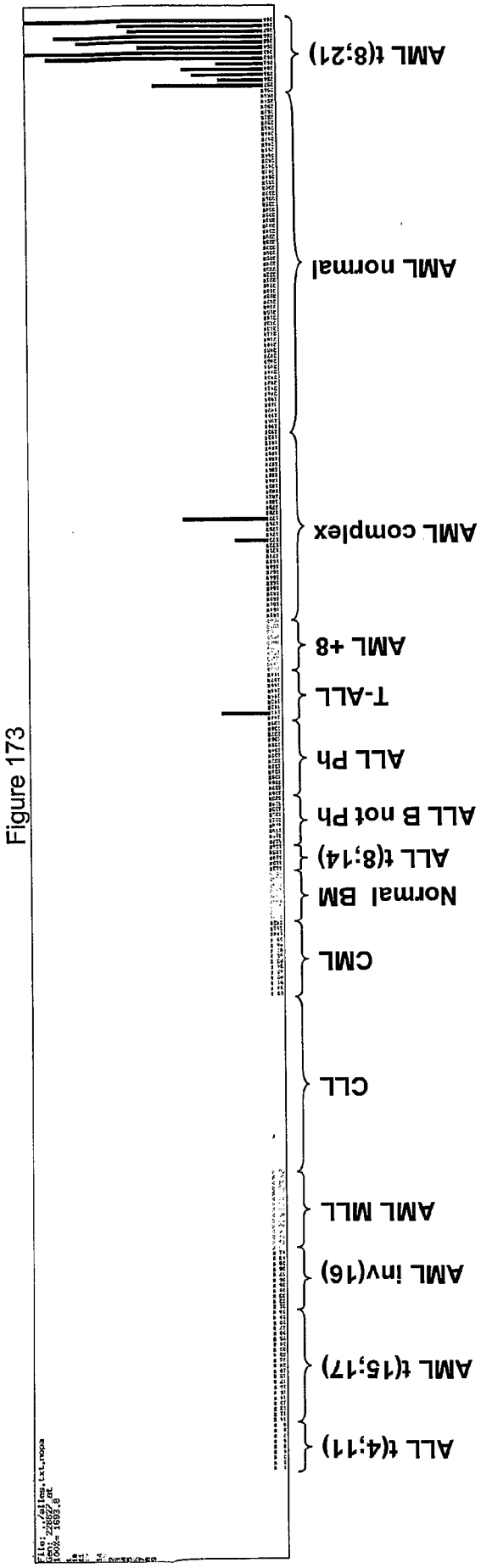


Figure 173

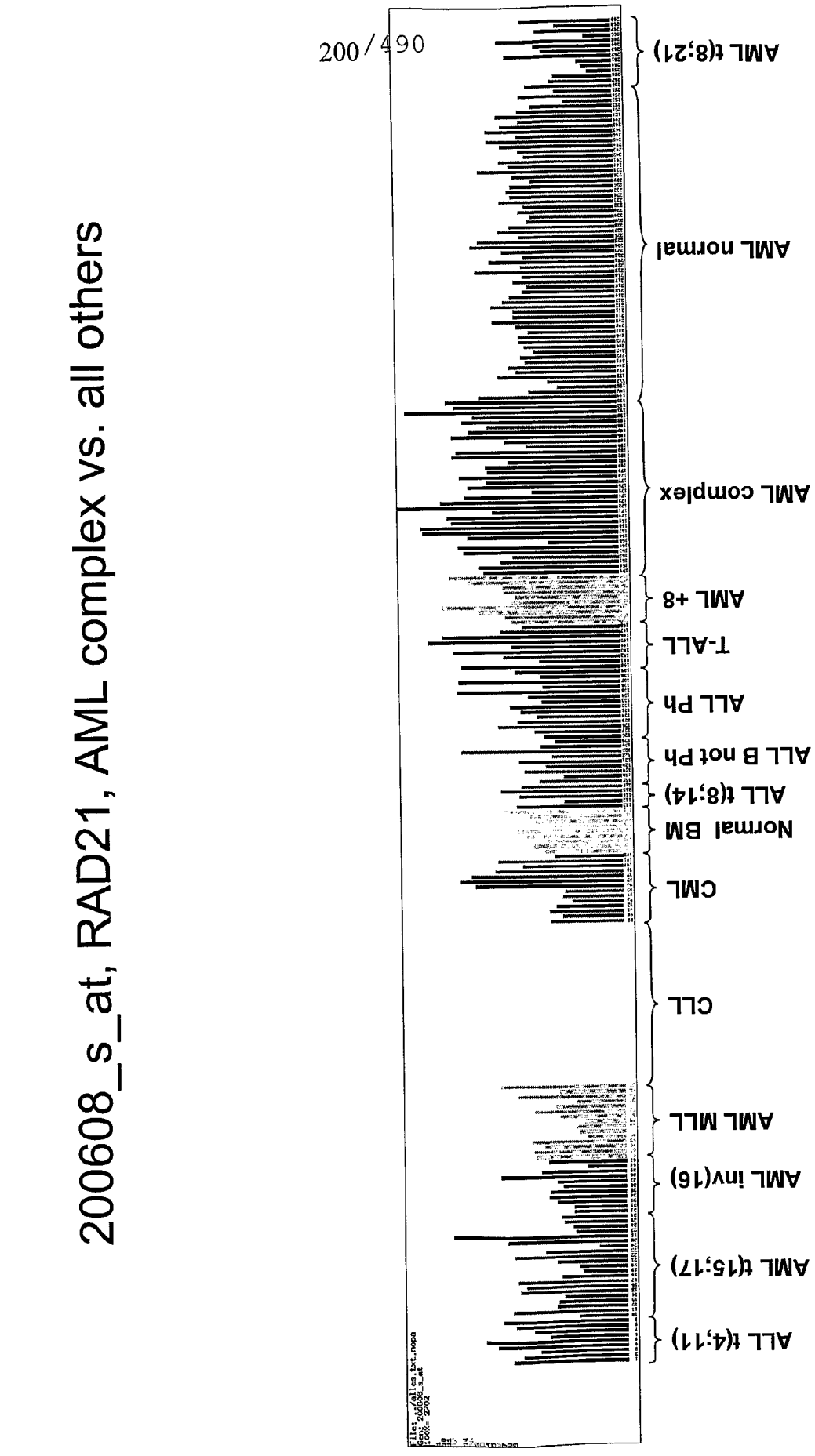

200608_s_at, RAD21, AML complex vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 174

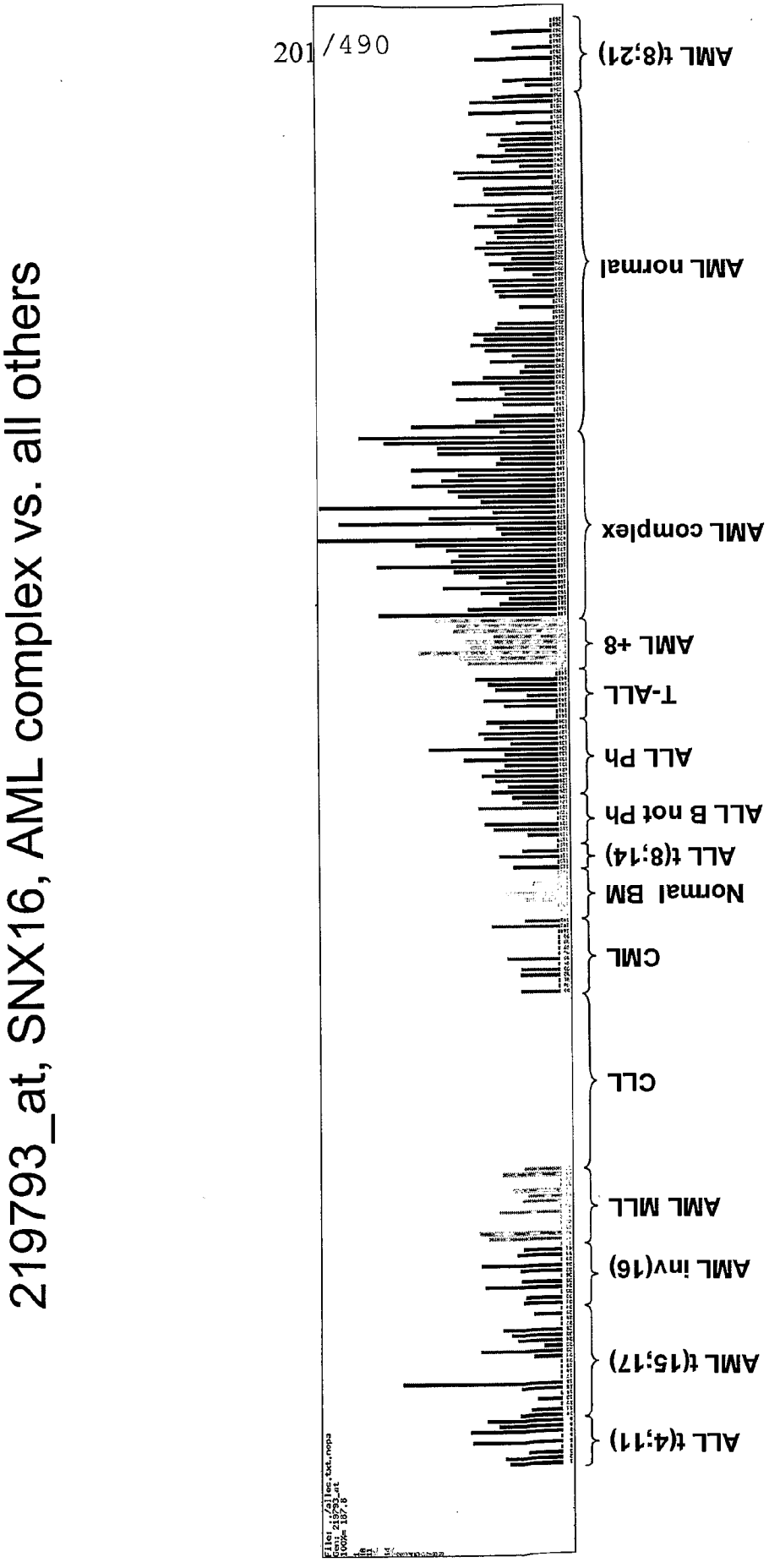

219793_at, SNX16, AML complex vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 175

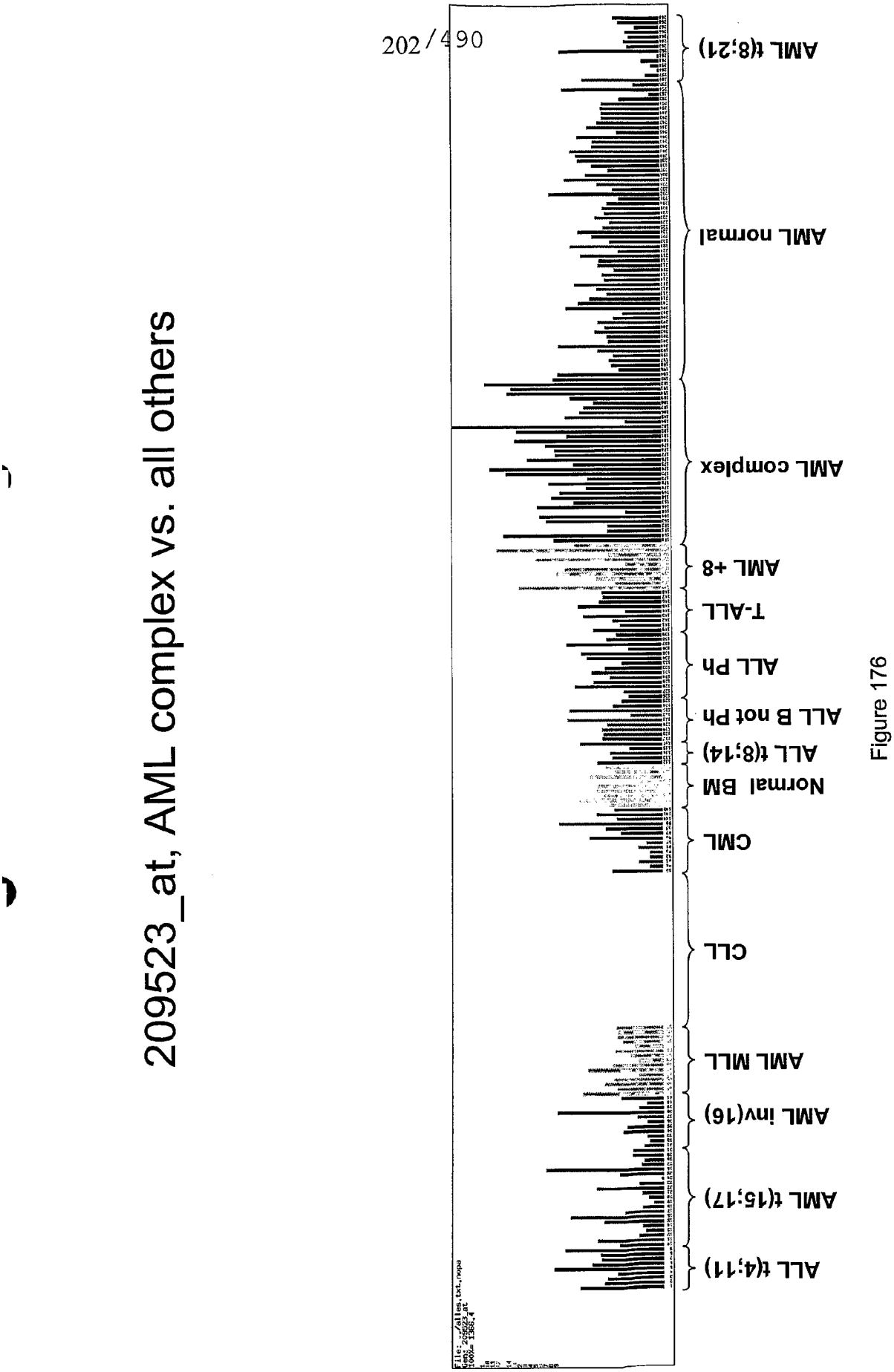

209523_at, AML complex vs. all others
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 176

200093_s_at - HG-U133B, HINT1, AML complex vs. AML normal

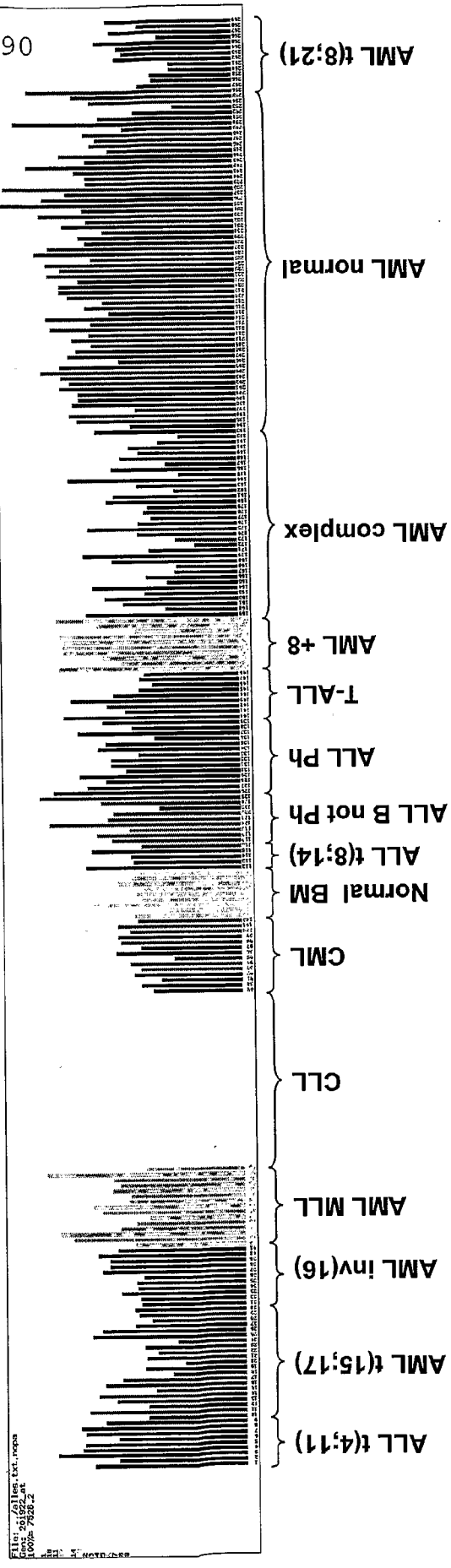


Figure 177

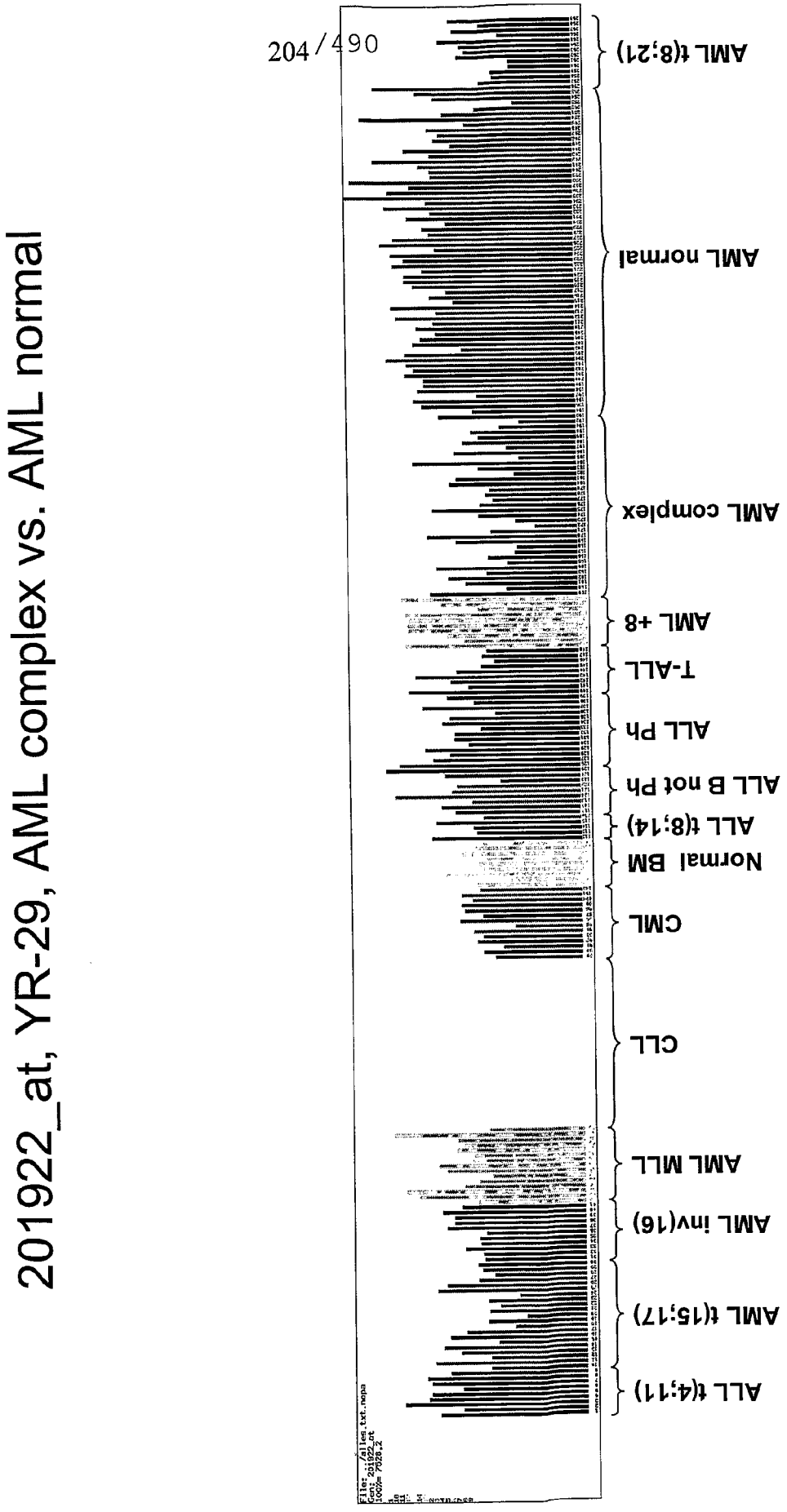

201922_at, YR-29, AML complex vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 178

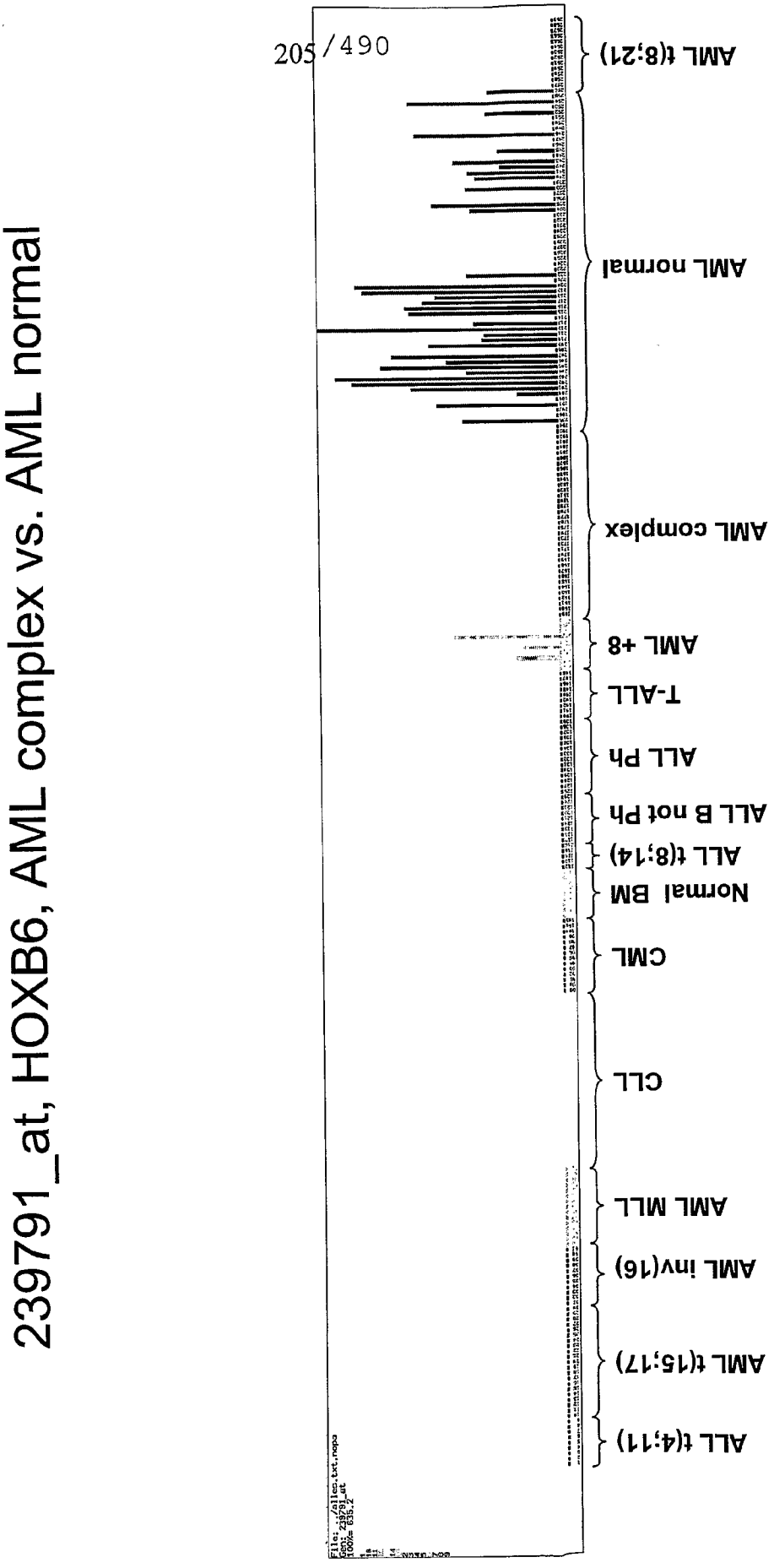

239791_at, HOXB6, AML complex vs. AML normal
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 179

200608_s_at, RAD21, AML complex vs. AML normal

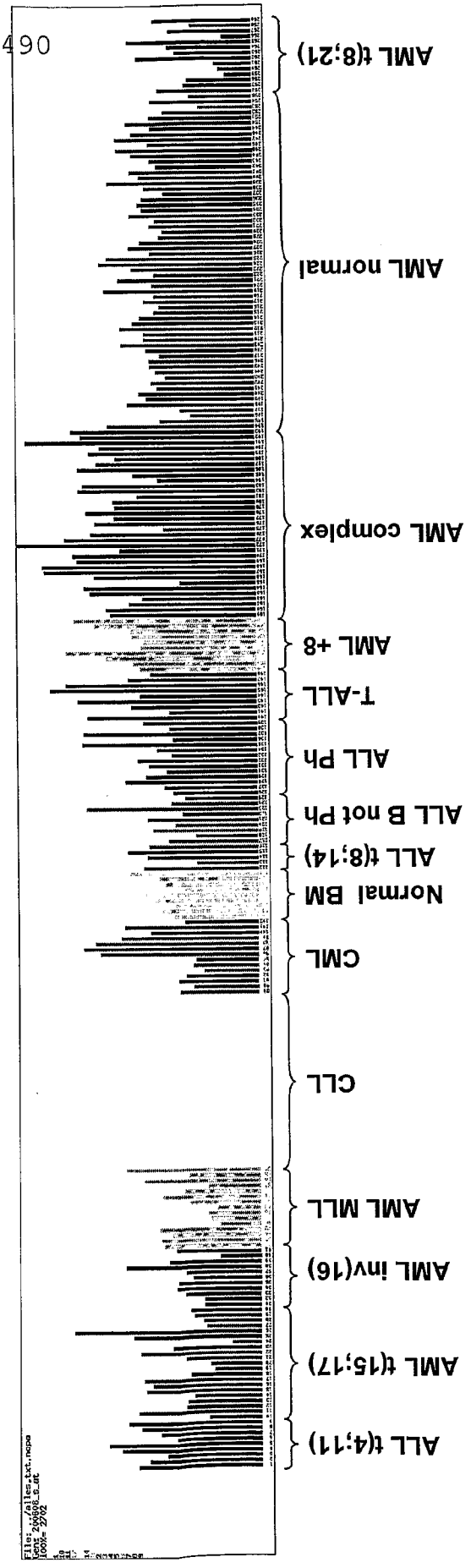


Figure 180

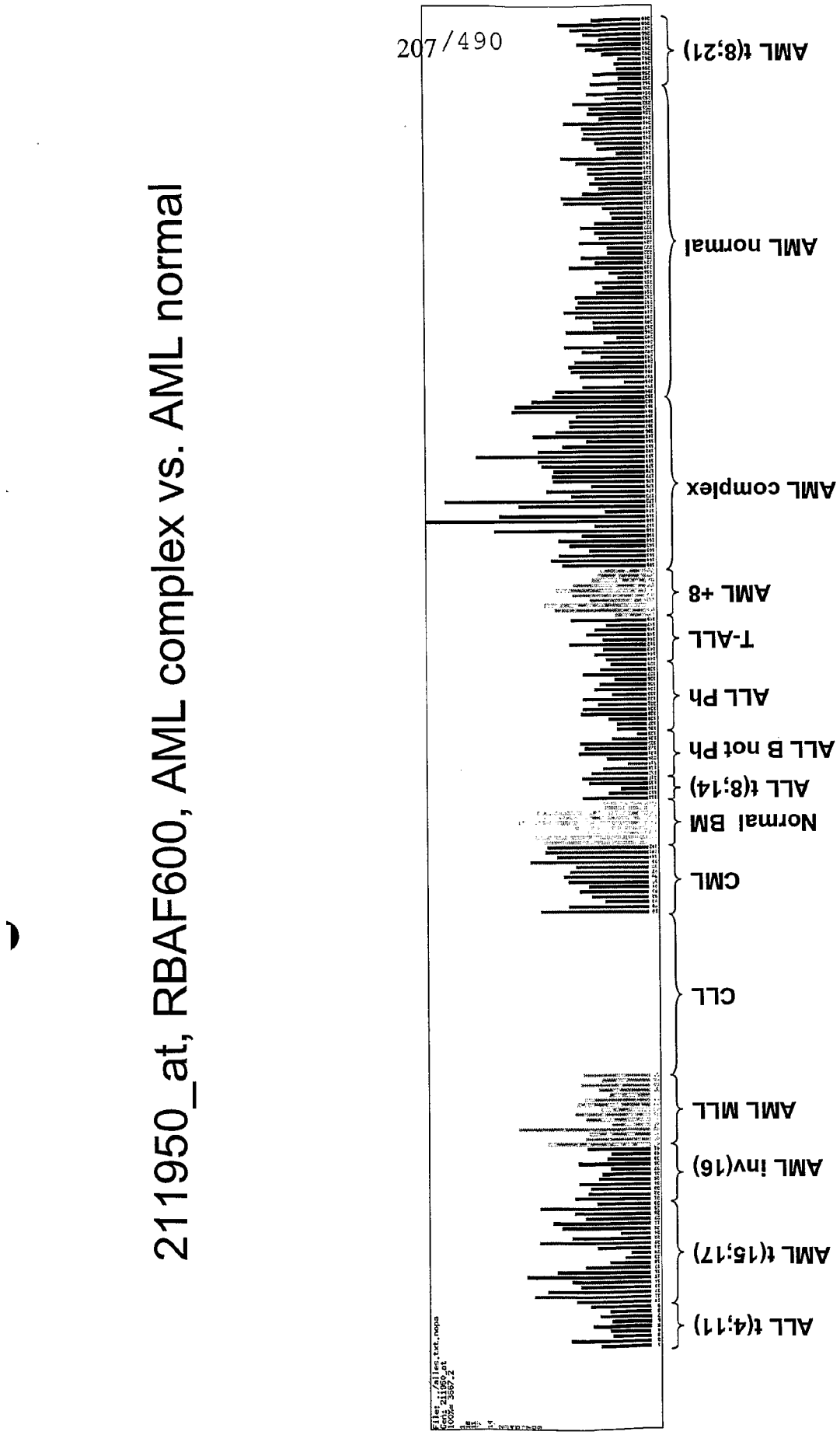

211950_at, RBAF600, AML complex vs. AML normal
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 181

228827_at, AML complex vs. AML t(8;21)

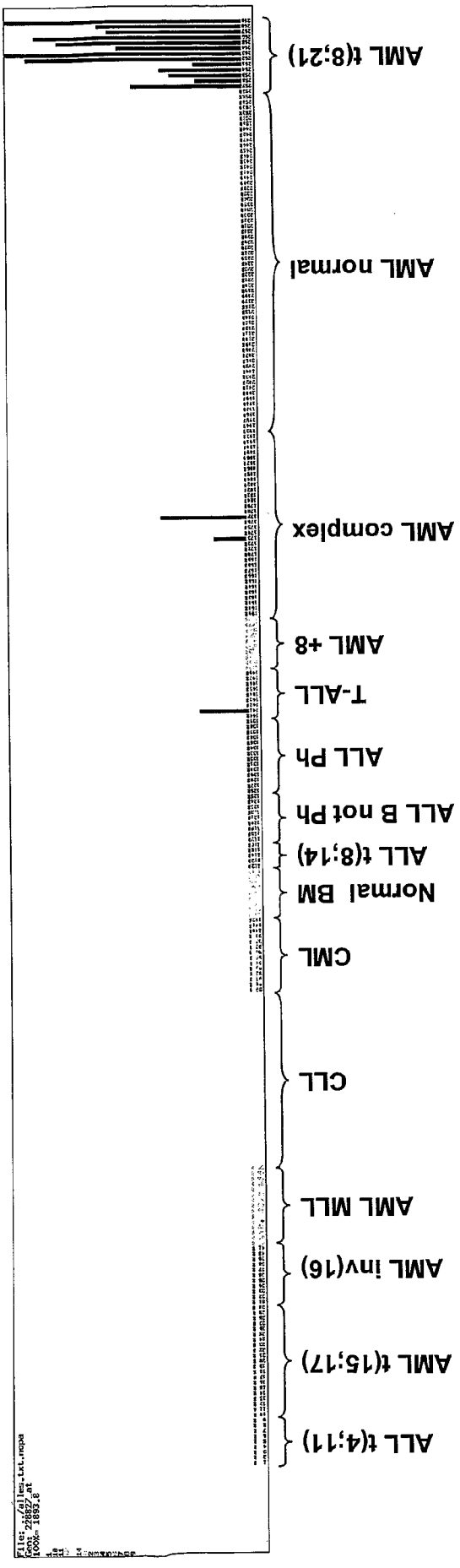


Figure 182

204249_s_at, LMO2, AML complex vs. AML t(8;21)

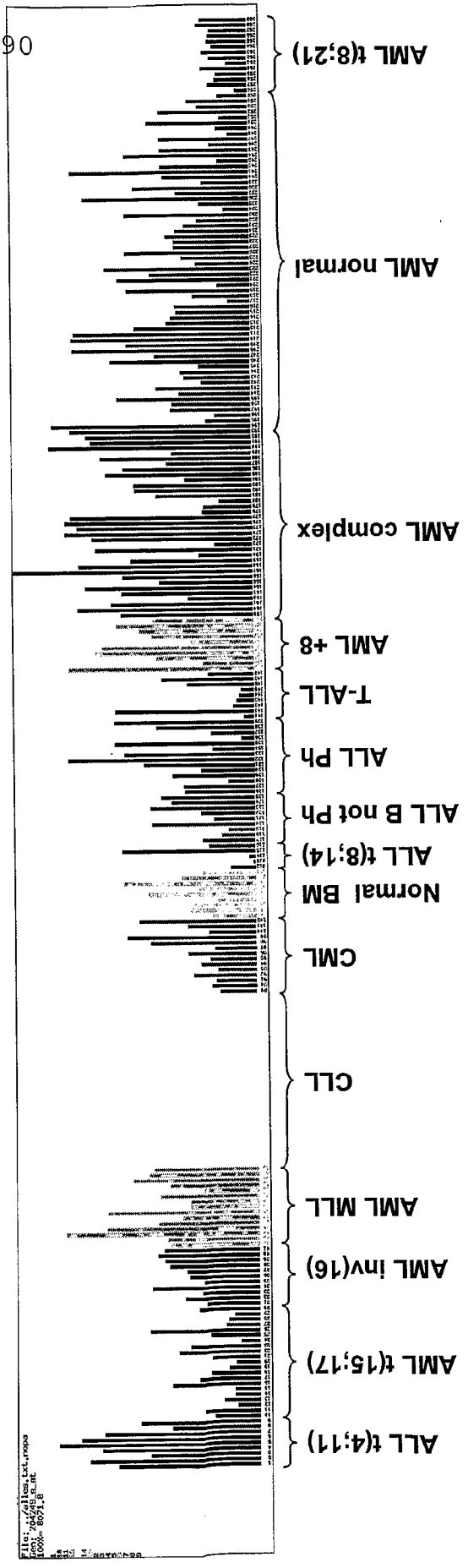


Figure 183

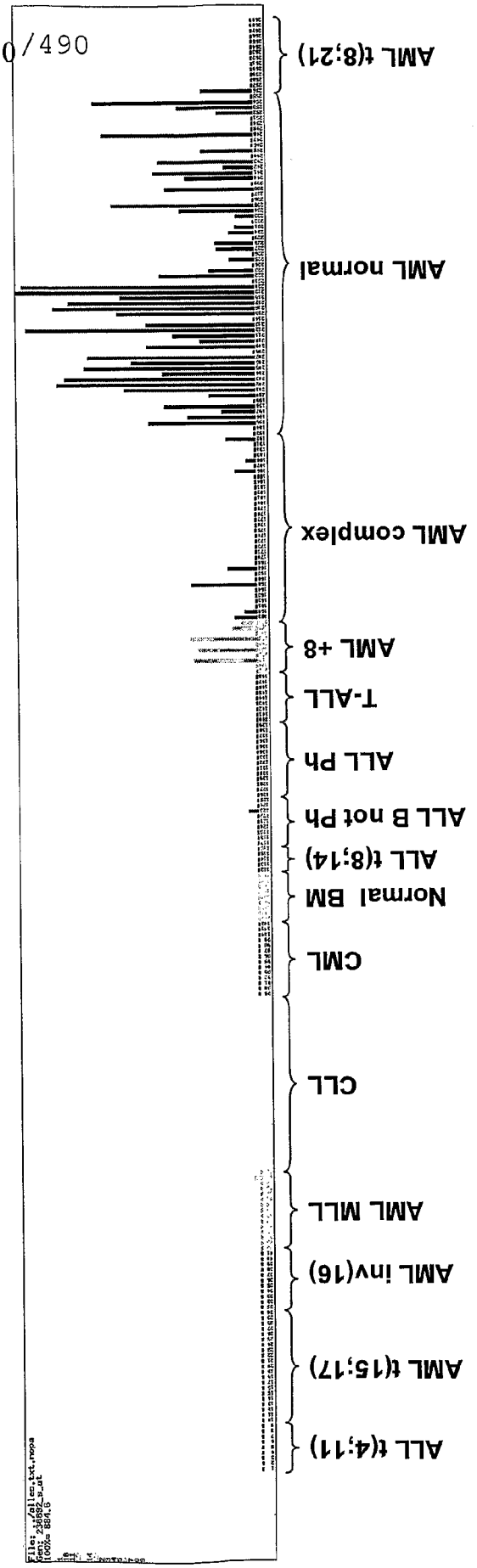

236892_s_at, HOXB6, AML normal vs. all others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 184

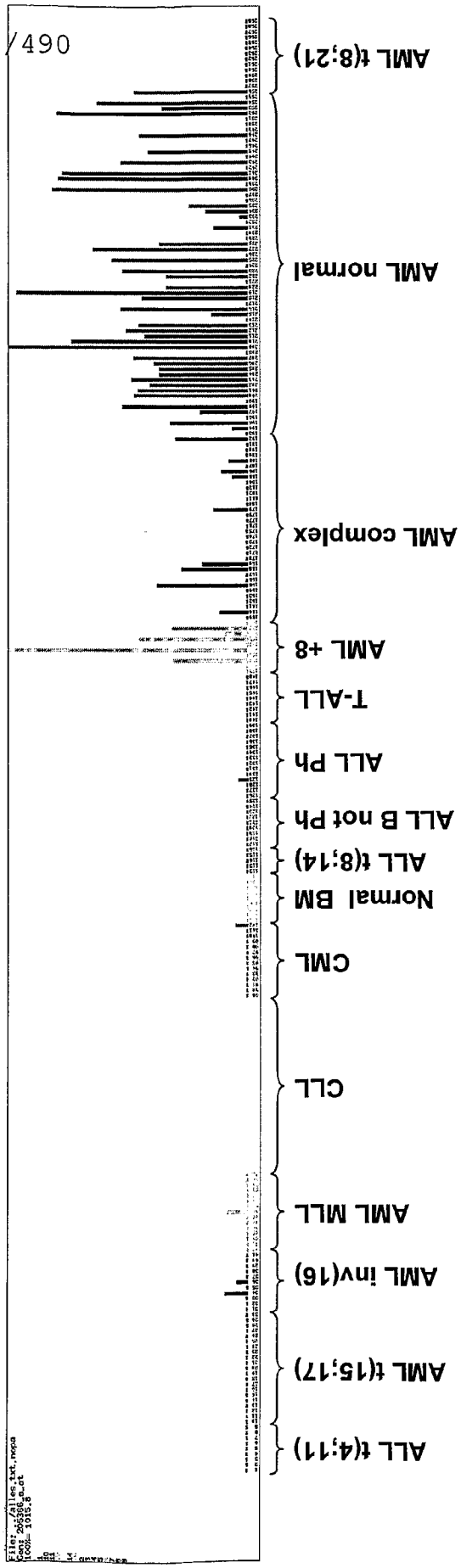

205366_s_at, HOXB6, AML normal vs. All others
AML t(8;21)
AML normal
AML complex
AML +8
T-ALL
ALL Ph
ALL B not Ph
ALL t(8;14)
Normal BM
CML
CLL
AML MLL
AML inv(16)
AML t(15;17)
ALL t(4;11)

Figure 185

228827_at, AML normal vs. AML t(8;21)

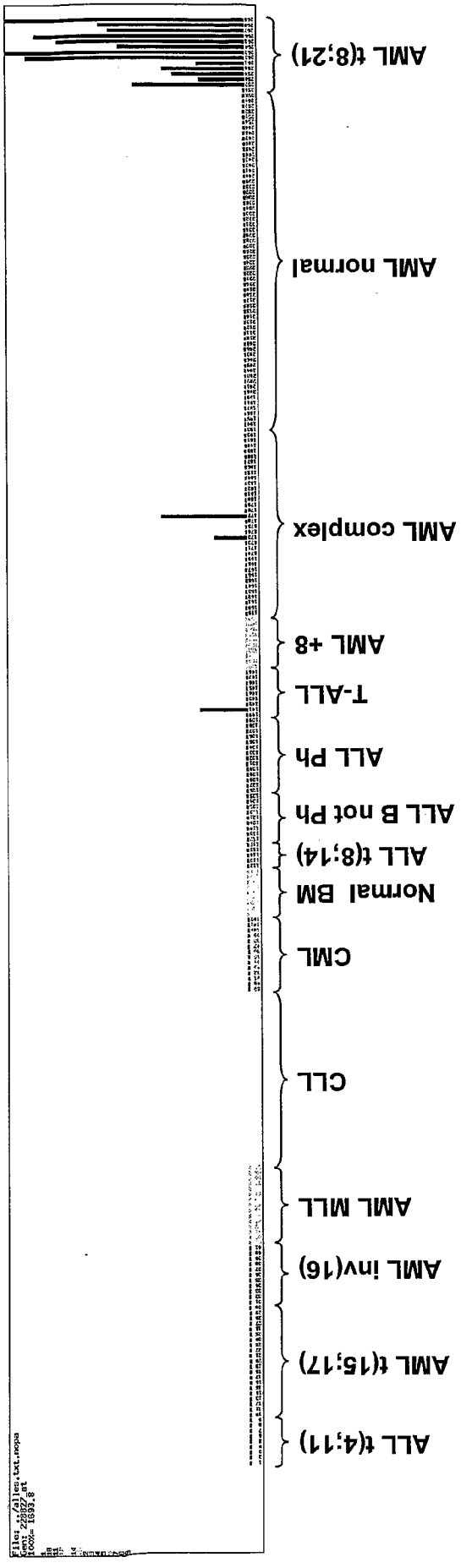


Figure 186

205529_s_at, CBFA2T1, AML t(8;21) vs. all others

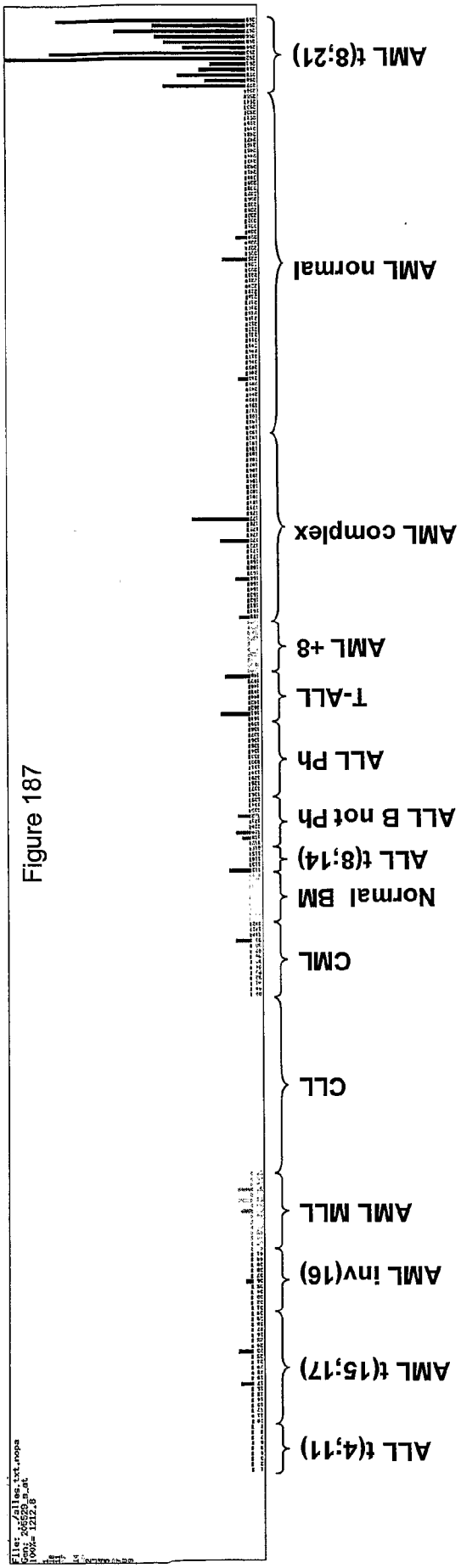


Figure 187

201998_at, SIAT1, CLL

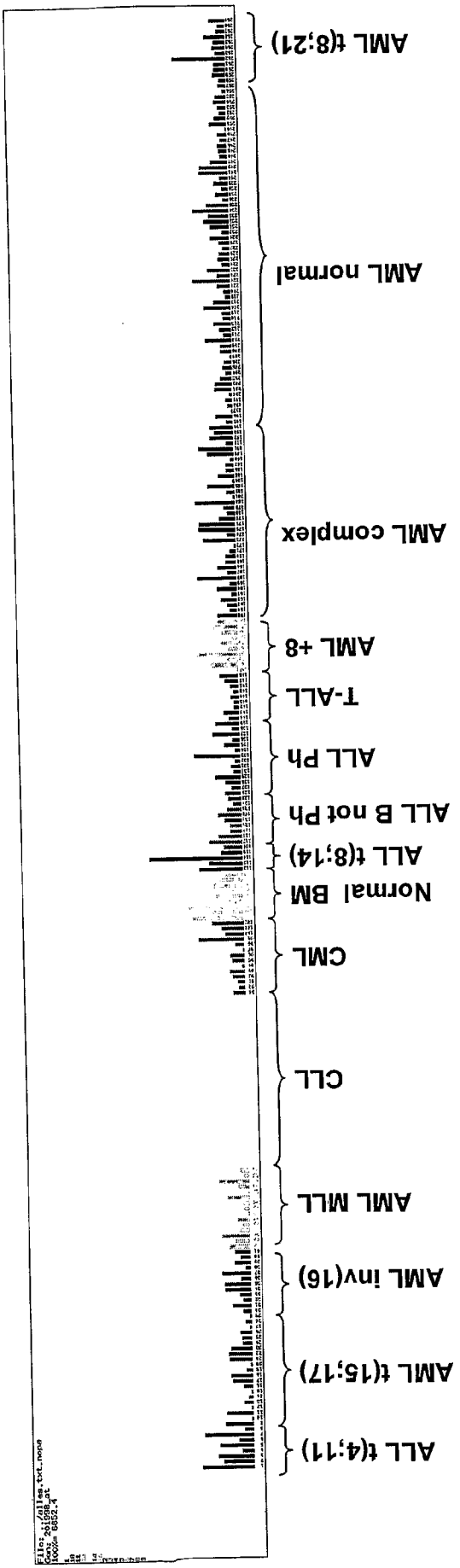


Figure 188

204150_at, STAB1, AML t(15;17)

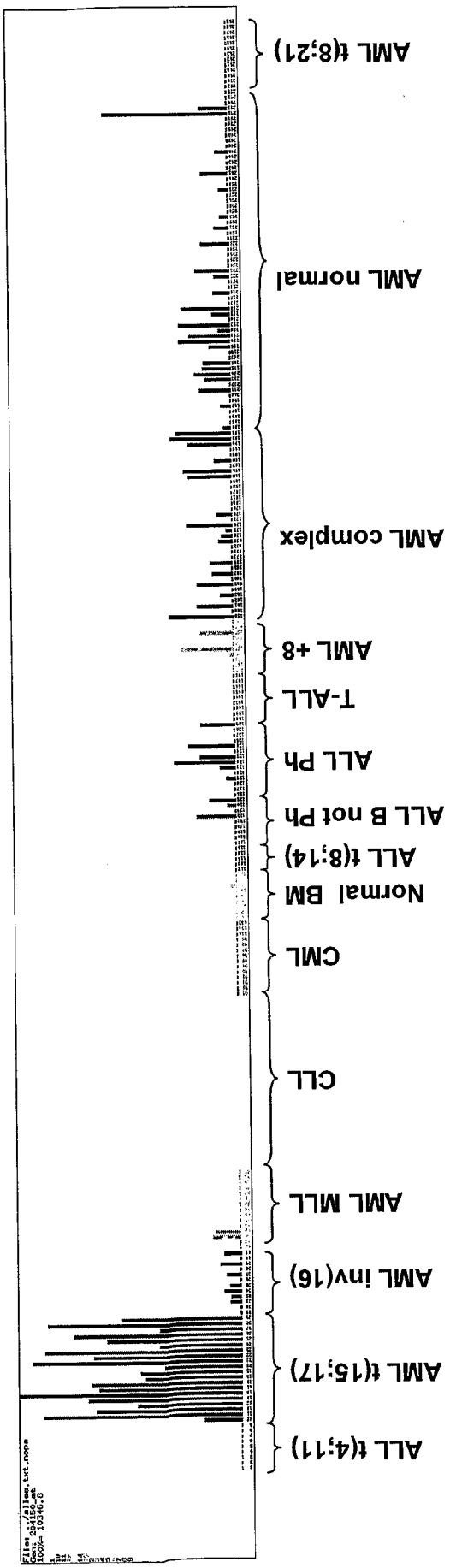


Figure 189

204511_at, KIAA0793, CLL

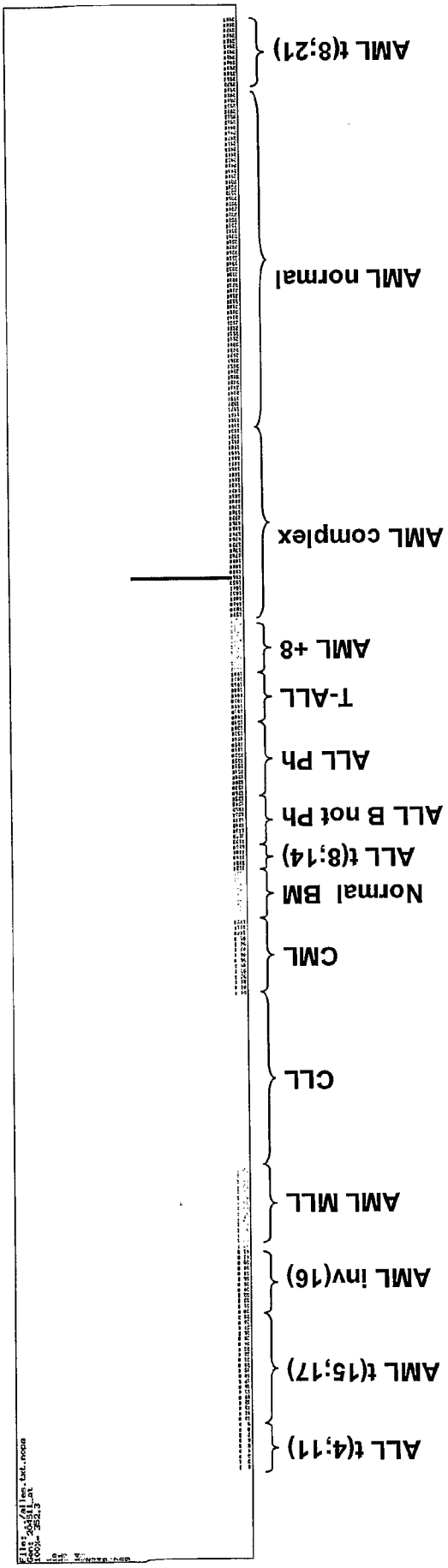


Figure 190

207819_s_at, ABCB4, CLL

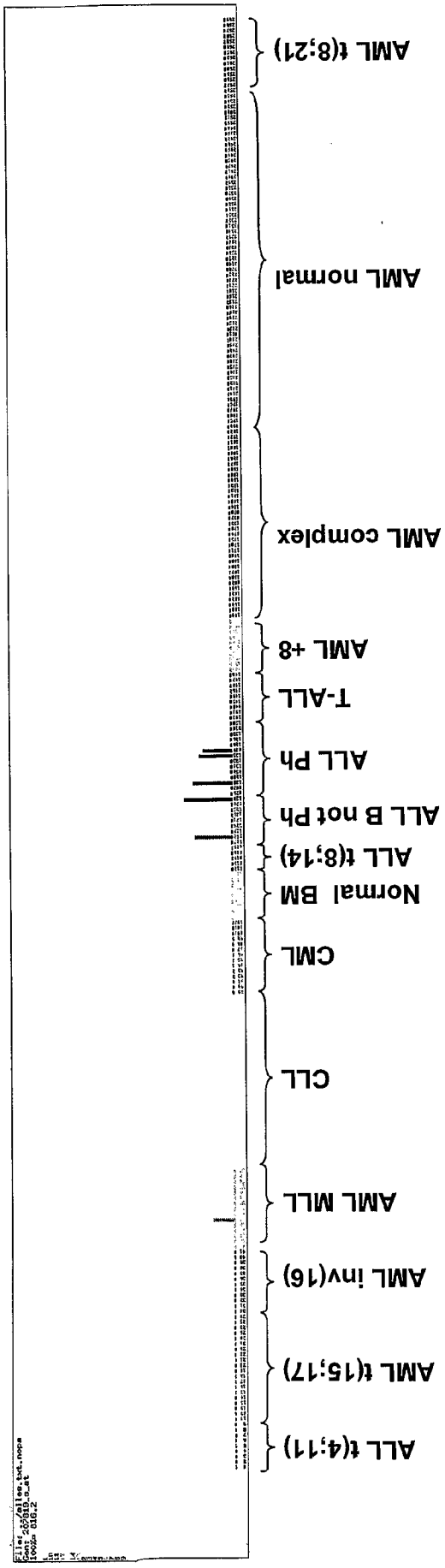


Figure 191

205805_s_at, ROR1, CLL

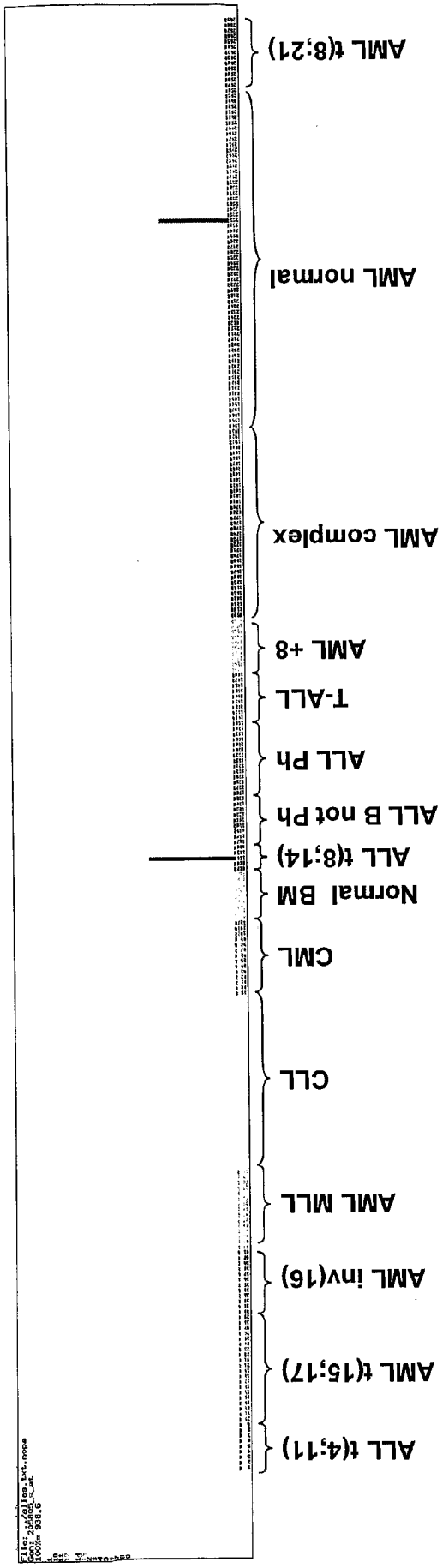


Figure 192

208091_s_at, DKFZP564K0822, CLL

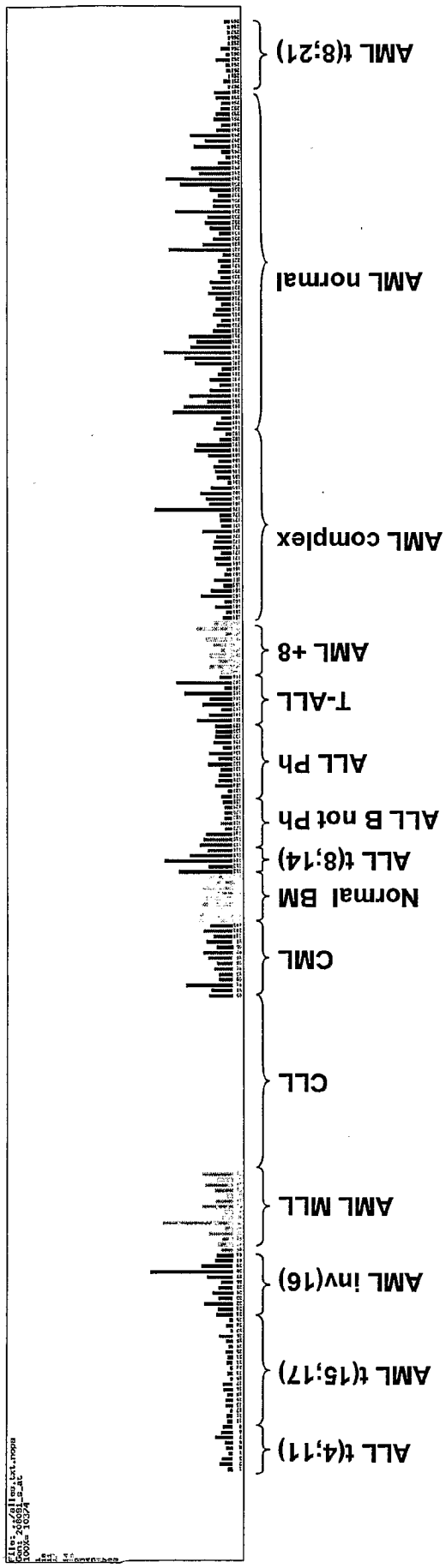


Figure 193

208456_s_at, RRAS2, CLL

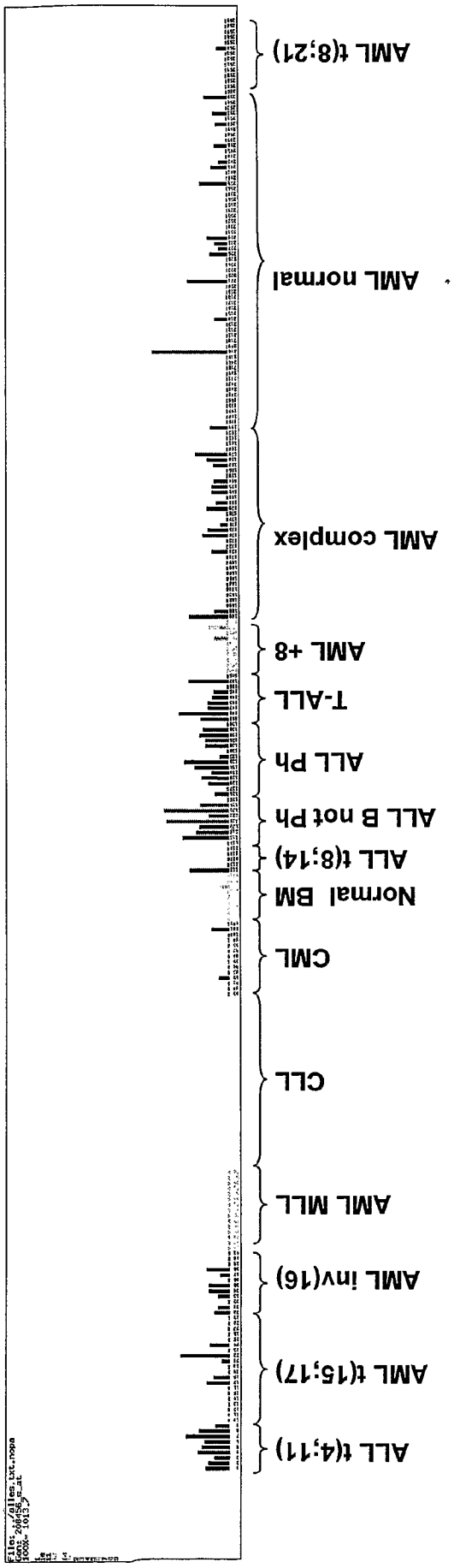


Figure 194

209061_at, NCOA3, CLL

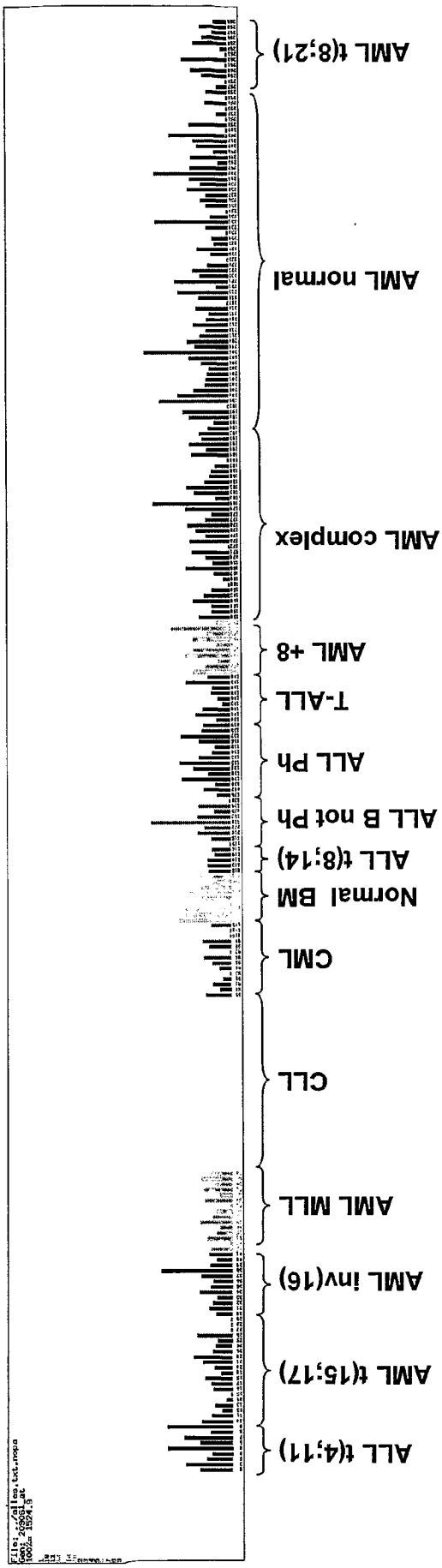


Figure 195

209374_s_at, IGHM, CLL

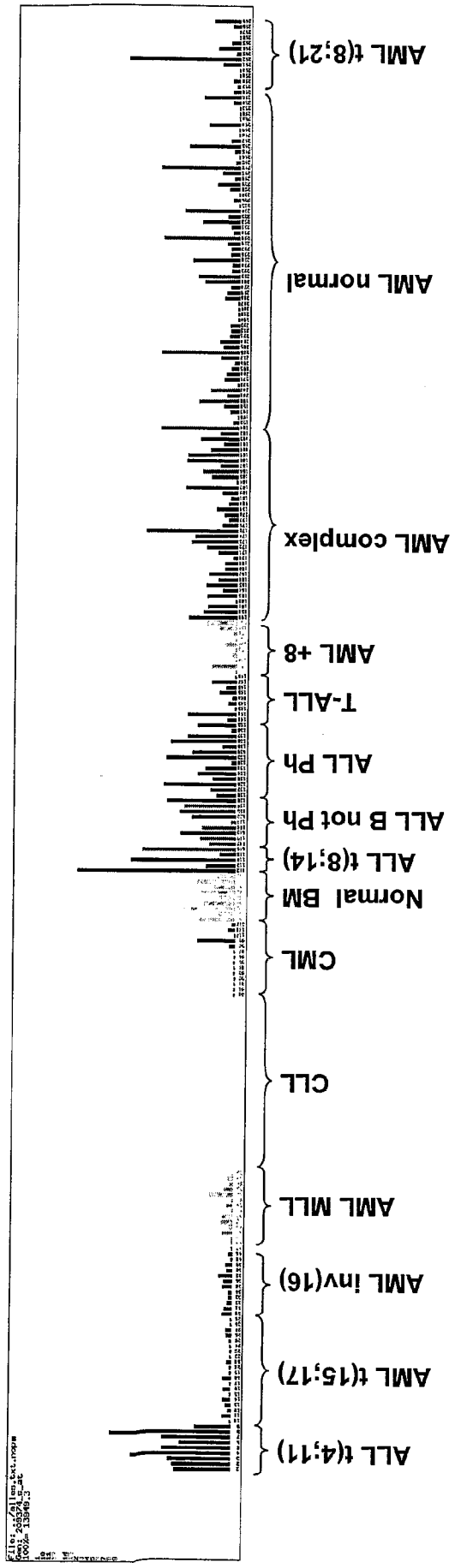


Figure 196

38487_at, FLJ12442, AML t(15;17)

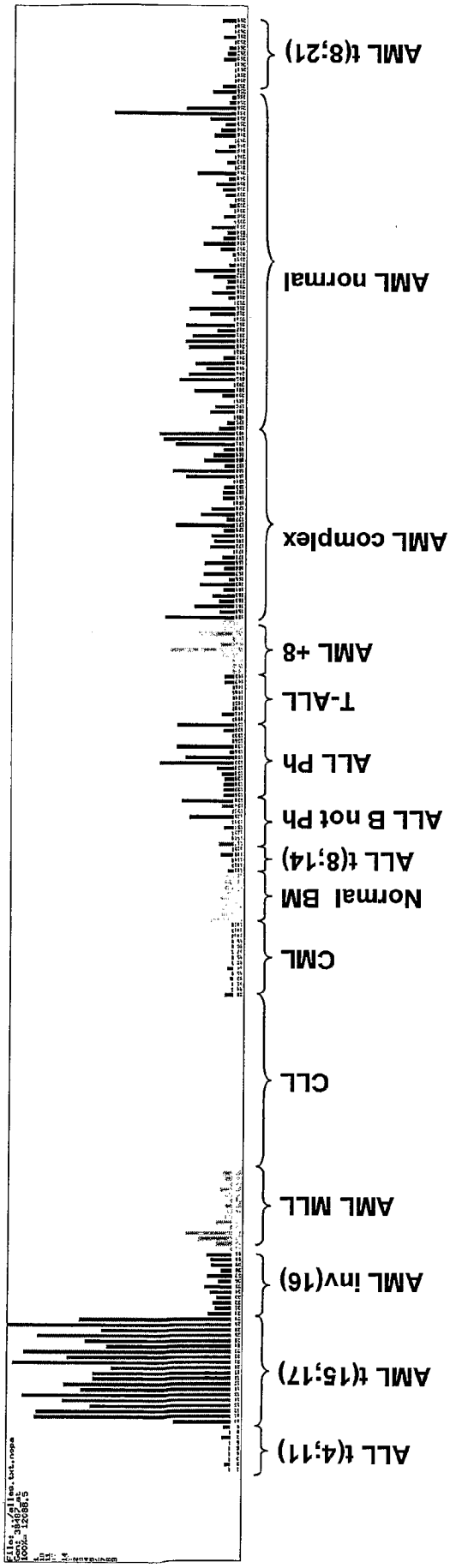


Figure 197

201162_at, IGFBP7, CLL

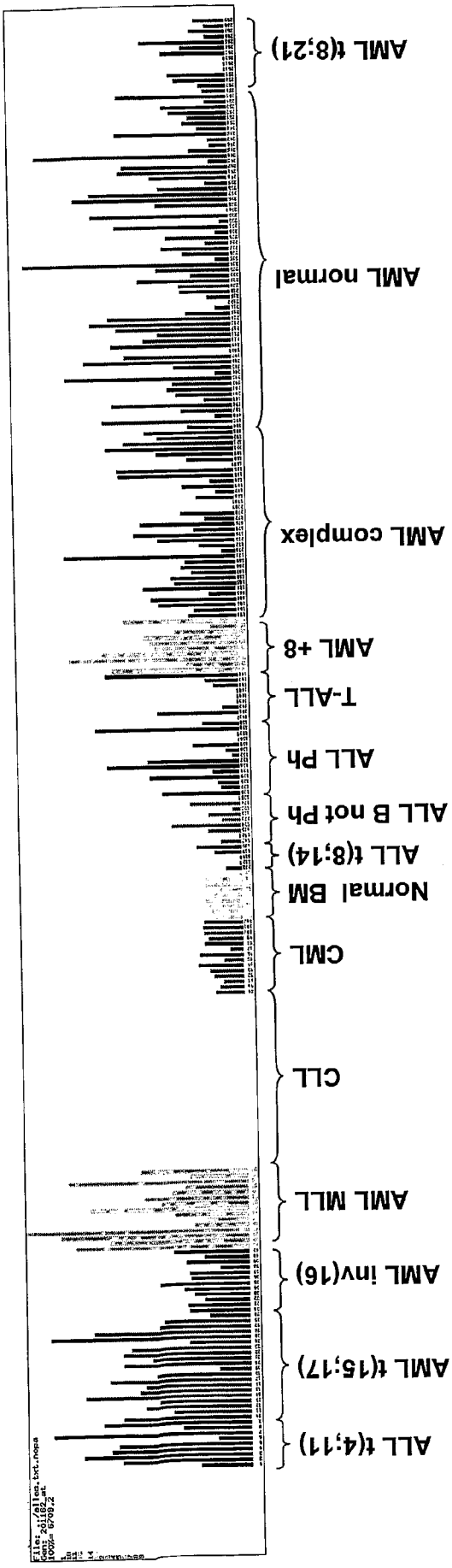


Figure 198

201163_s_at, IGFBP7, CLL

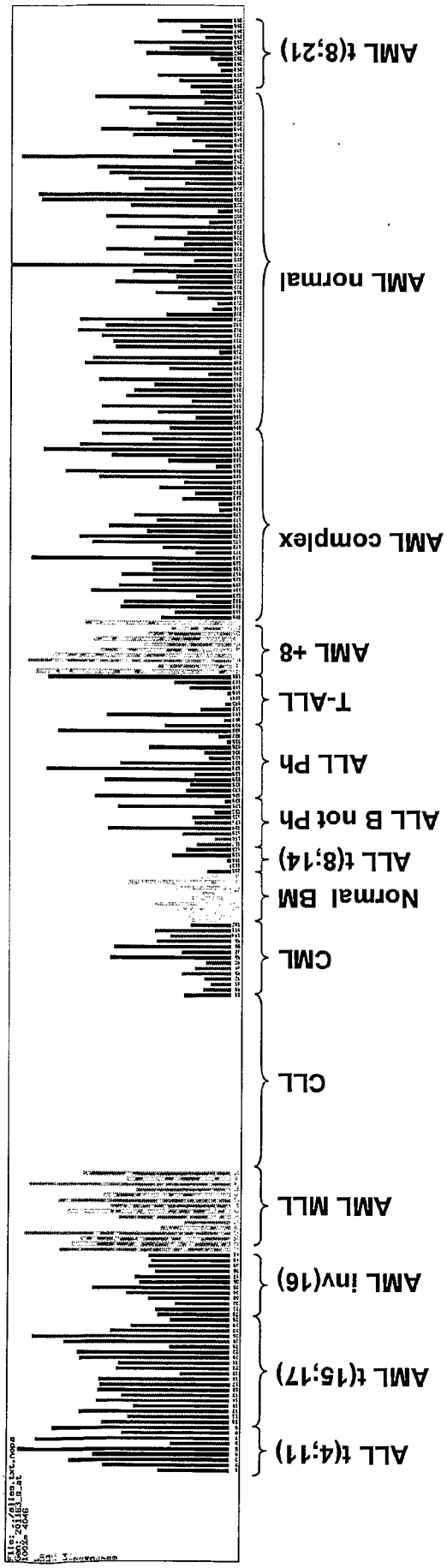


Figure 199

202095_s_at, BIRC5, CLL

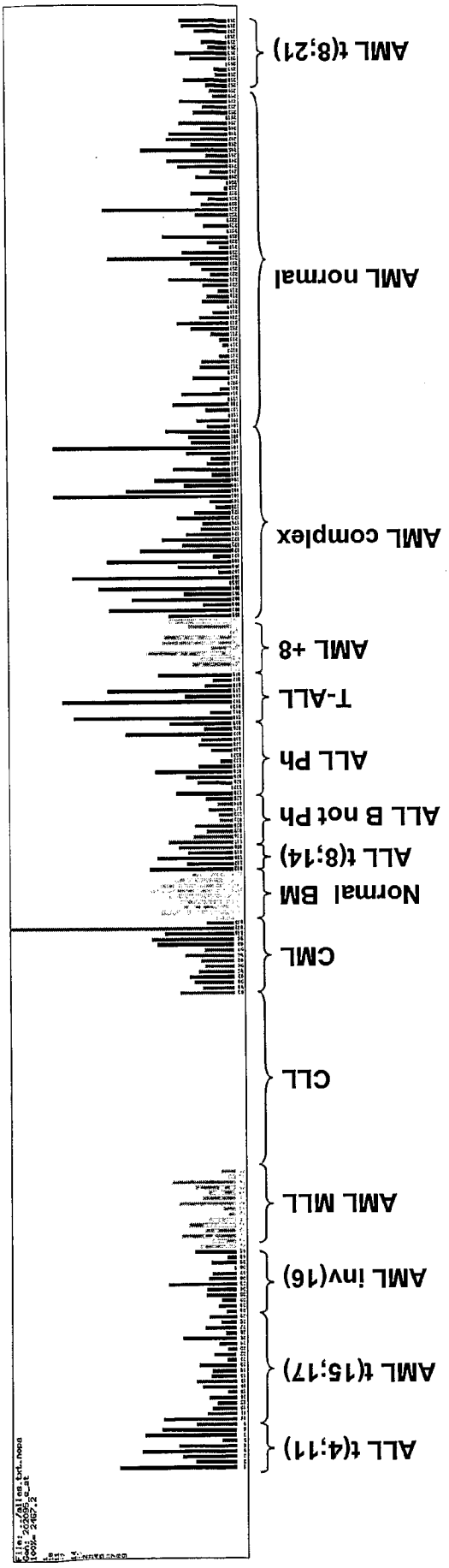


Figure 200

201362_at, NS1-BP, CML

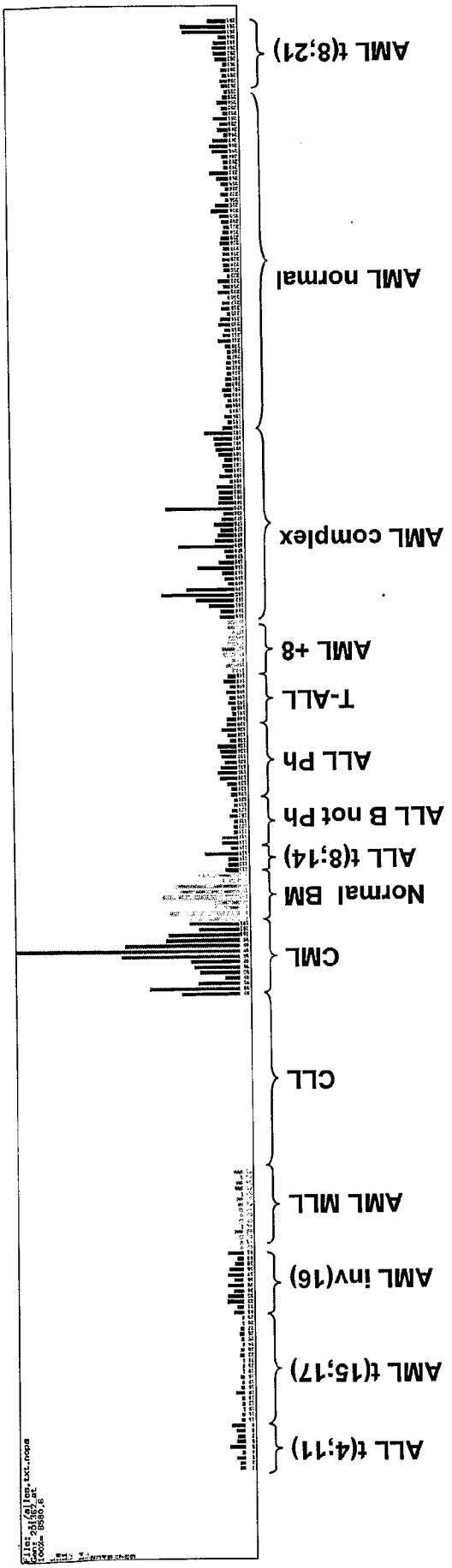


Figure 201

203074_at, ANXA8, AML t(15;17)

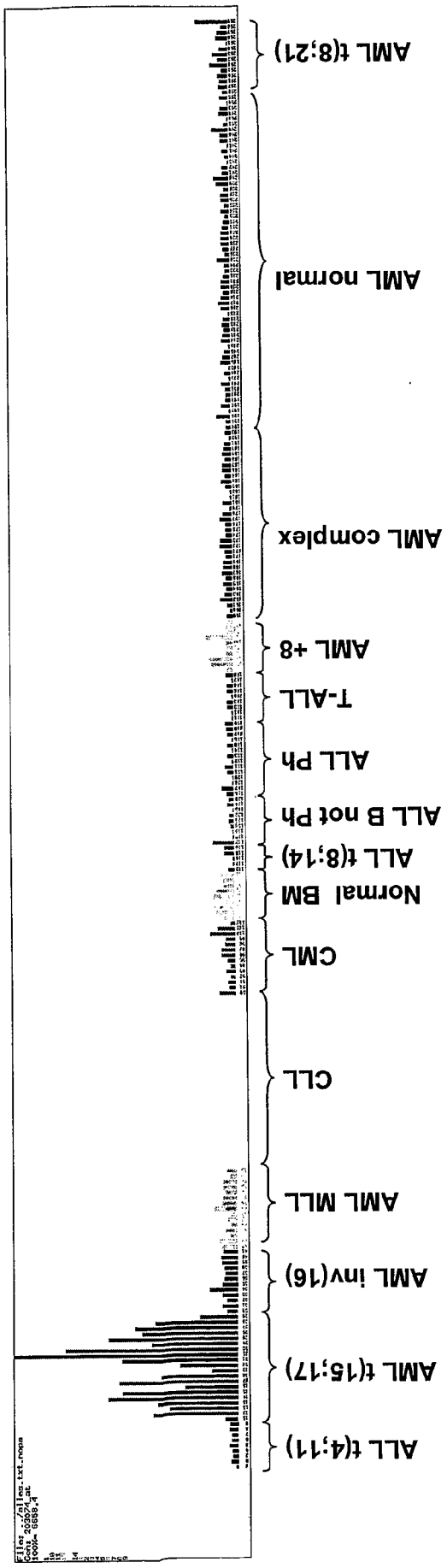


Figure 202

201496_x_at, MYH11, AML inv(16)

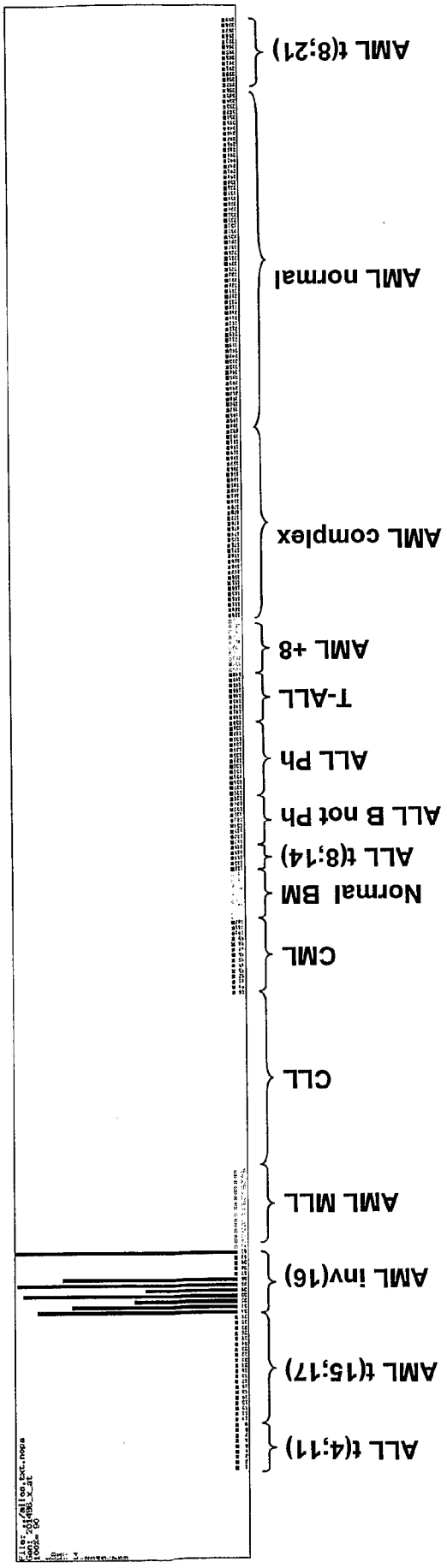


Figure 203

205528_s_at, CBFA2T1, AML t(8;21)

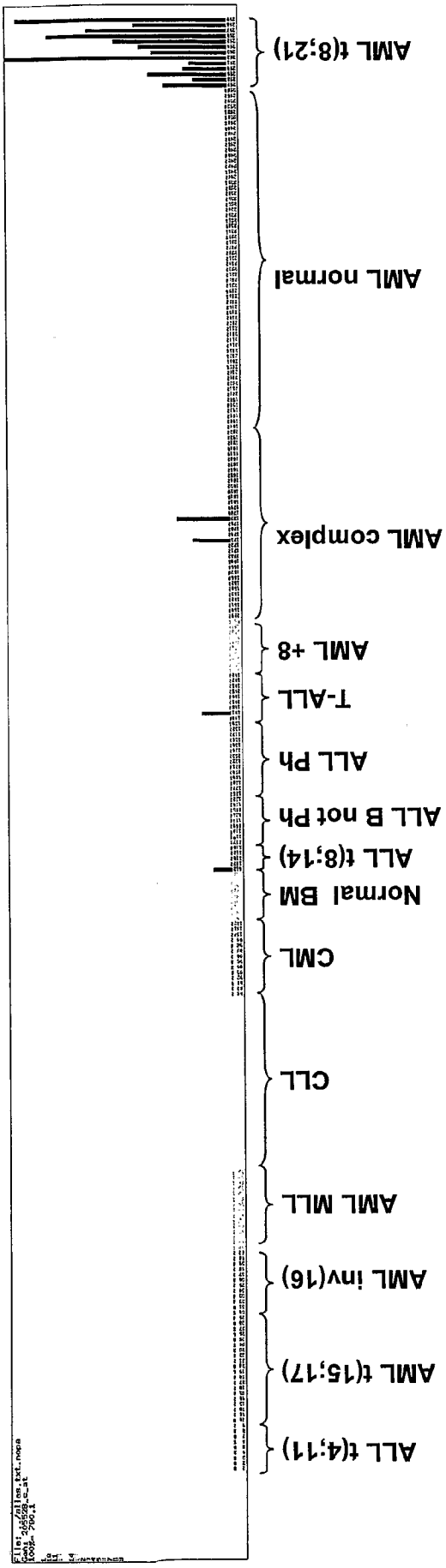


Figure 204

201497_x_at, MYH11, AML inv(16)

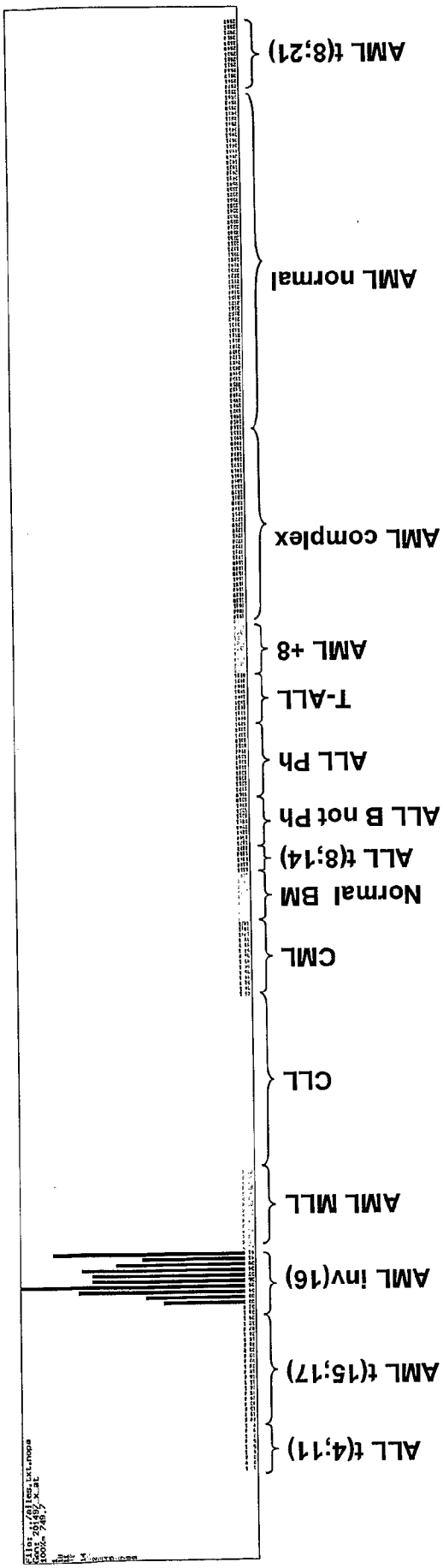


Figure 205

205529_s_at, CBFA2T1, AML t(8;21)

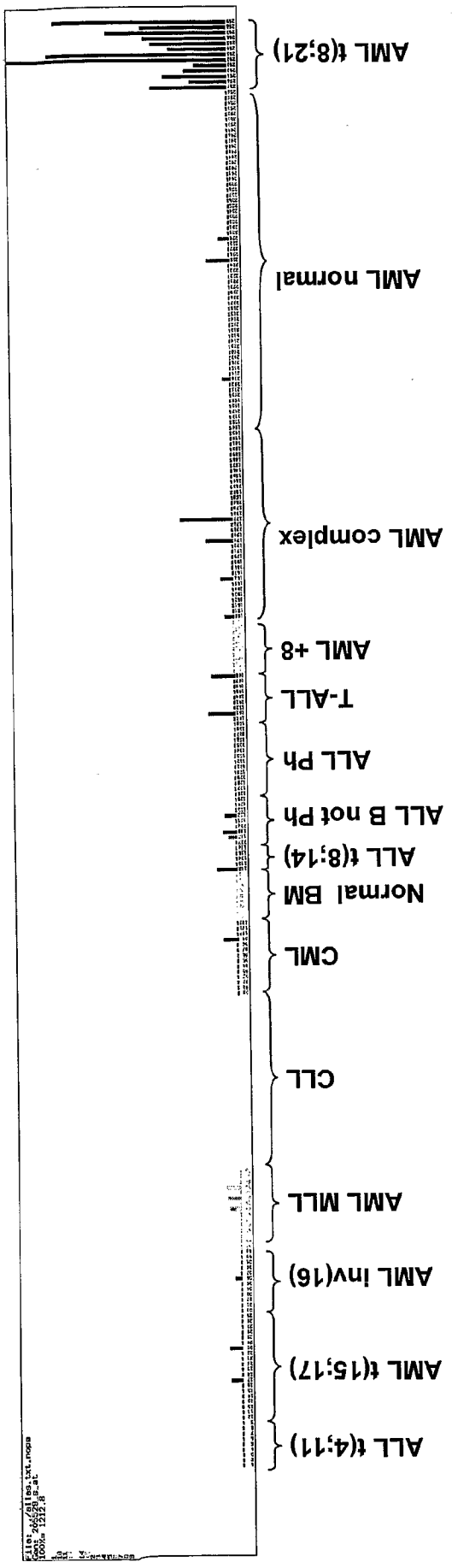


Figure 206

206940_s_at, POU4F1, AML t(8;21)

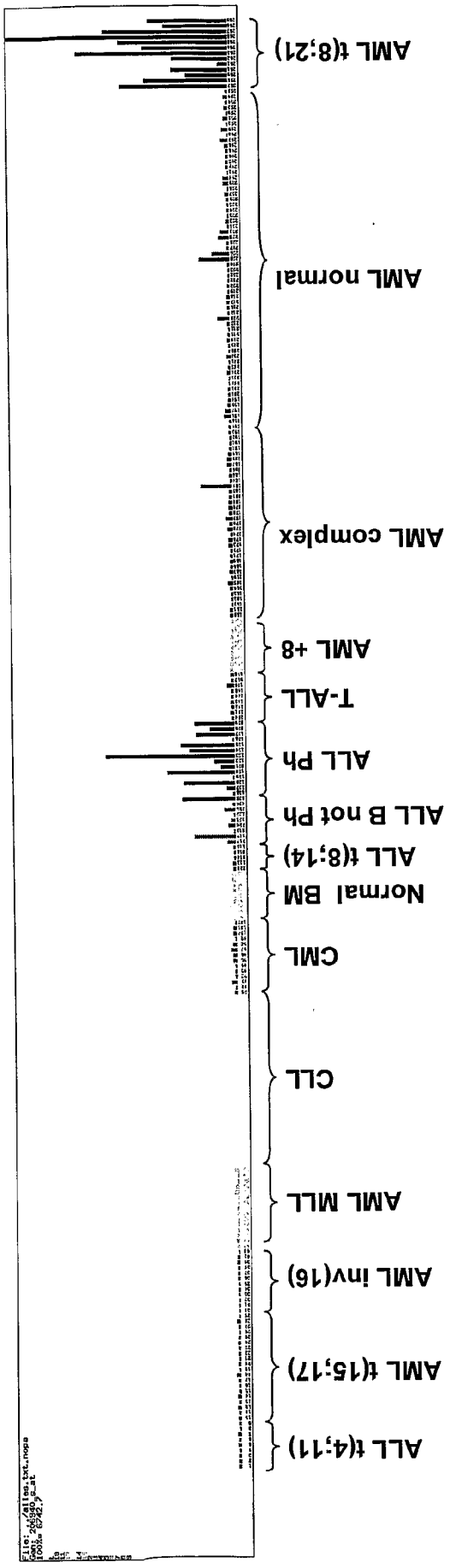


Figure 207

212285_s_at, AGRN, AML t(15;17)

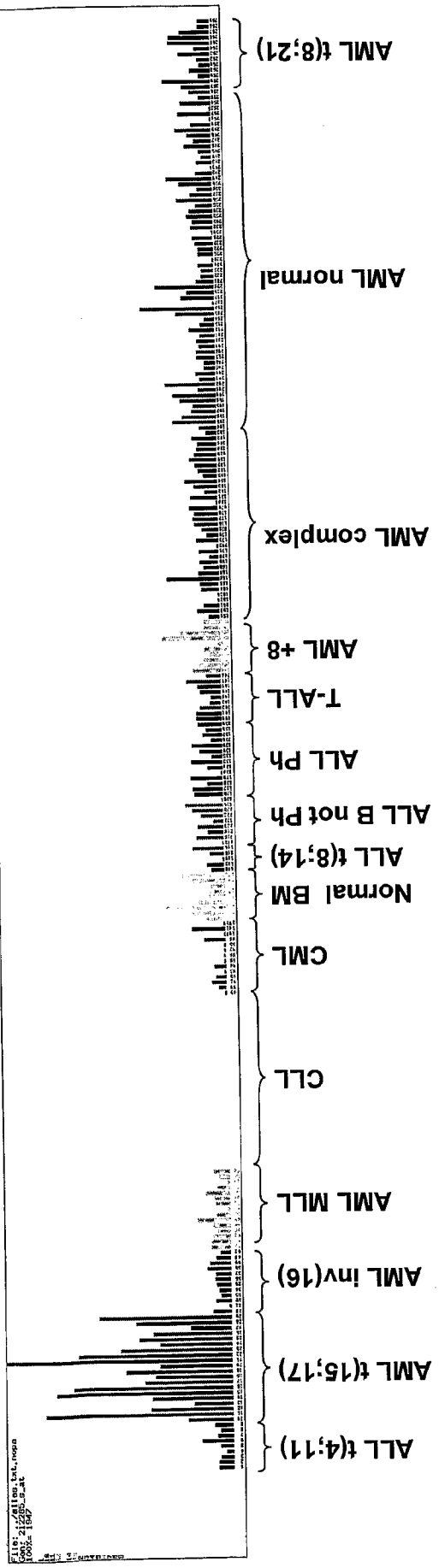


Figure 208

209616_s_at, CES1, AML MLL

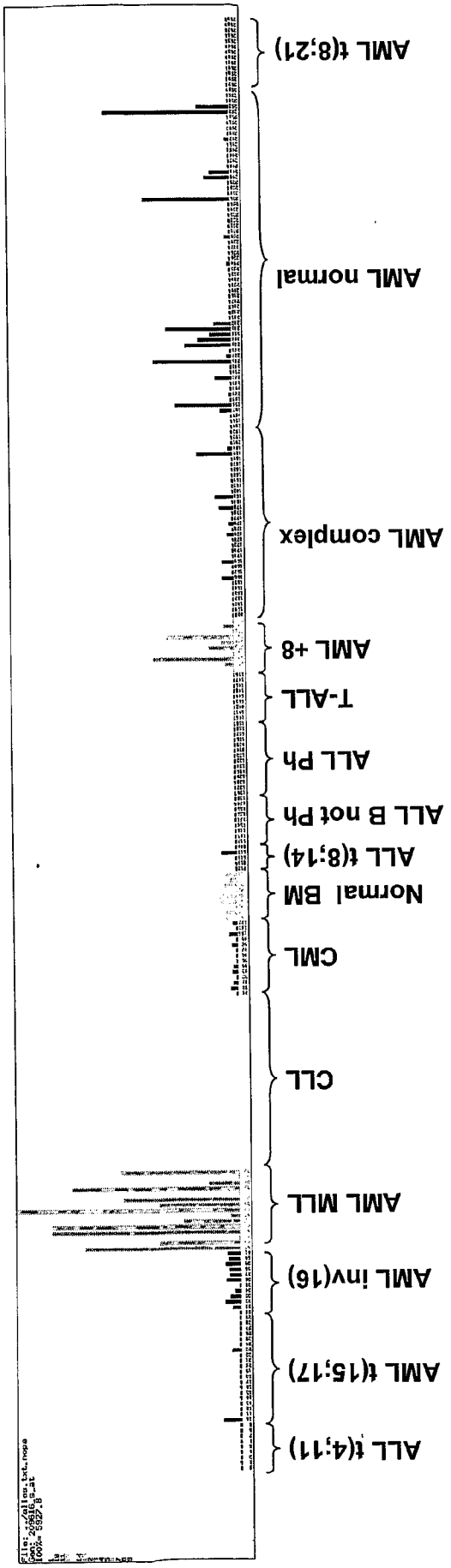


Figure 209

213539_at, CD3D, T-ALL

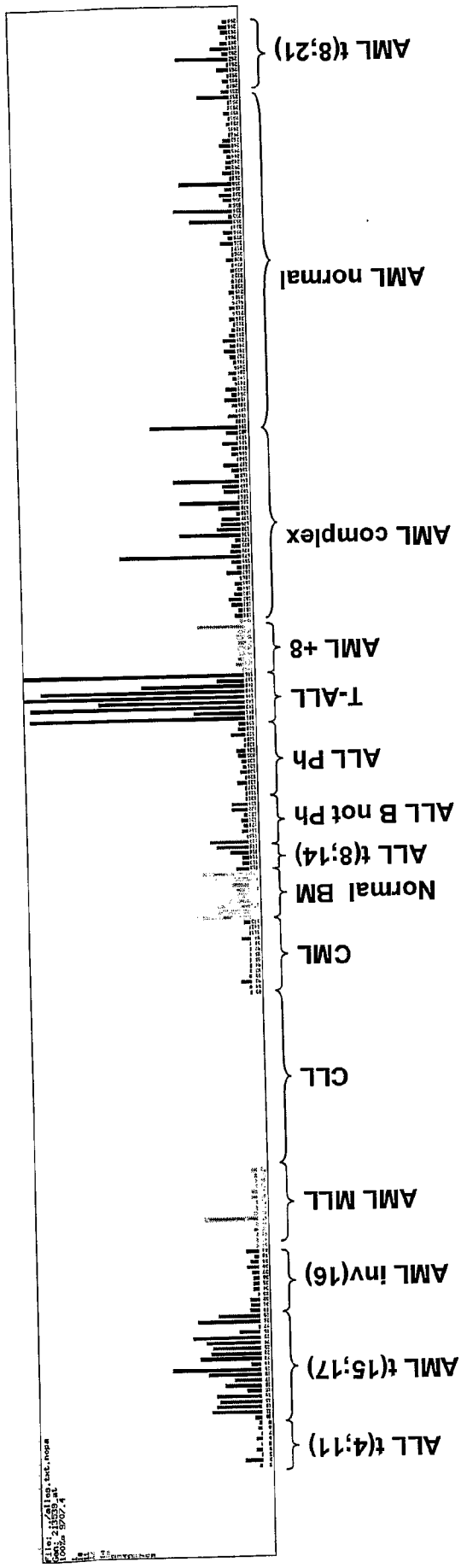


Figure 210

214450_at, CTSW, AML t(15;17)

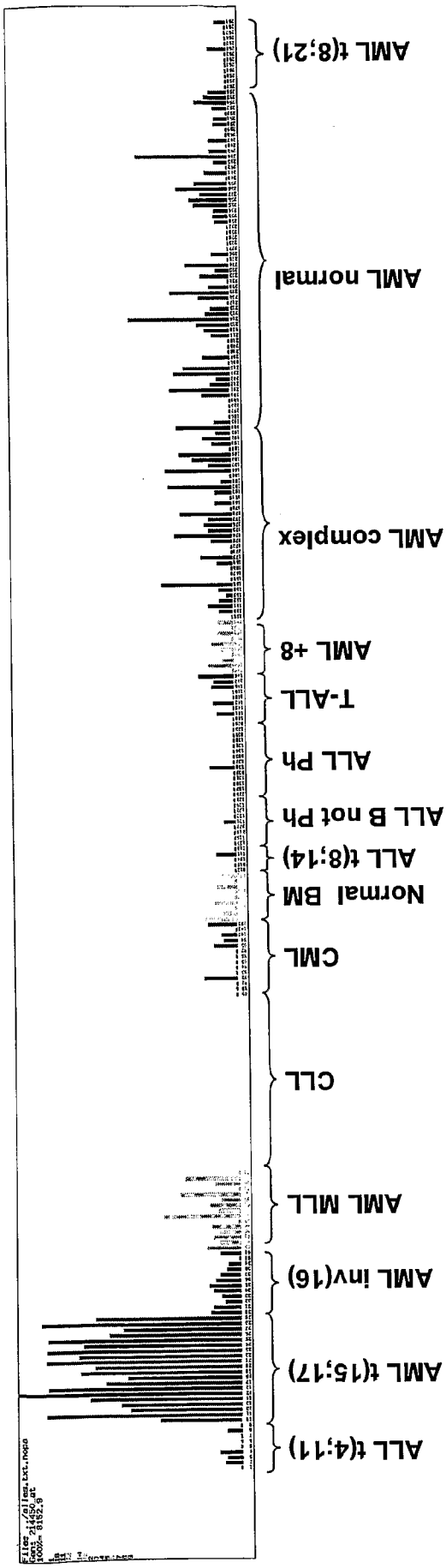


Figure 211

218223_s_at, LOC51177, CML

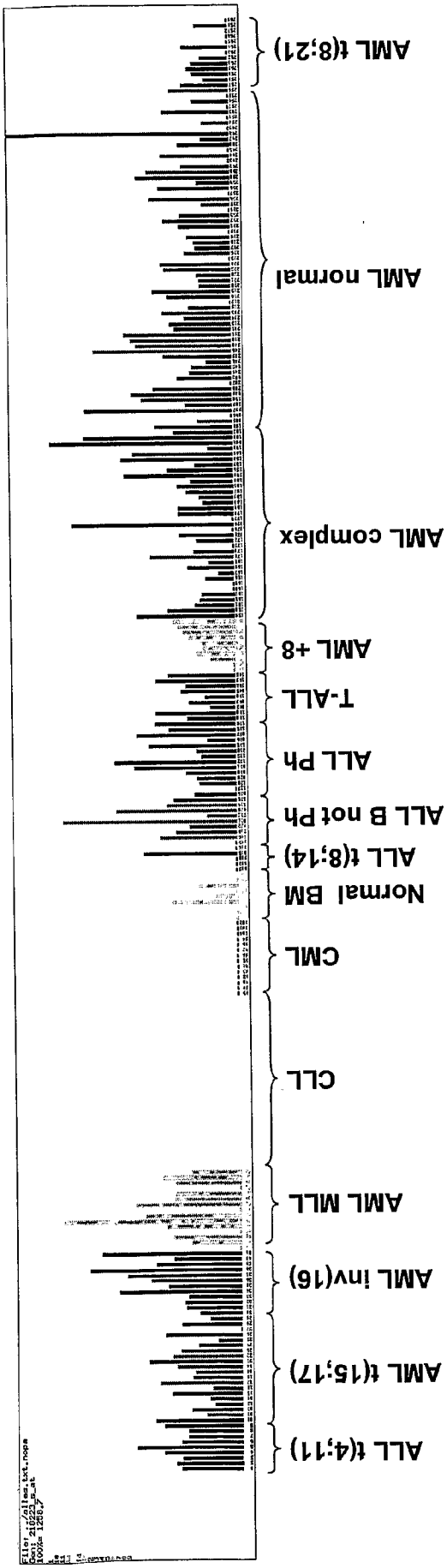


Figure 212

210997_at, HGF, AML t(15;17)

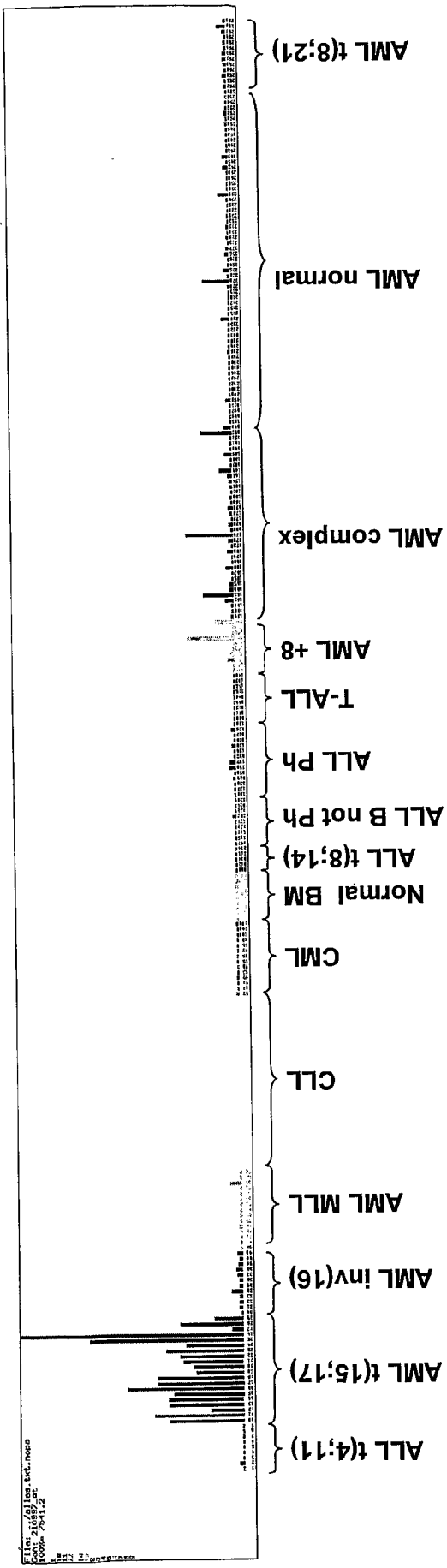


Figure 213

209101_at, CTGF, ALL t(4;11), ALL Ph, T-ALL

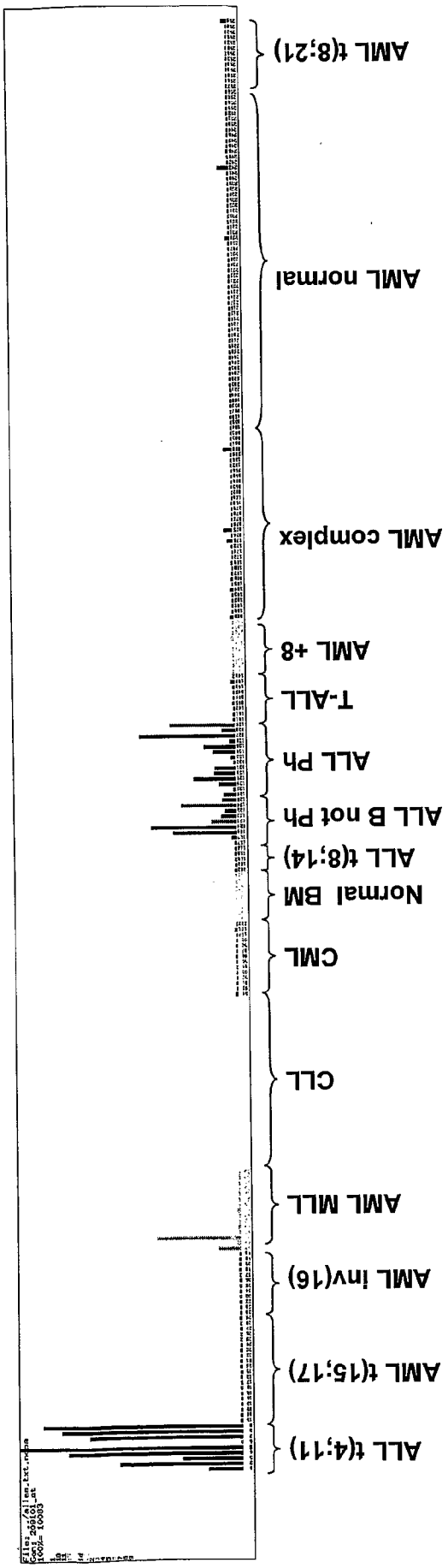


Figure 214

215925_s_at, ALL t(4;11)

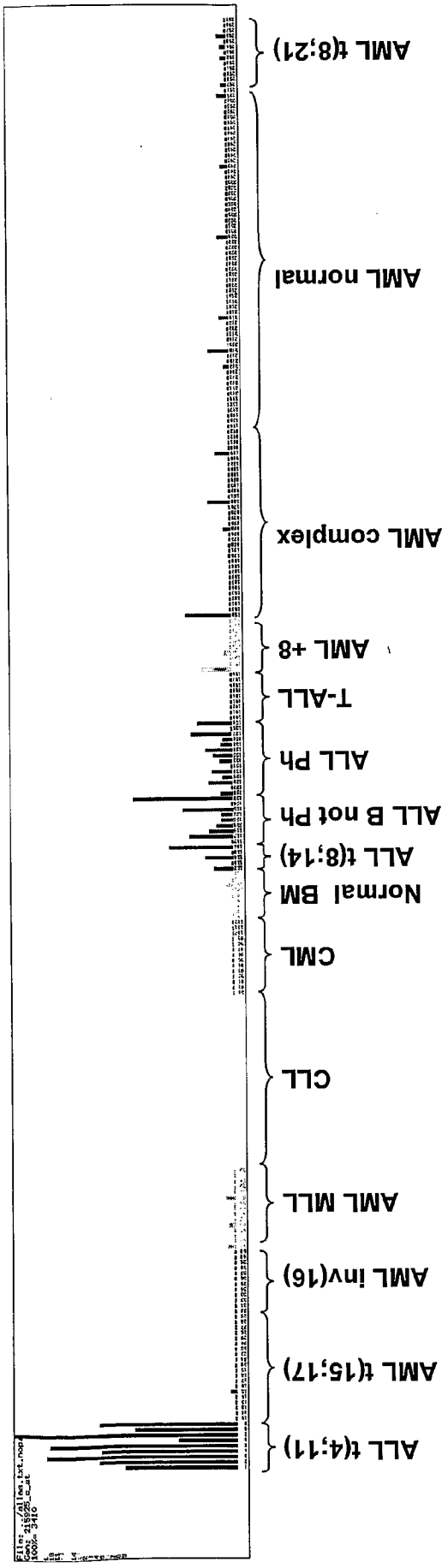


Figure 215

239393_at, ALL t(4;11)

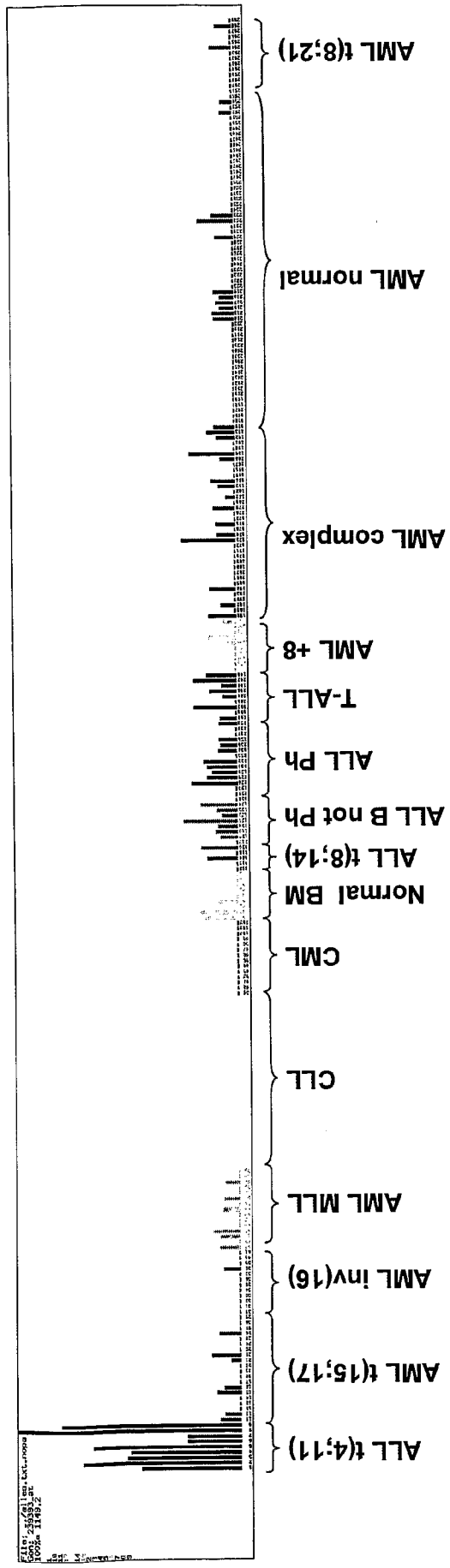


Figure 216

239791_at, HOXB6, AML normal, AML +8

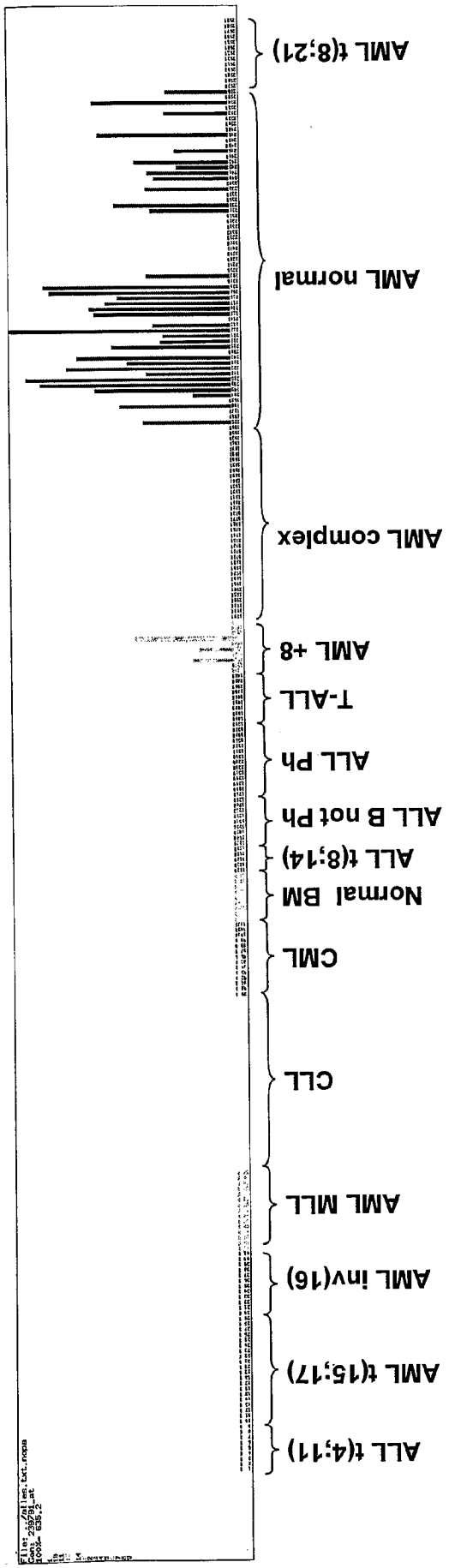


Figure 217

240581_at, ALL t(4;11)

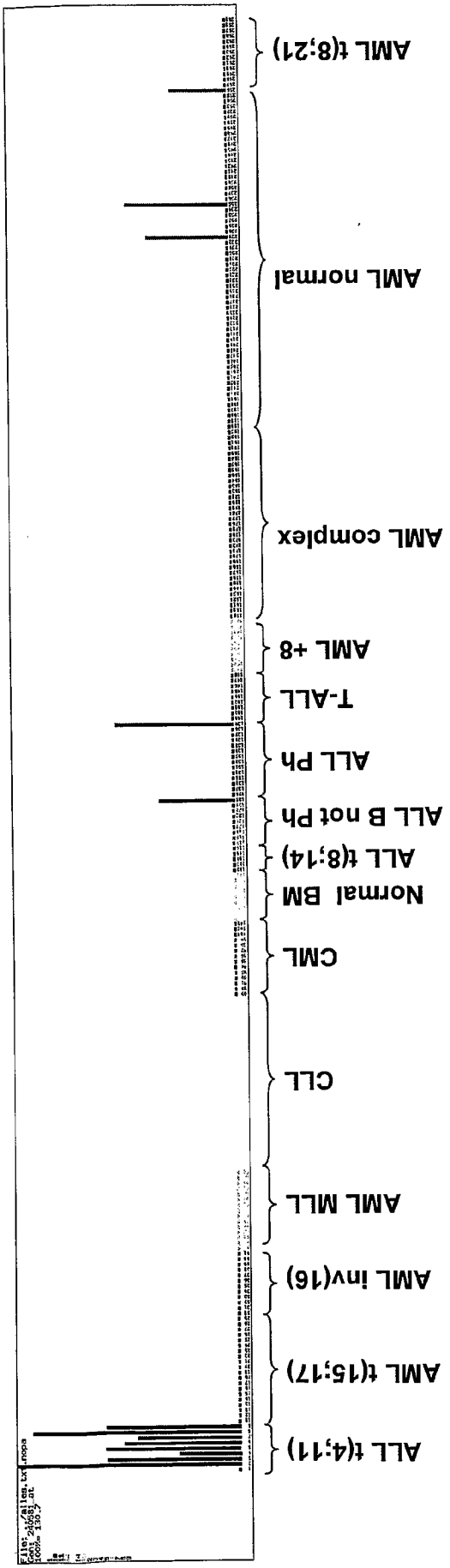


Figure 218

241464_s_at, AML MLL, AML normal, AML +8, AML complex

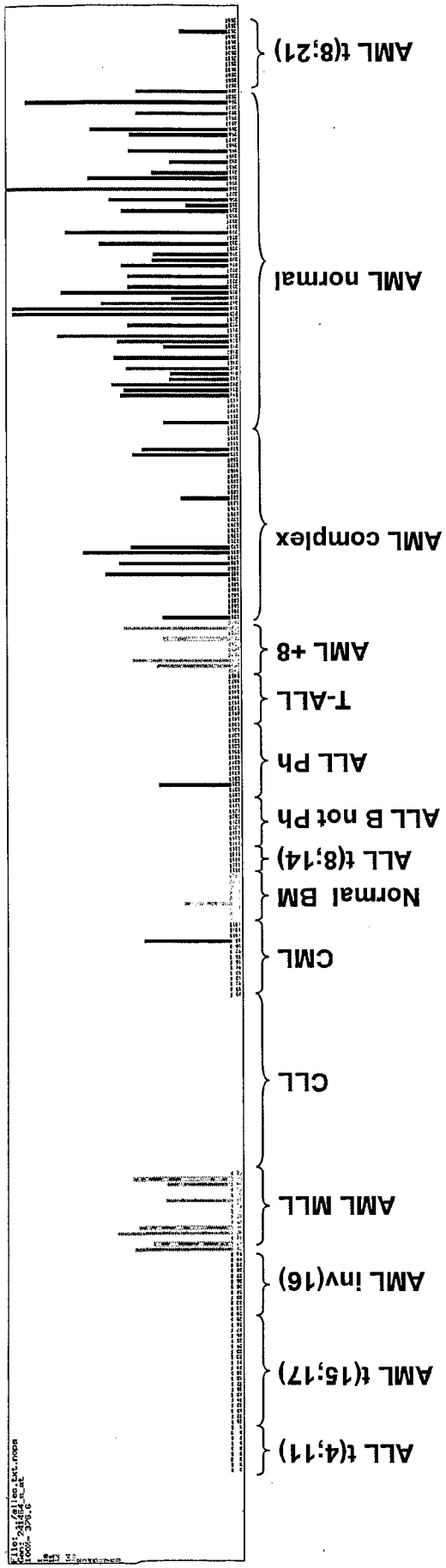


Figure 219

241525_at, AML inv(16)

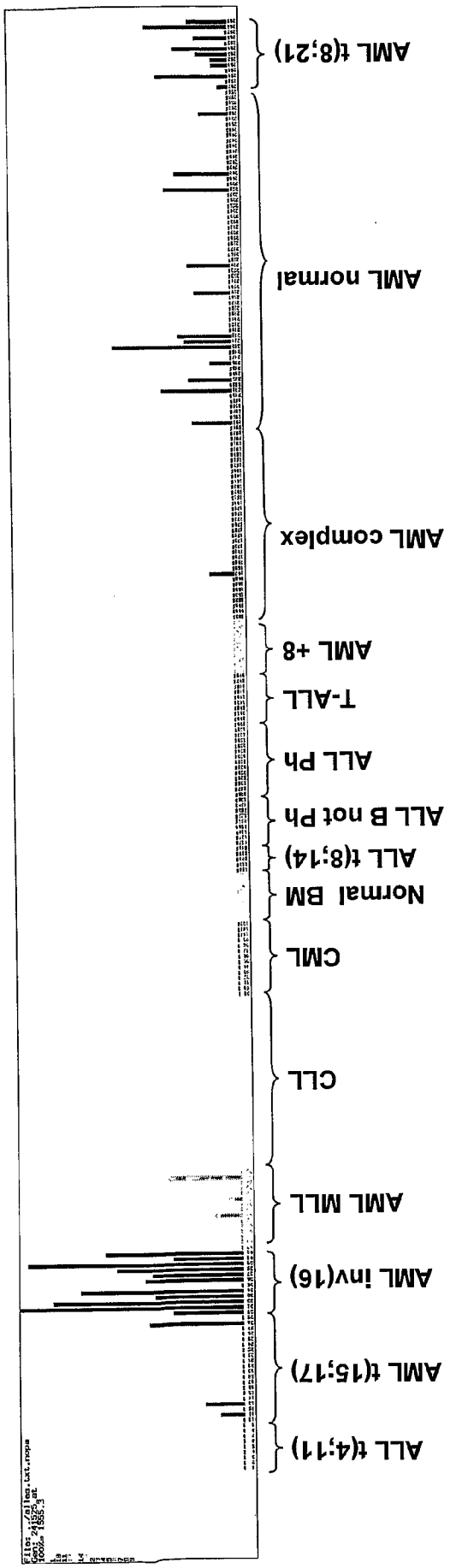


Figure 220

243362_s_at, LEF1, ALL, CLL

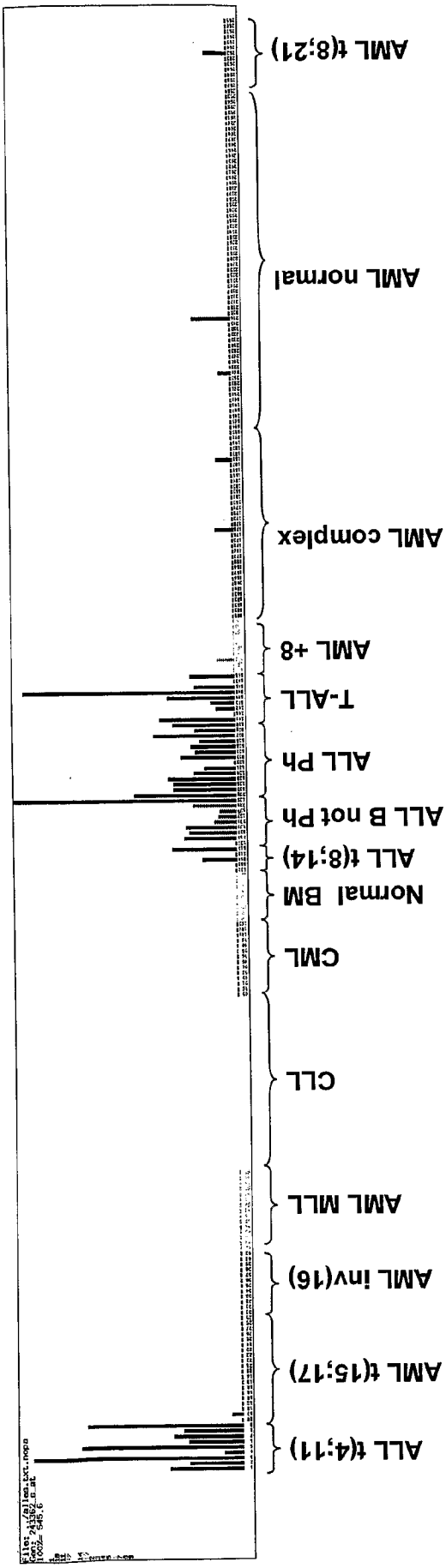


Figure 221

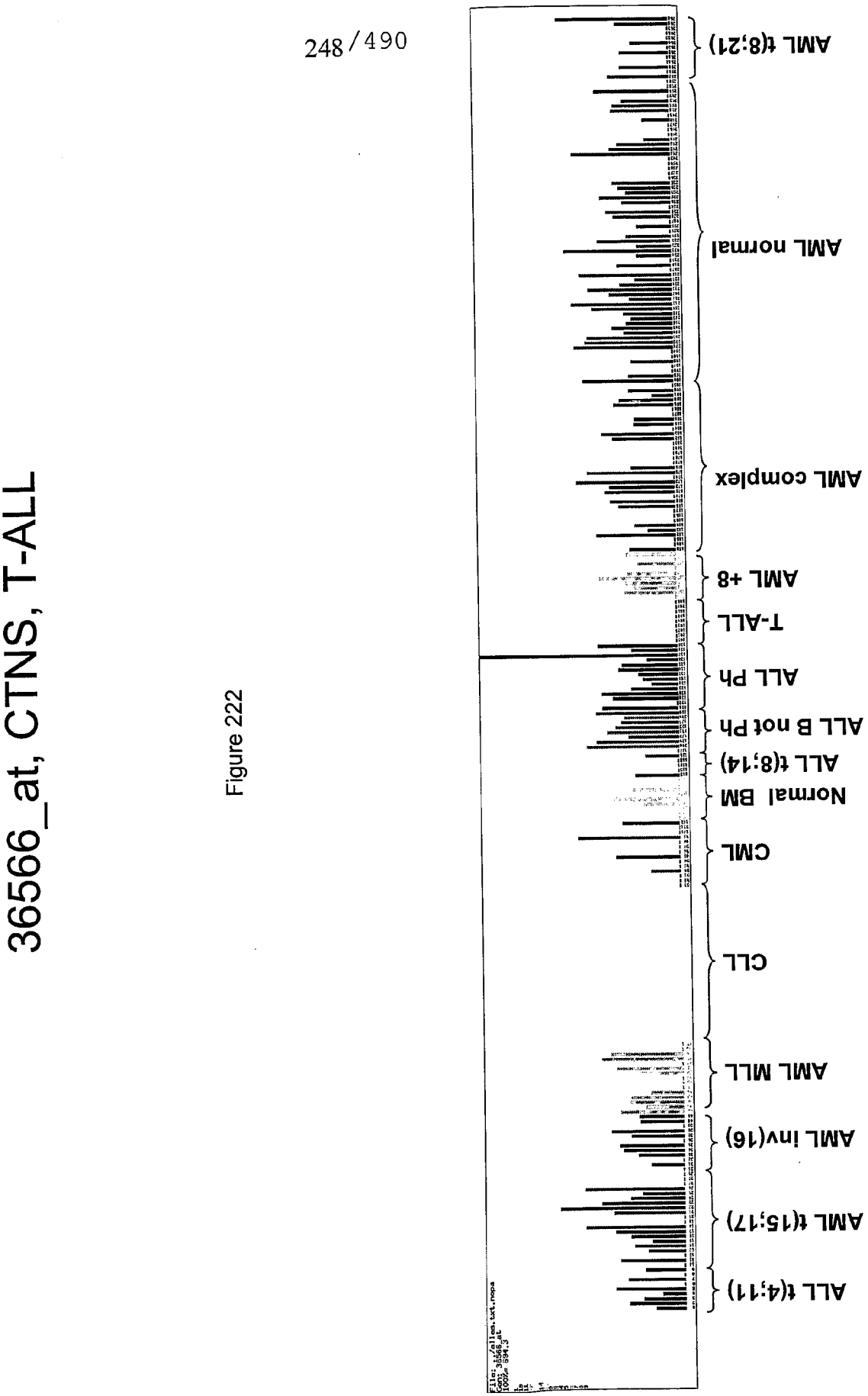

36566_at, CTNS, T-ALL
ALL t(4;11)
AML t(15;17)
AML inv(16)
AML MLL
CLL
CML
Normal BM
ALL t(8;14)
ALL B not Ph
ALL Ph
T-ALL
AML +8
AML complex
AML normal
AML t(8;21)

Figure 222

38487_at, FLJ12442, AML t(15;17)

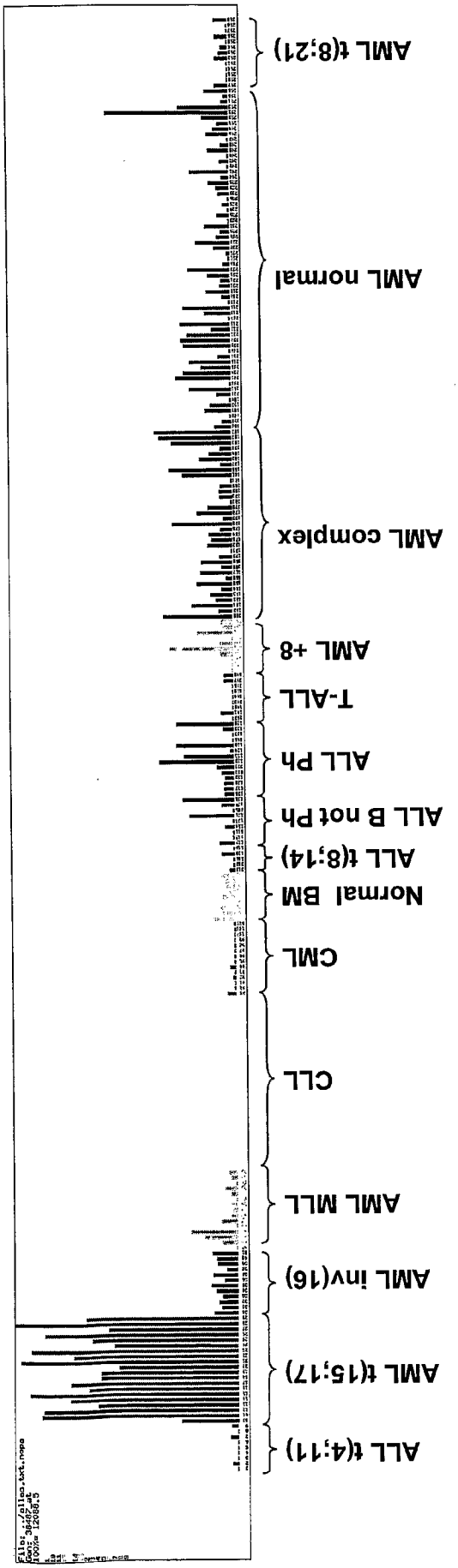


Figure 223

224794_s_at, LOC51148, AML t(15;17)

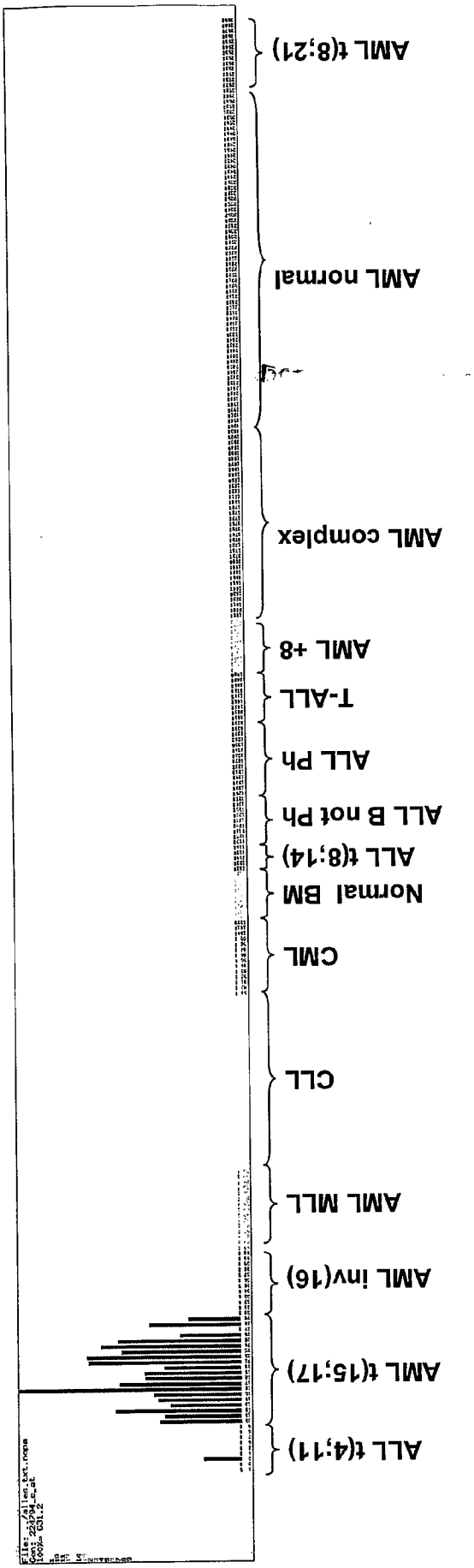


Figure 224

228904_at, AML normal, AML +8, AML complex

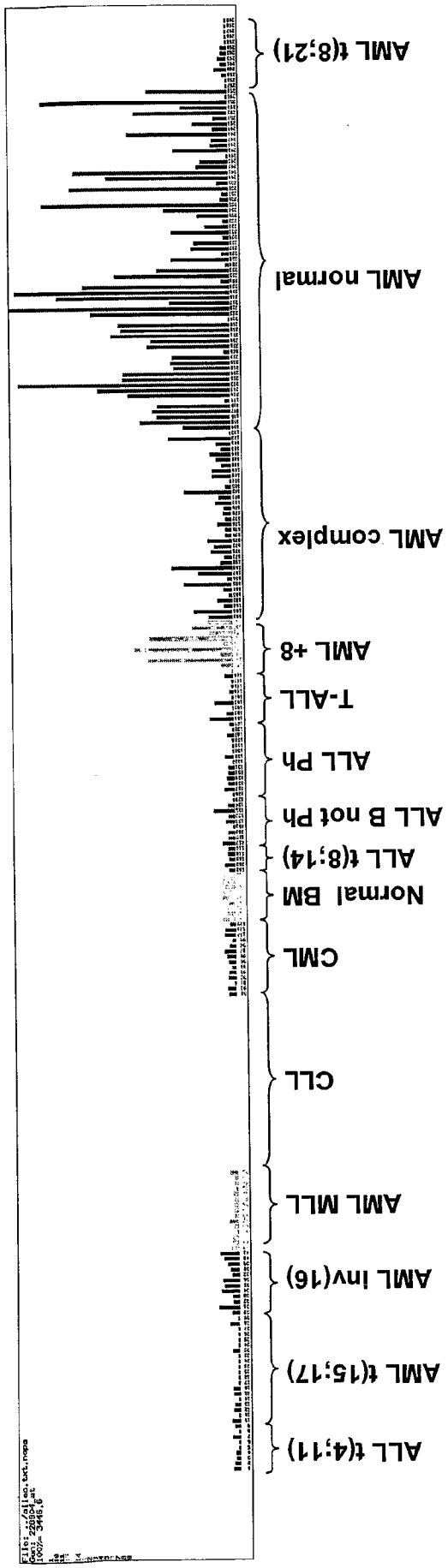


Figure 225

224520_s_at, MGC13168, ALL t(8;14)

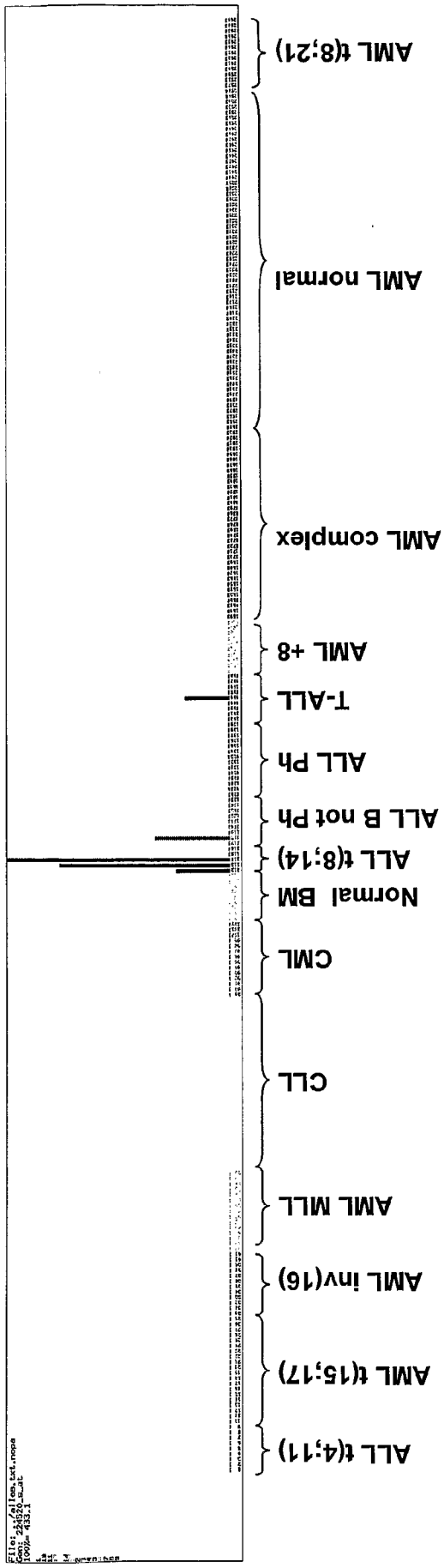


Figure 226

226496_at, ALL, CLL

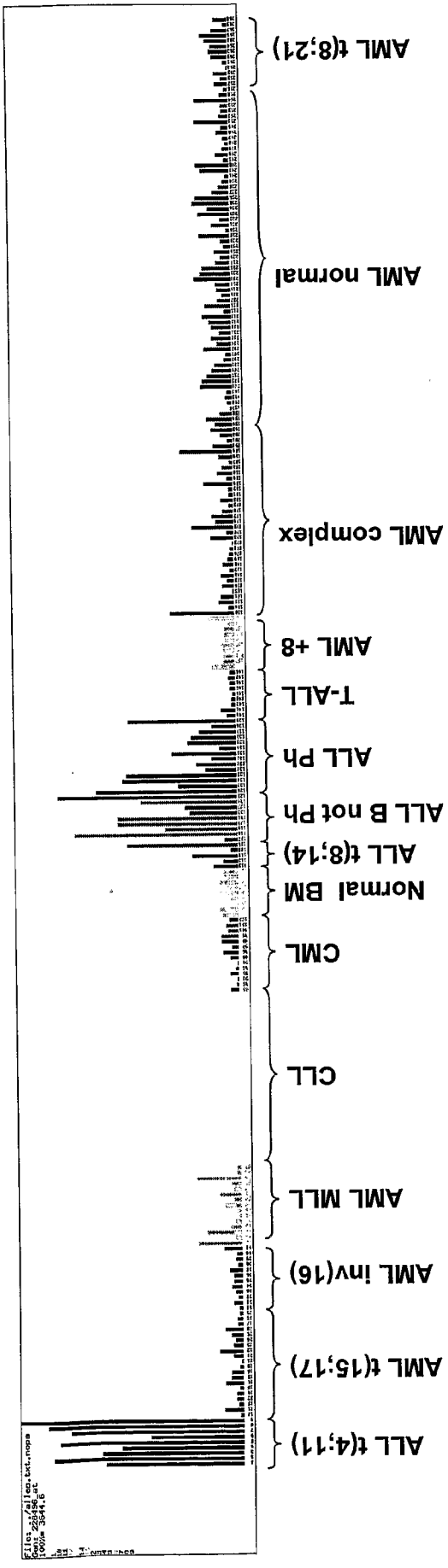


Figure 227

222166_at, AML +8

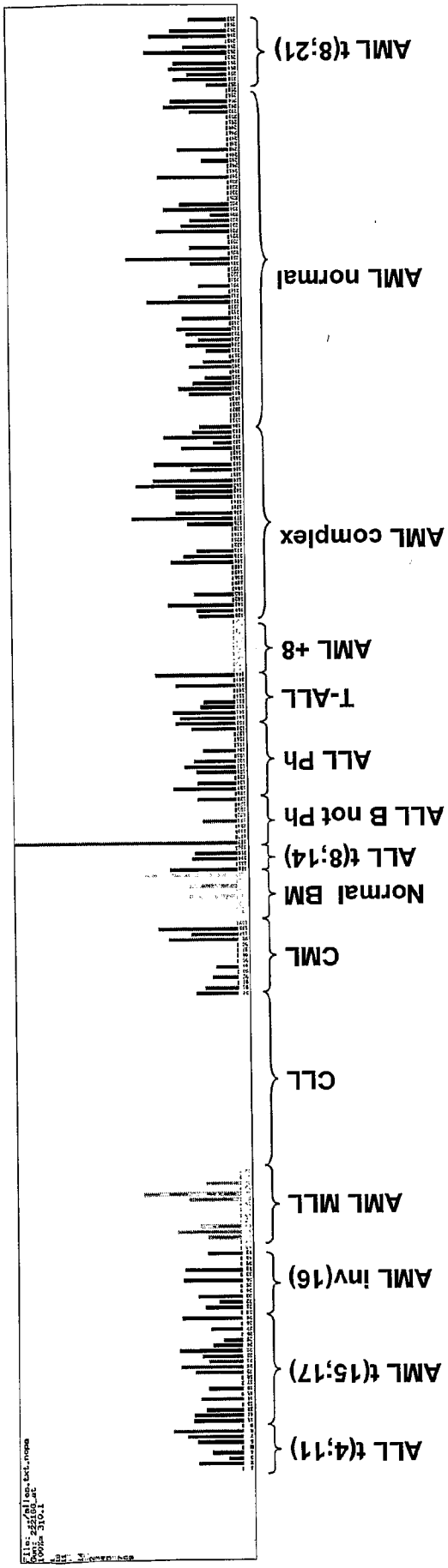


Figure 228

225660_at, SEMA6A, ALL B not Ph, ALL Ph

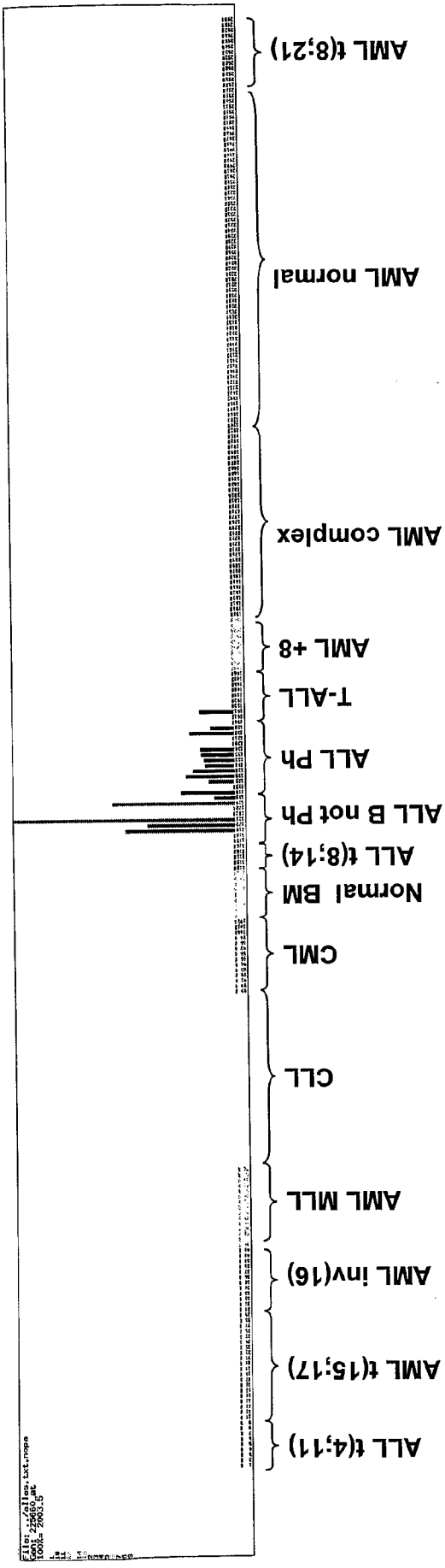


Figure 229

228827_at, AML t(8;21)

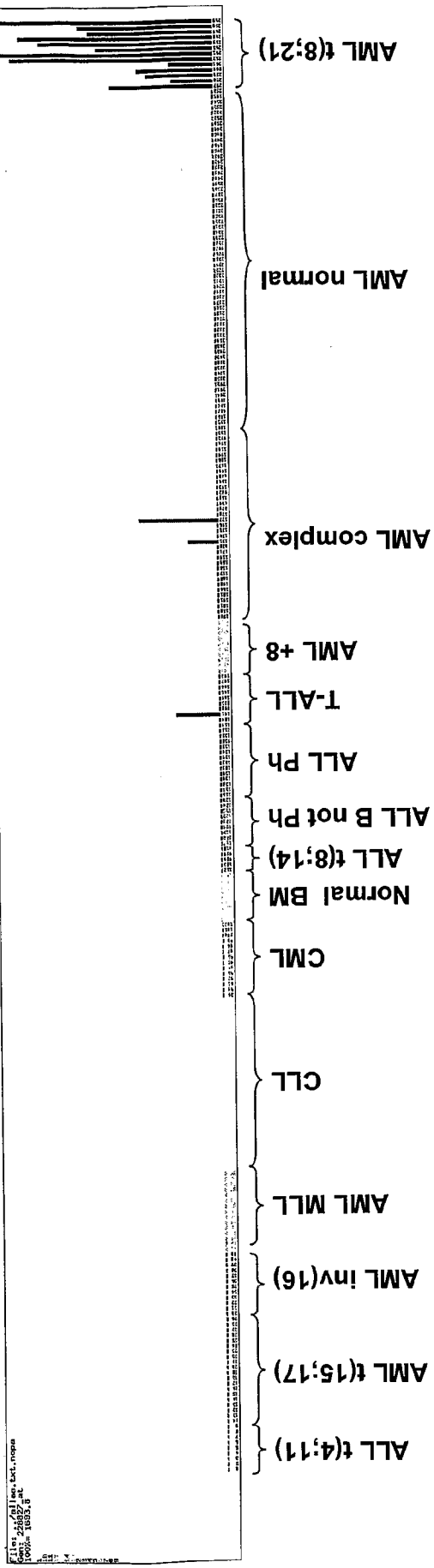


Figure 230

236301_at, CLL

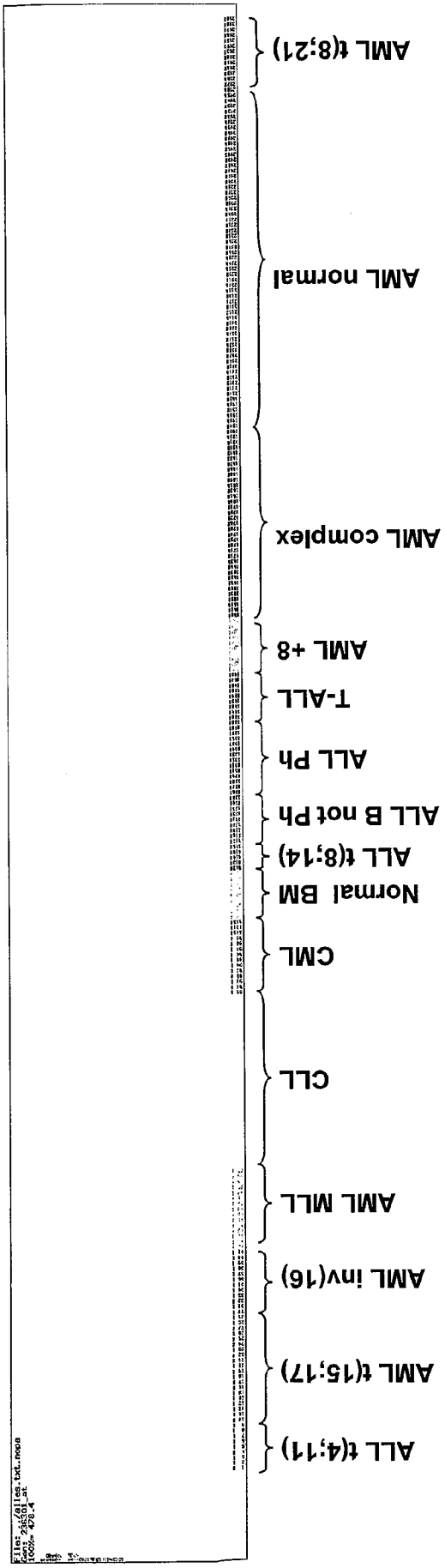


Figure 231

236892_s_at, HOXB6, AML normal, AML +8, AML complex

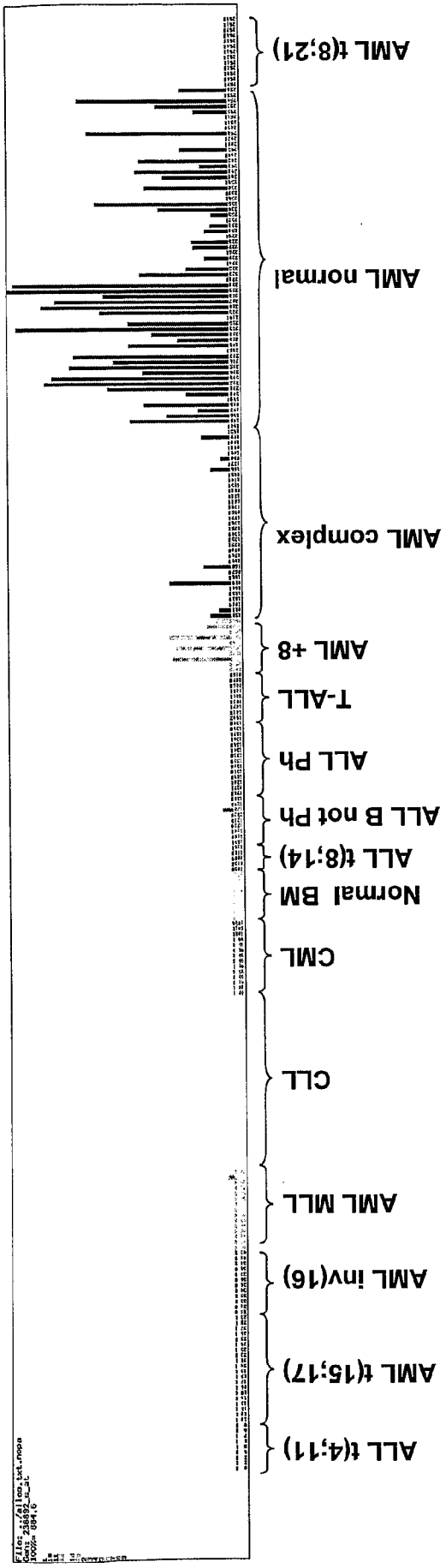


Figure 232

239214_at, ALL t(4;11)

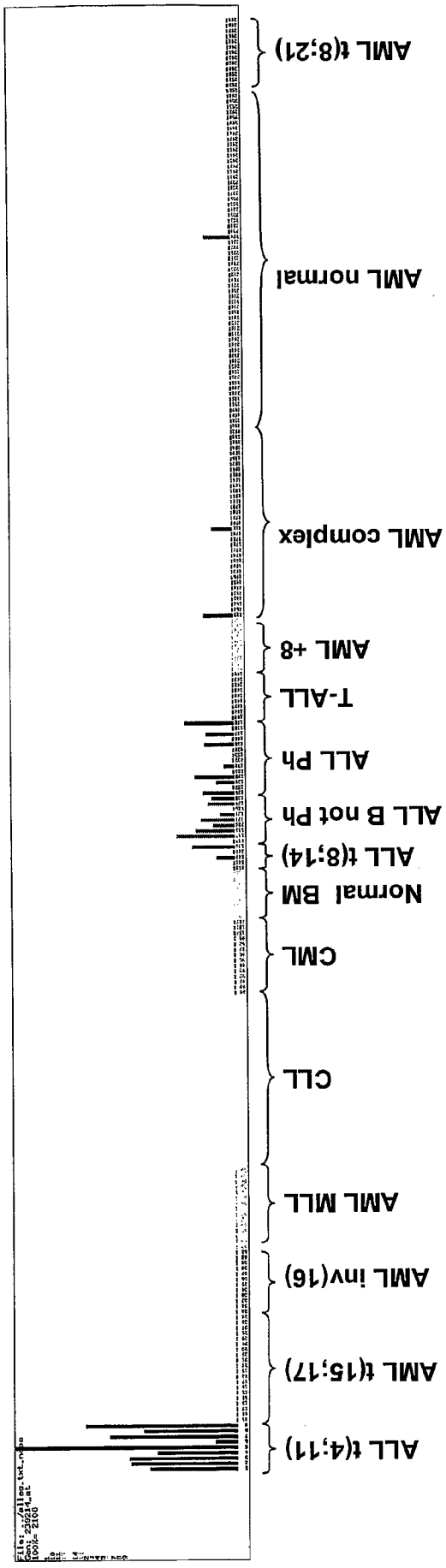


Figure 233

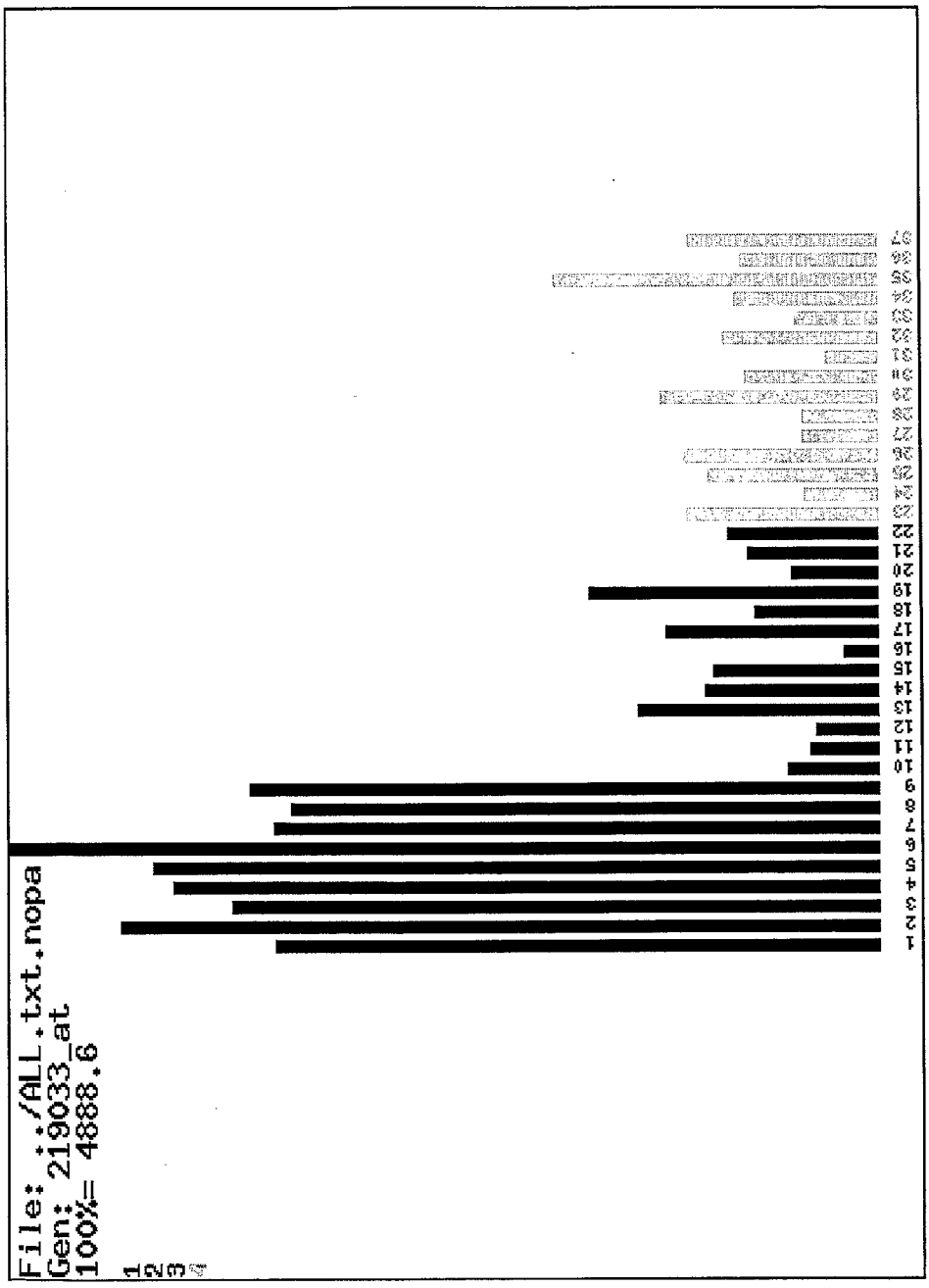

219033_at, FLJ21308, ALL t(4;11) vs. all other
File: ../ALL.txt.nopa
Gen: 219033_at
100%= 4888.6
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 234

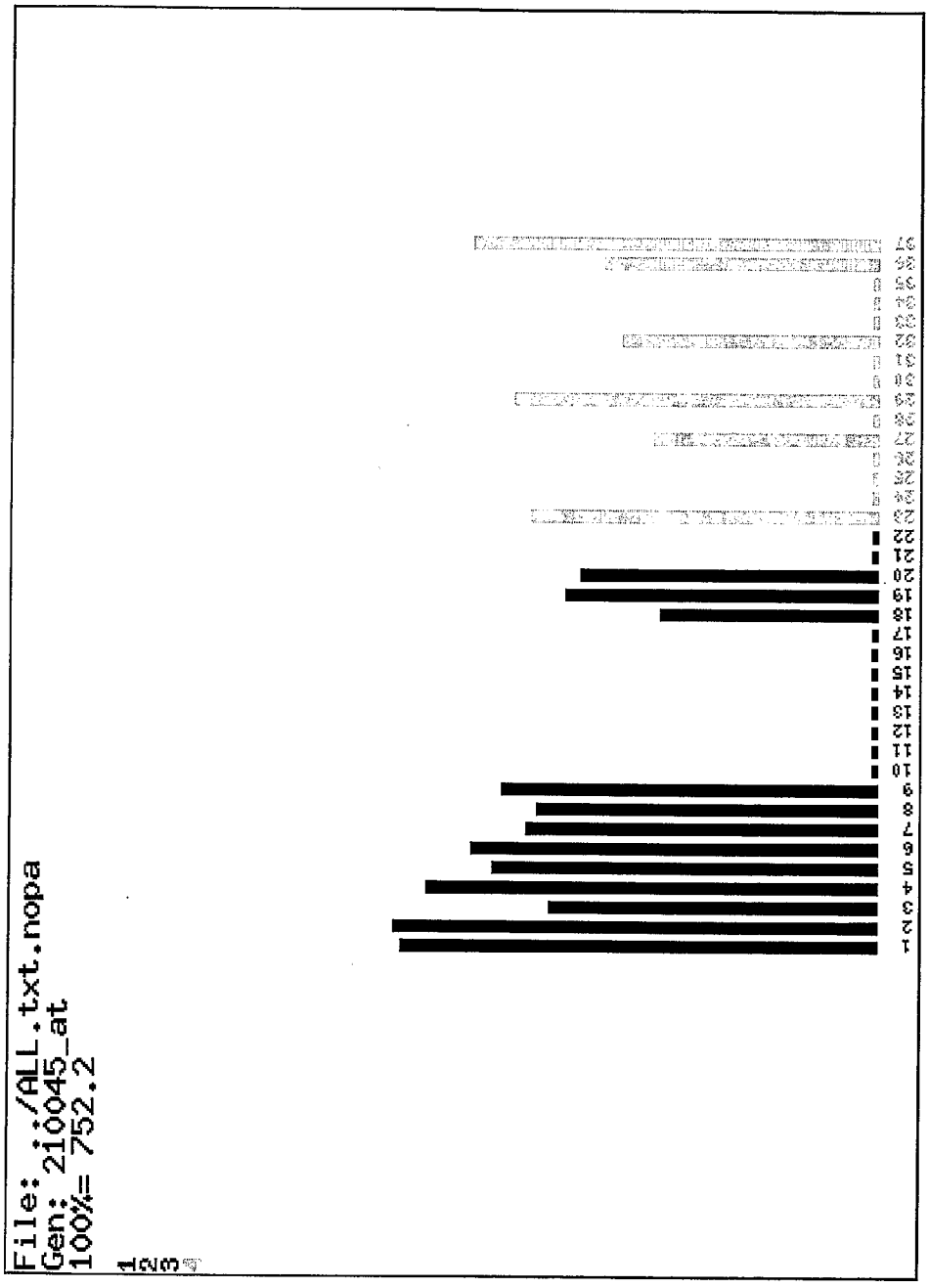

210045_at, IDH2, ALL t(4;11) vs. ALL t(8;14)
File: ../ALL.txt.nopa
Gen: 210045_at
100%= 752.2
1263
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 235

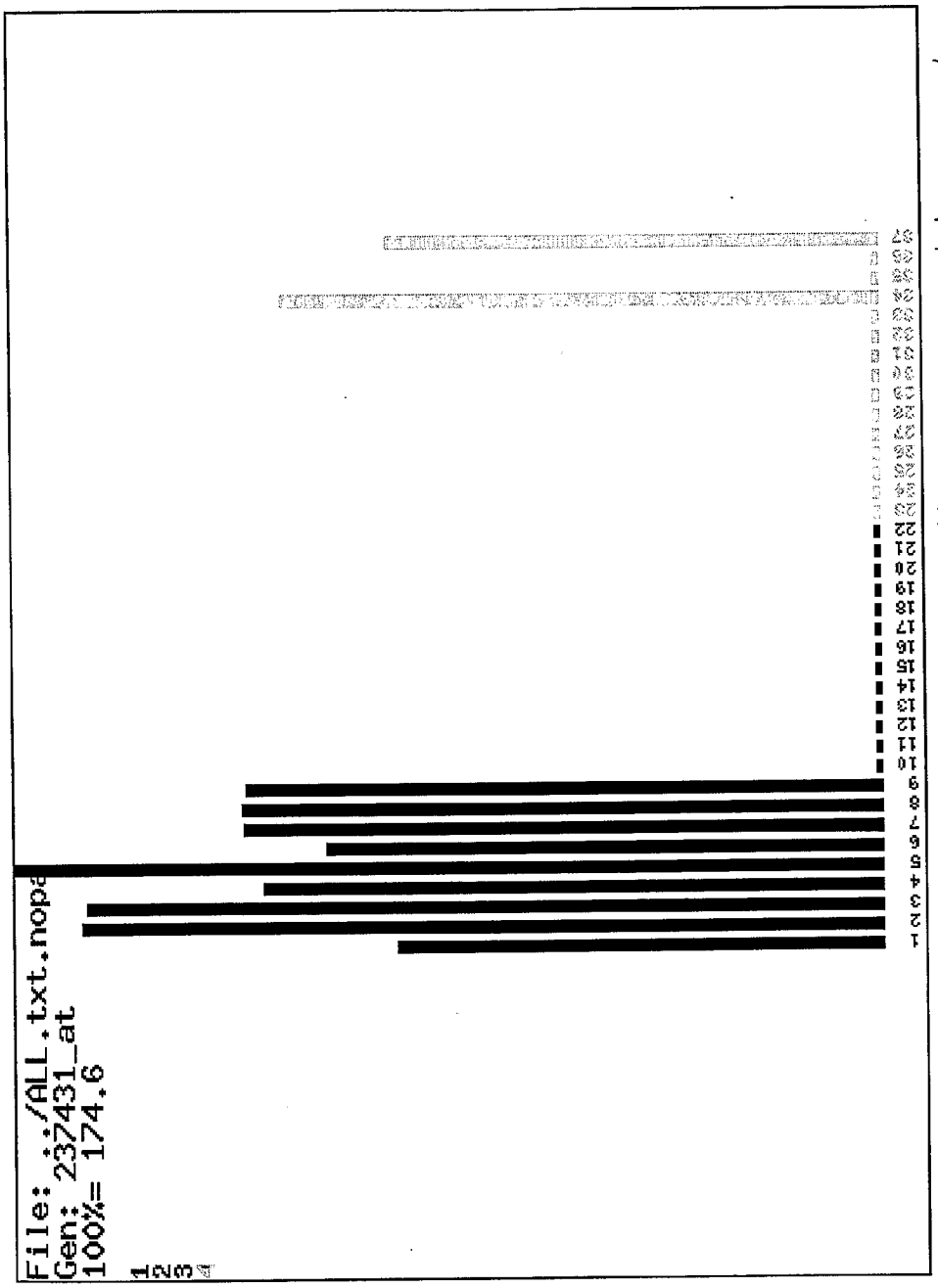

237431_at, ALL t(4;11) vs. ALL B not Ph
File: ../ALL.txt.nopa
Gen: 237431_at
100%= 174.6
1 2 3 4
t(4;11) t(8;14) ALLBnotPh ALLPh T-ALL

Figure 236

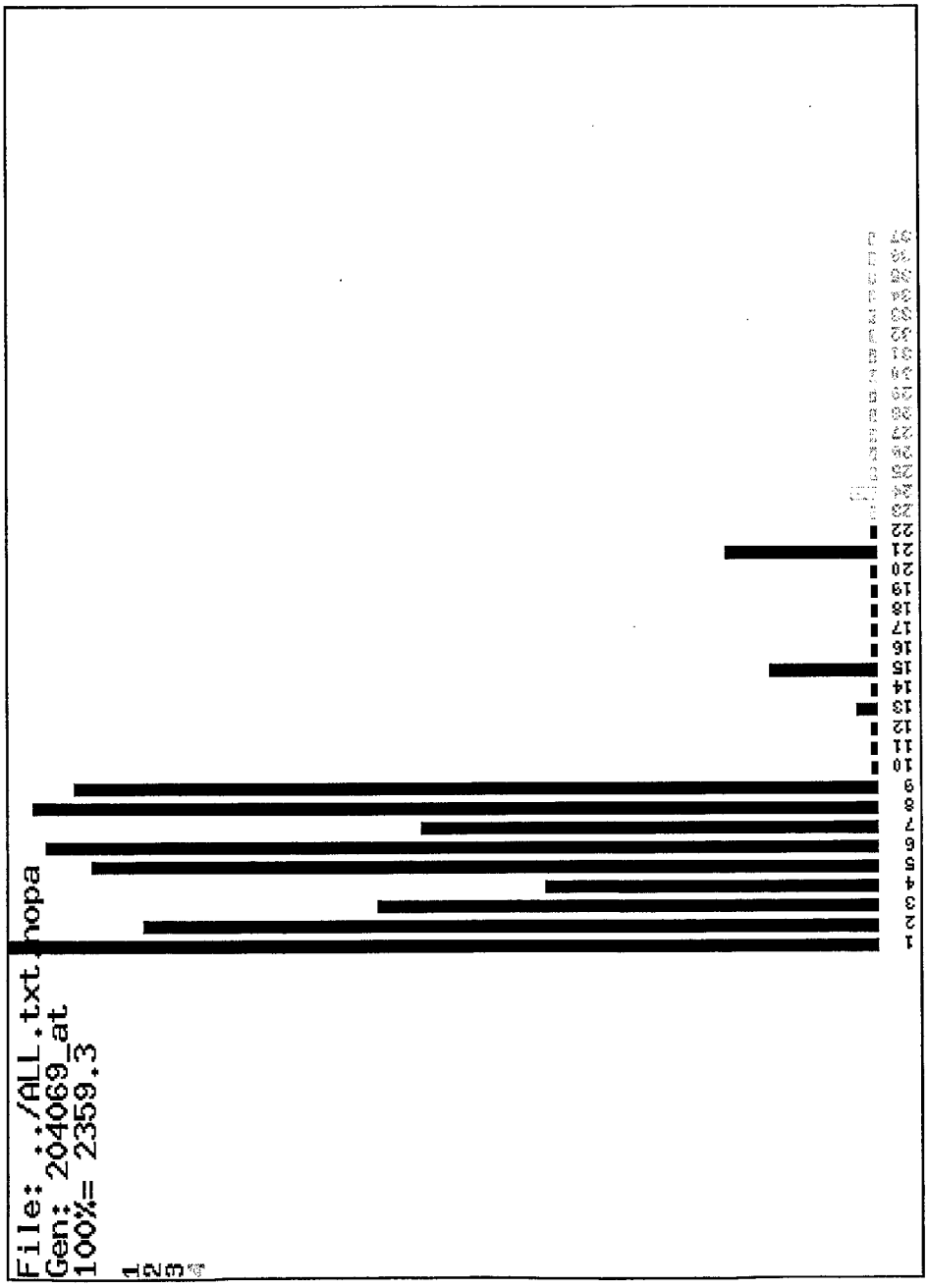

204069_at, MEIS1, ALL t(4;11) vs. ALL Ph
File: ../ALL.txt.hopa
Gen: 204069_at
100%= 2359.3
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 237

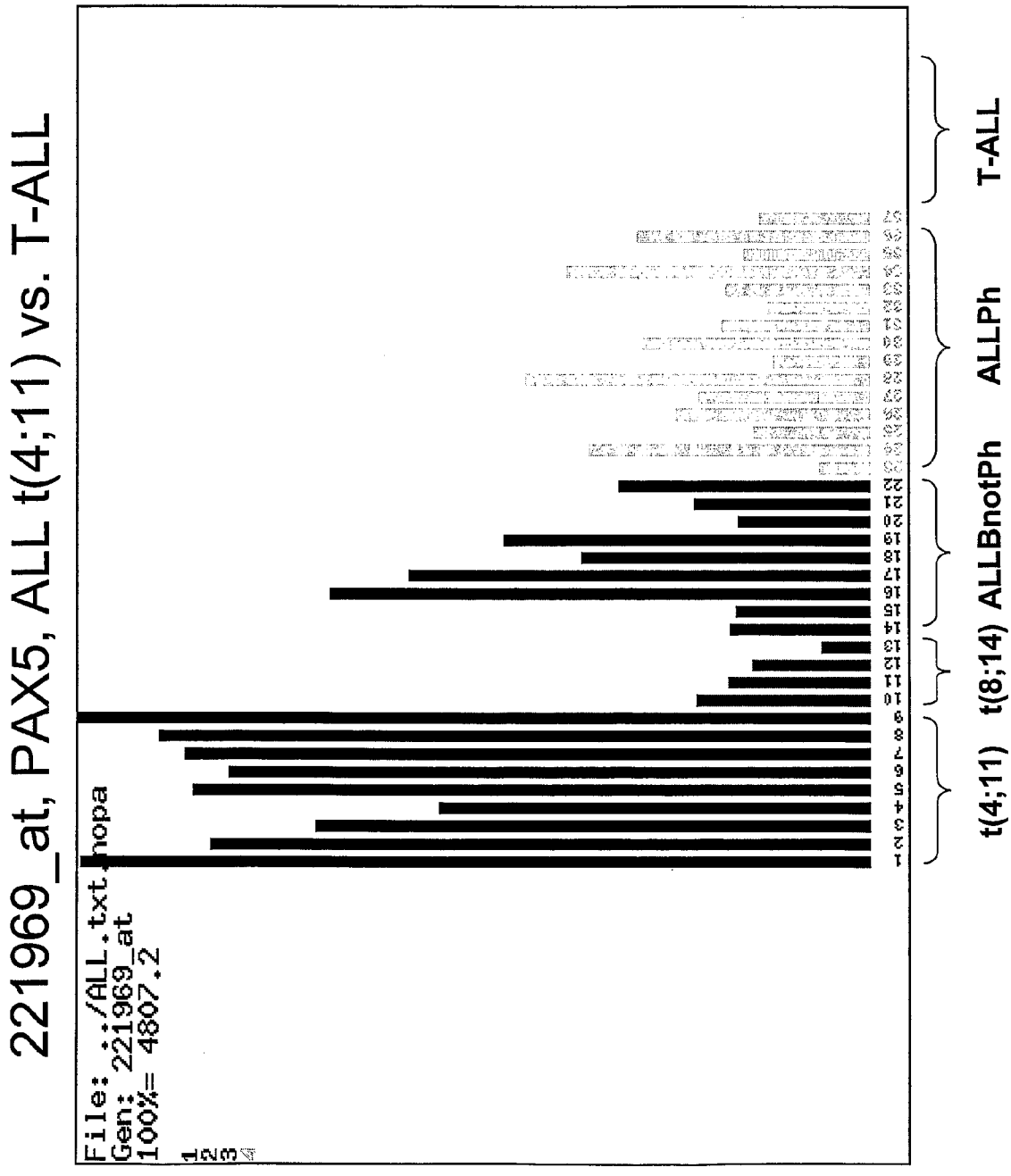

221969_at, PAX5, ALL t(4;11) vs. T-ALL
File: ../ALL.txt.hopa
Gen: 221969_at
100%= 4807.2
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 238

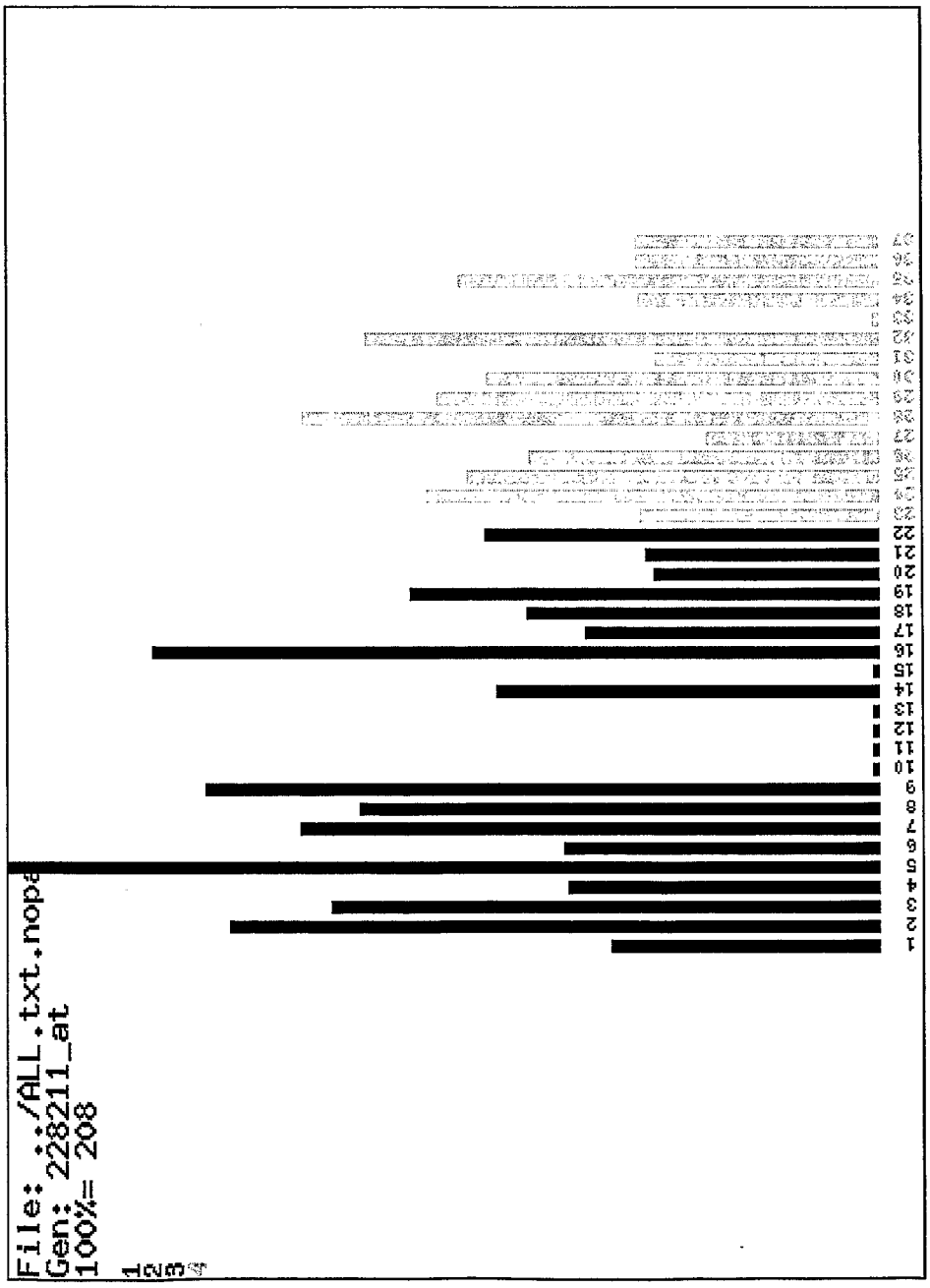

228211_at, ALL t(8;14) vs. all other
File: ../ALL.txt.nopa
Gen: 228211_at
100%= 208
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 239

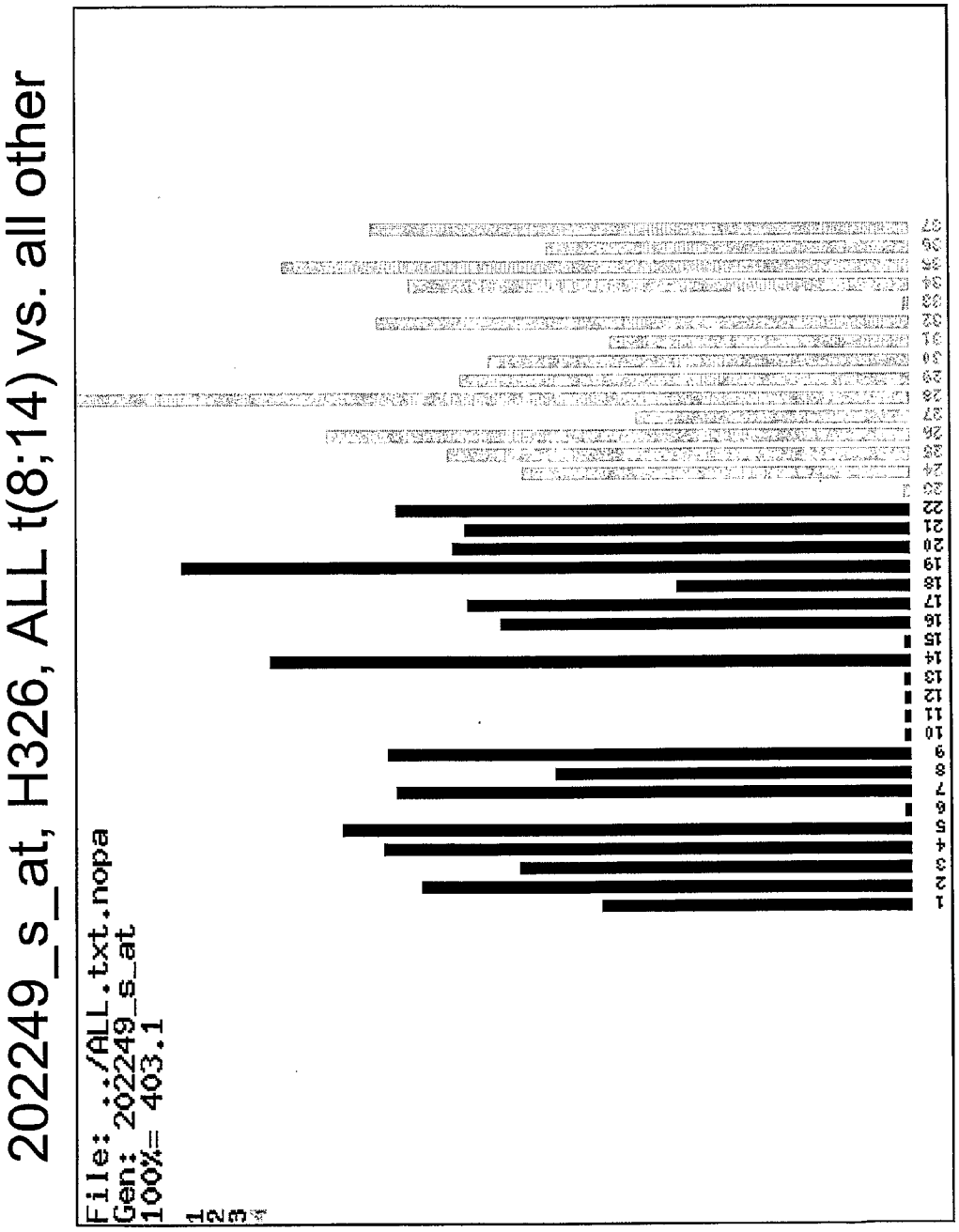

202249_s_at, H326, ALL t(8;14) vs. all other
File: ../ALL.txt.nopa
Gen: 202249_s_at
100%= 403.1
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 240

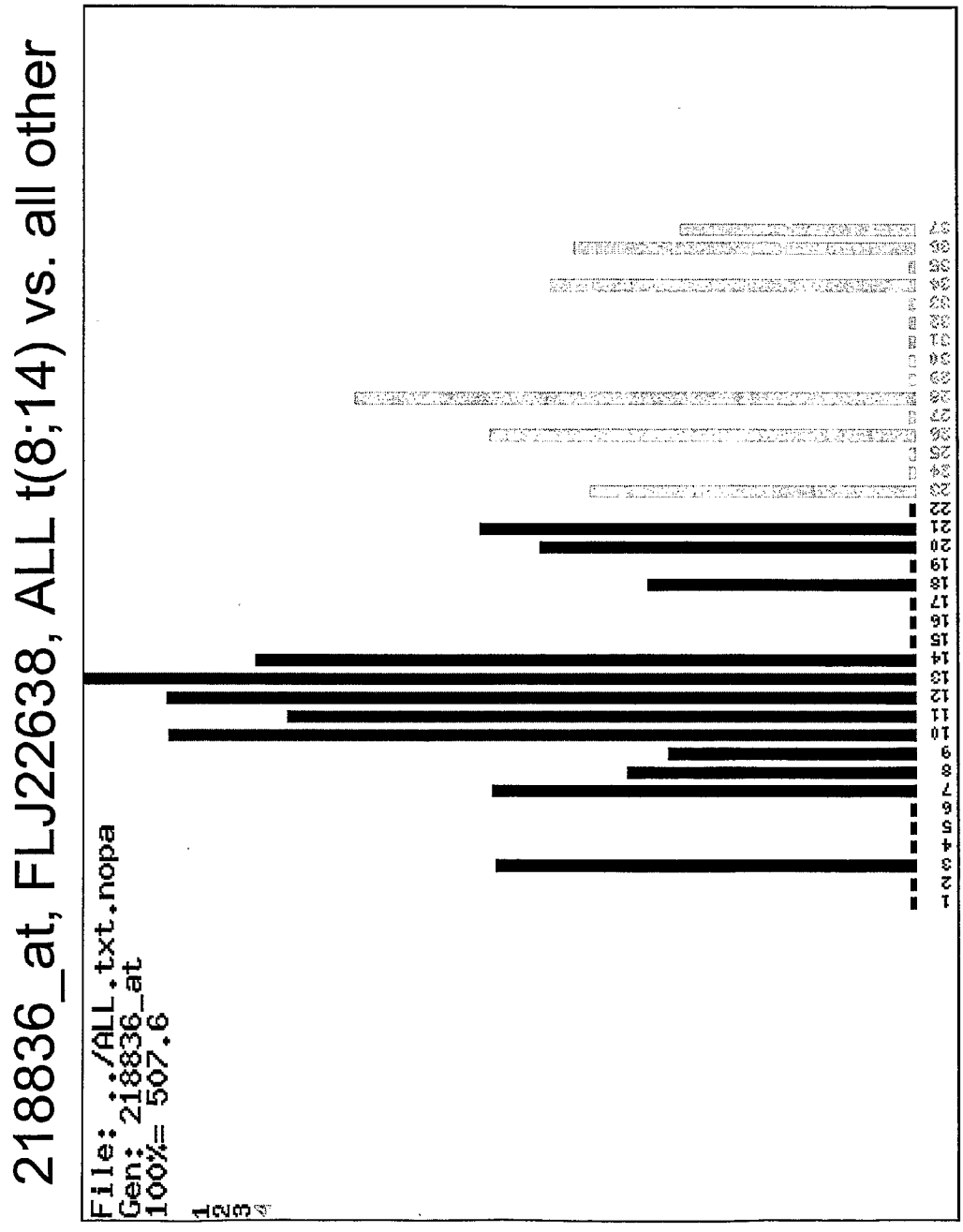

218836_at, FLJ22638, ALL t(8;14) vs. all other
File: ../ALL.txt.nopa
Gen: 218836_at
100%= 507.6
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 241

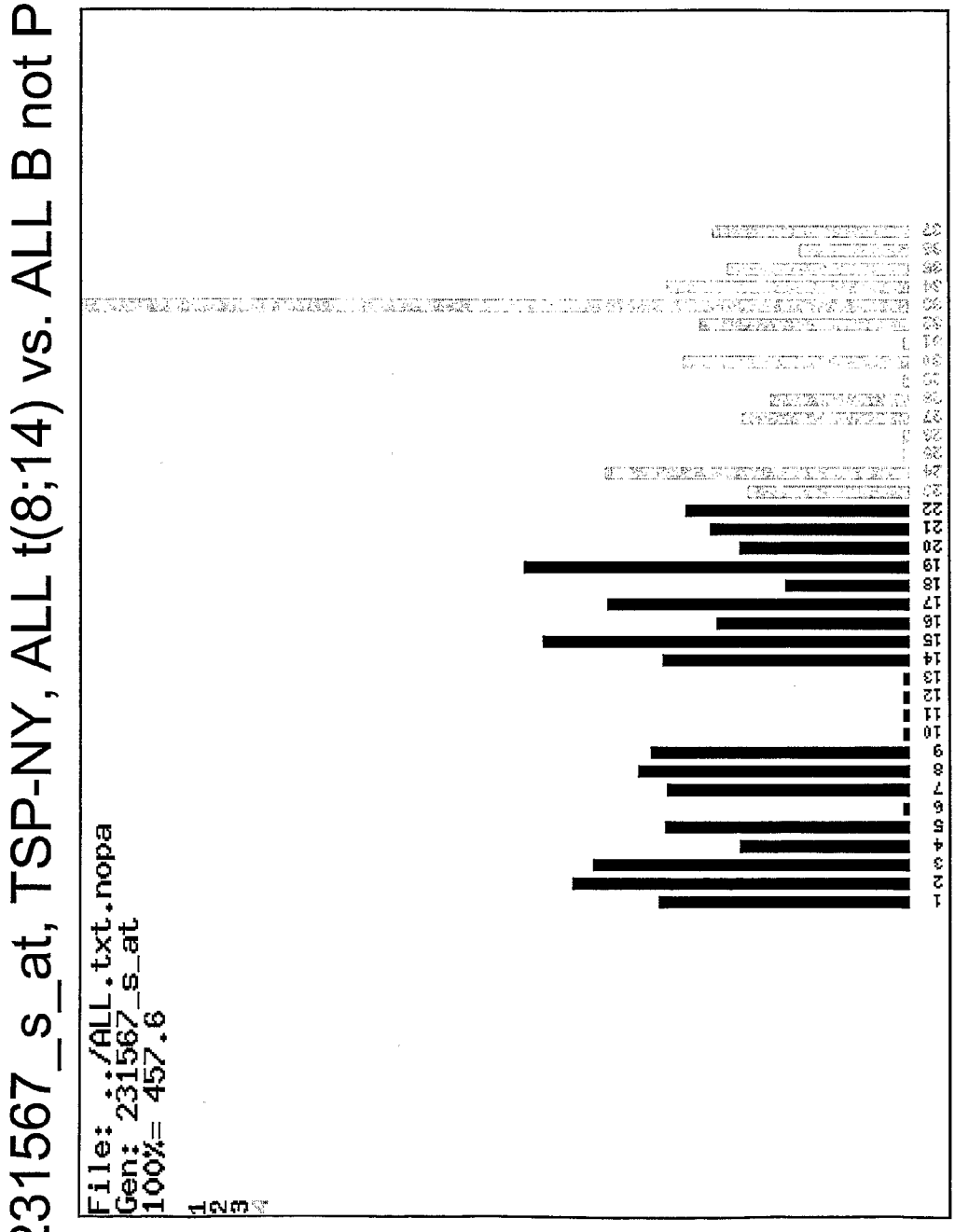

231567_s_at, TSP-NY, ALL t(8;14) vs. ALL B not Ph
File: ../ALL.txt.nopa
Gen: 231567_s_at
100%= 457.6
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 242

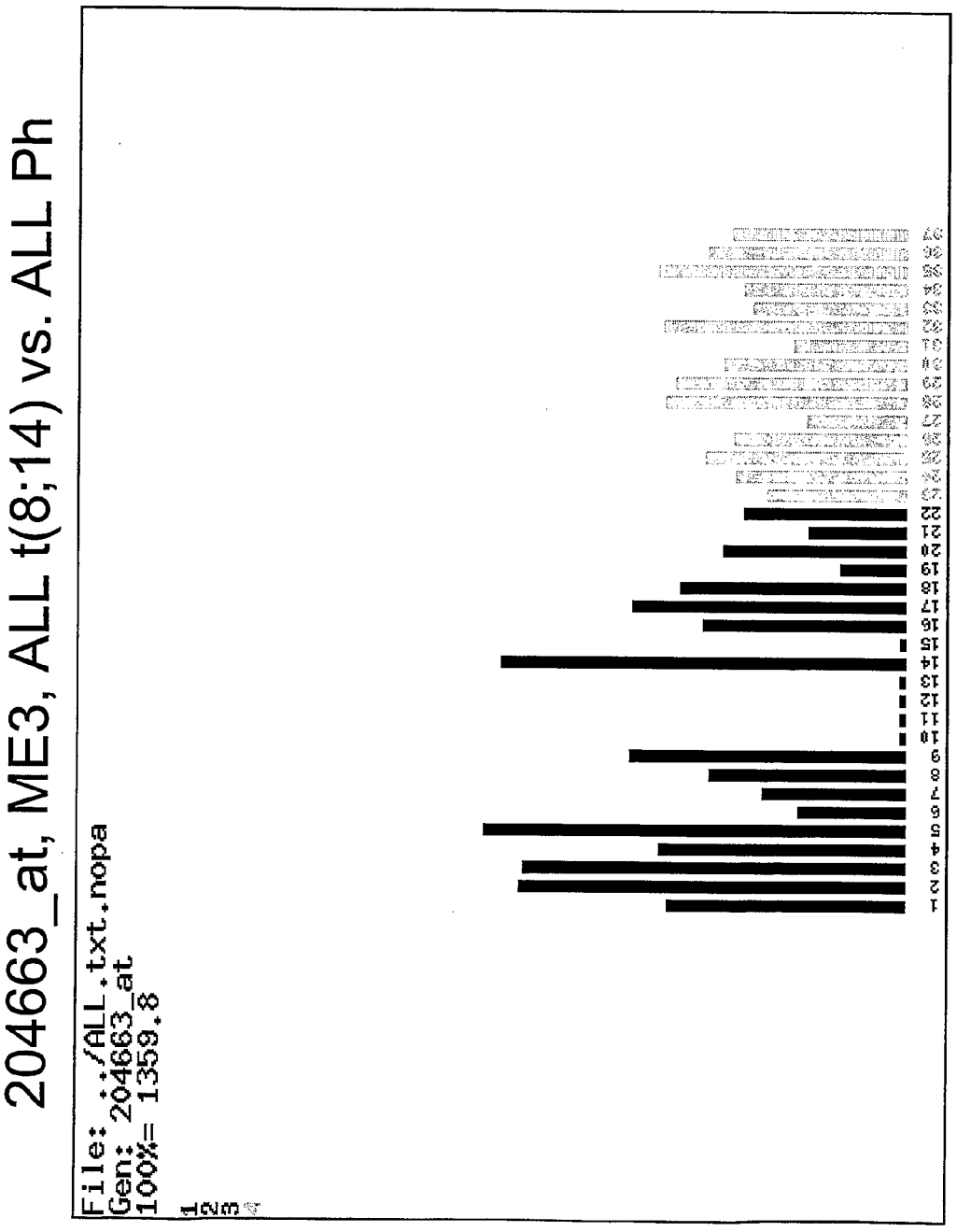

204663_at, ME3, ALL t(8;14) vs. ALL Ph
File: ../ALL.txt.mopa
Gen: 204663_at
100%= 1359.8
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 243

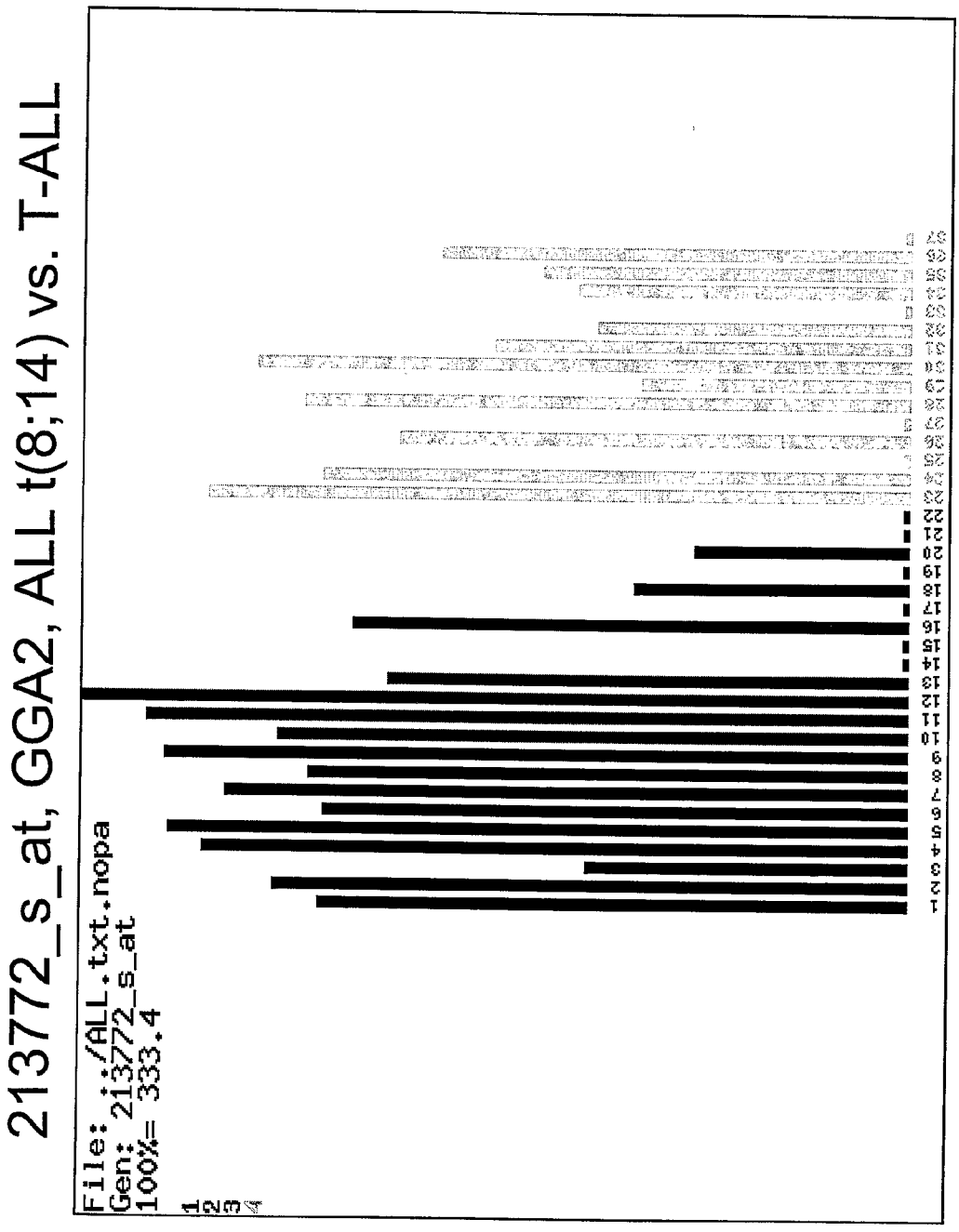

213772_s_at, GGA2, ALL t(8;14) vs. T-ALL
File: ../ALL.txt.nopa
Gen: 213772_s_at
100%= 333.4
1 2 3 4
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 244

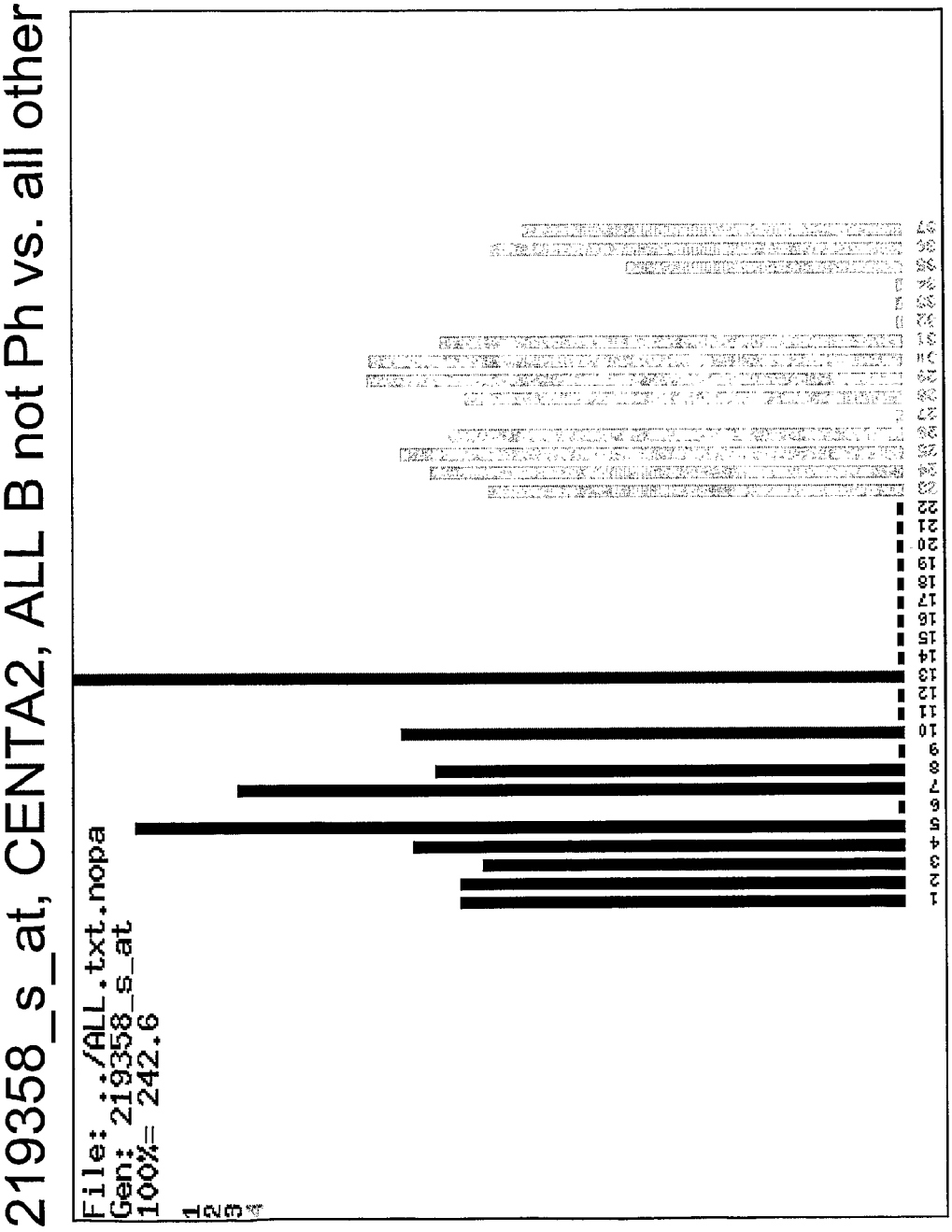

219358_s_at, CENTA2, ALL B not Ph vs. all other
File: ../ALL.txt.nopa
Gen: 219358_s_at
100%= 242.6
1
2
3
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 245

WO03039443 file://E:\WO03039443.com\

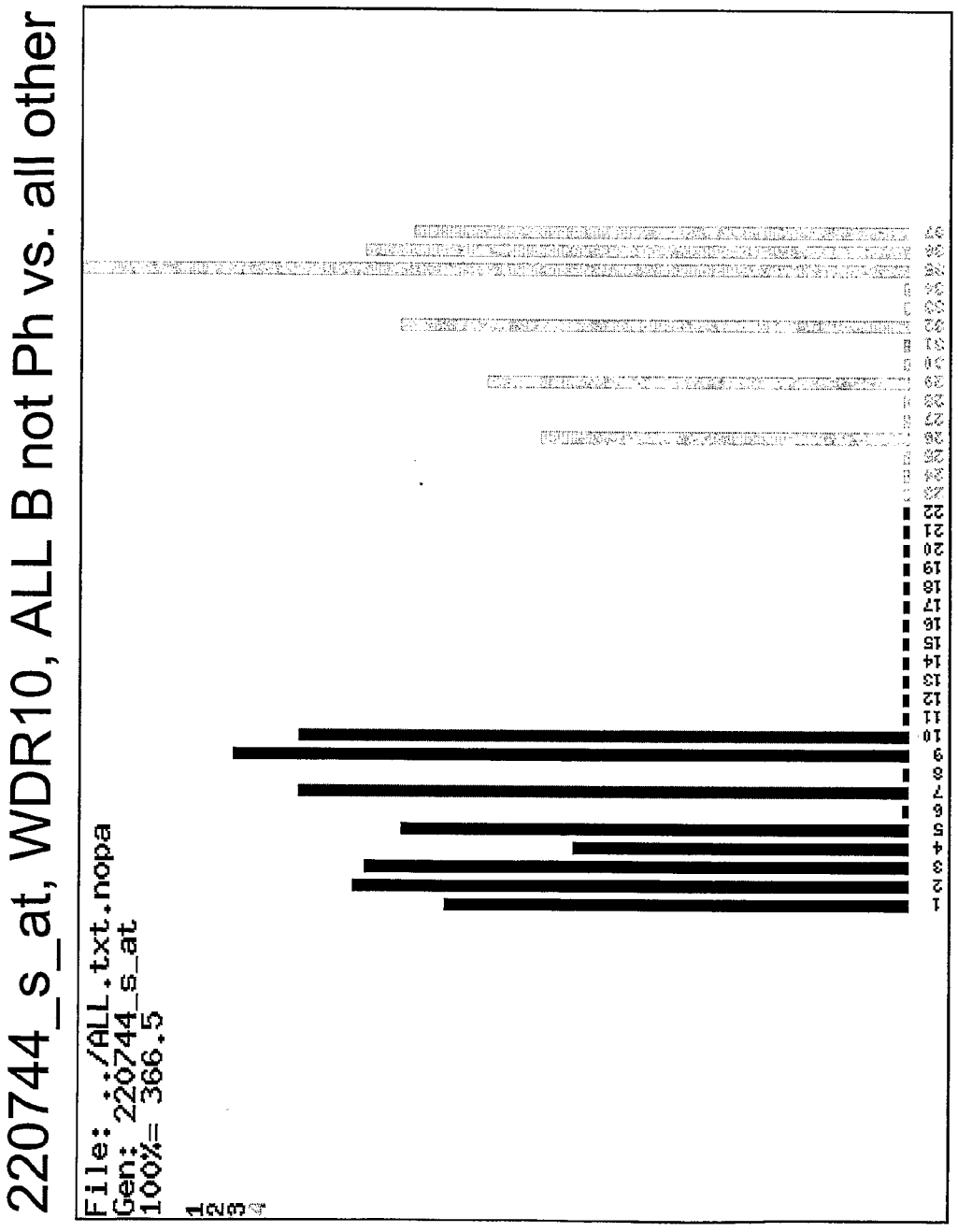


Figure 246

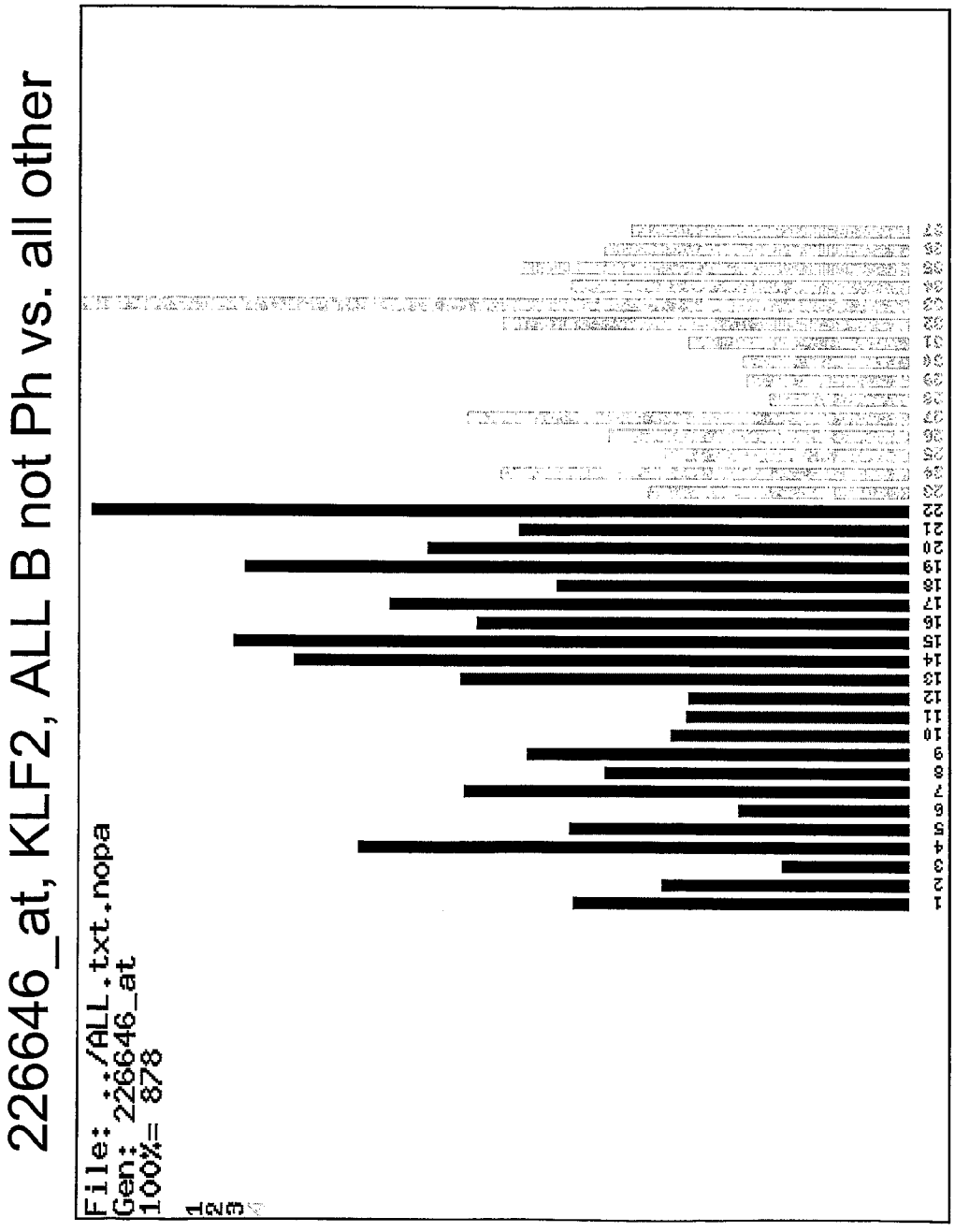

226646_at, KLF2, ALL B not Ph vs. all other
File: ../ALL.txt.nopa
Gen: 226646_at
100%= 878
1
2
3
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 247

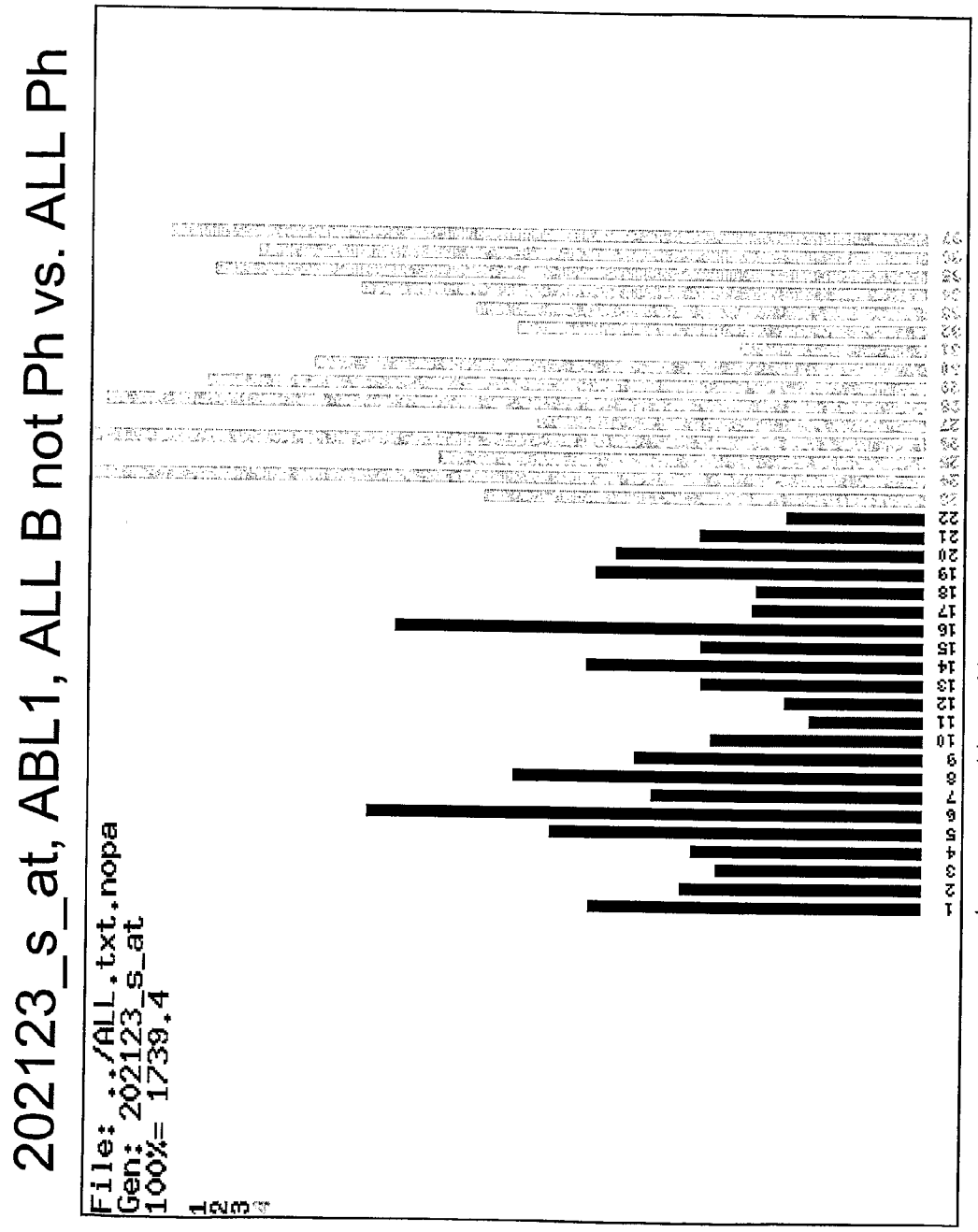

202123_s_at, ABL1, ALL B not Ph vs. ALL Ph
File: ../ALL.txt.nopa
Gen: 202123_s_at
100%= 1739.4
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 248

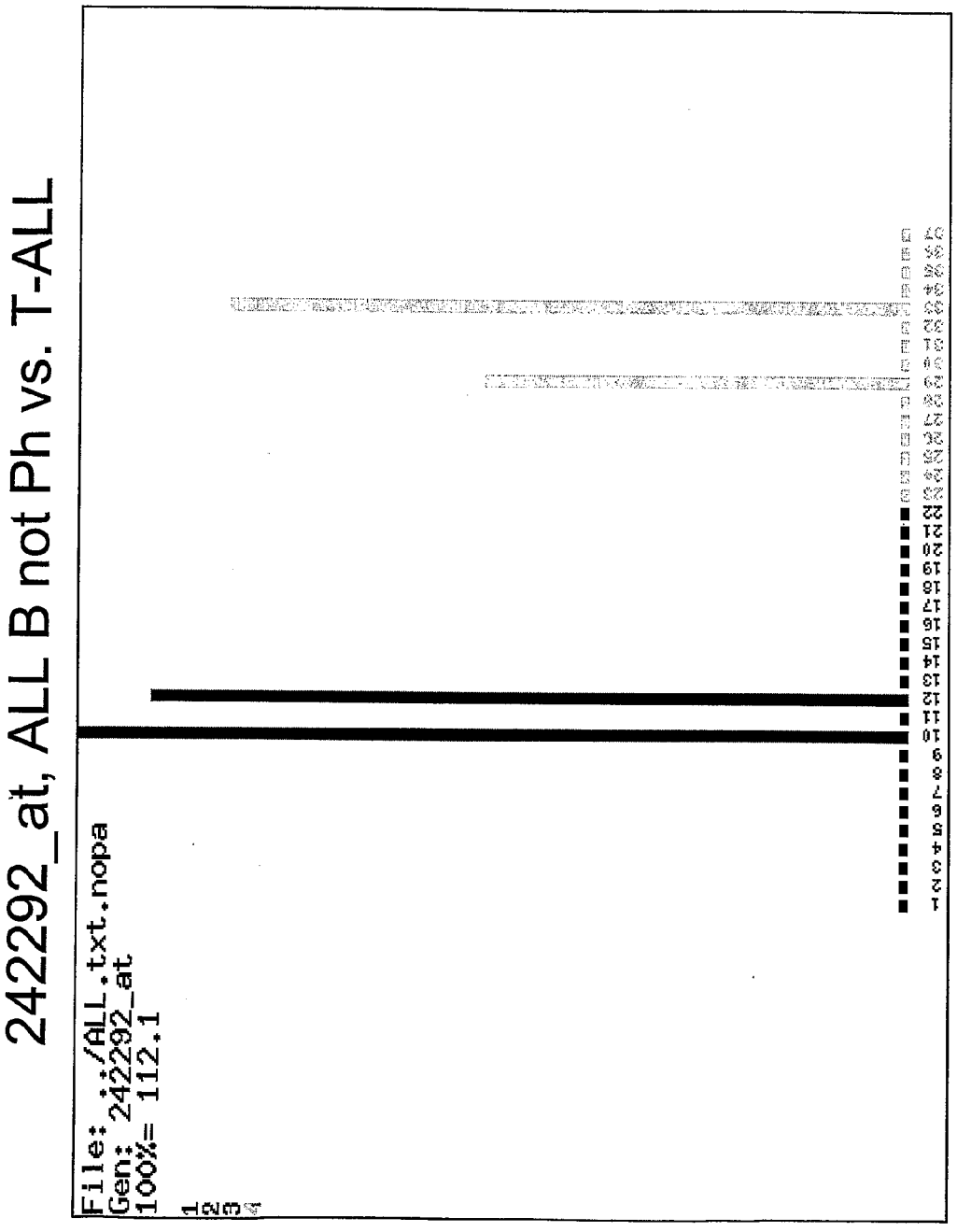

242292_at, ALL B not Ph vs. T-ALL
File: ../ALL.txt.nopa
Gen: 242292_at
100%= 112.1
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 249

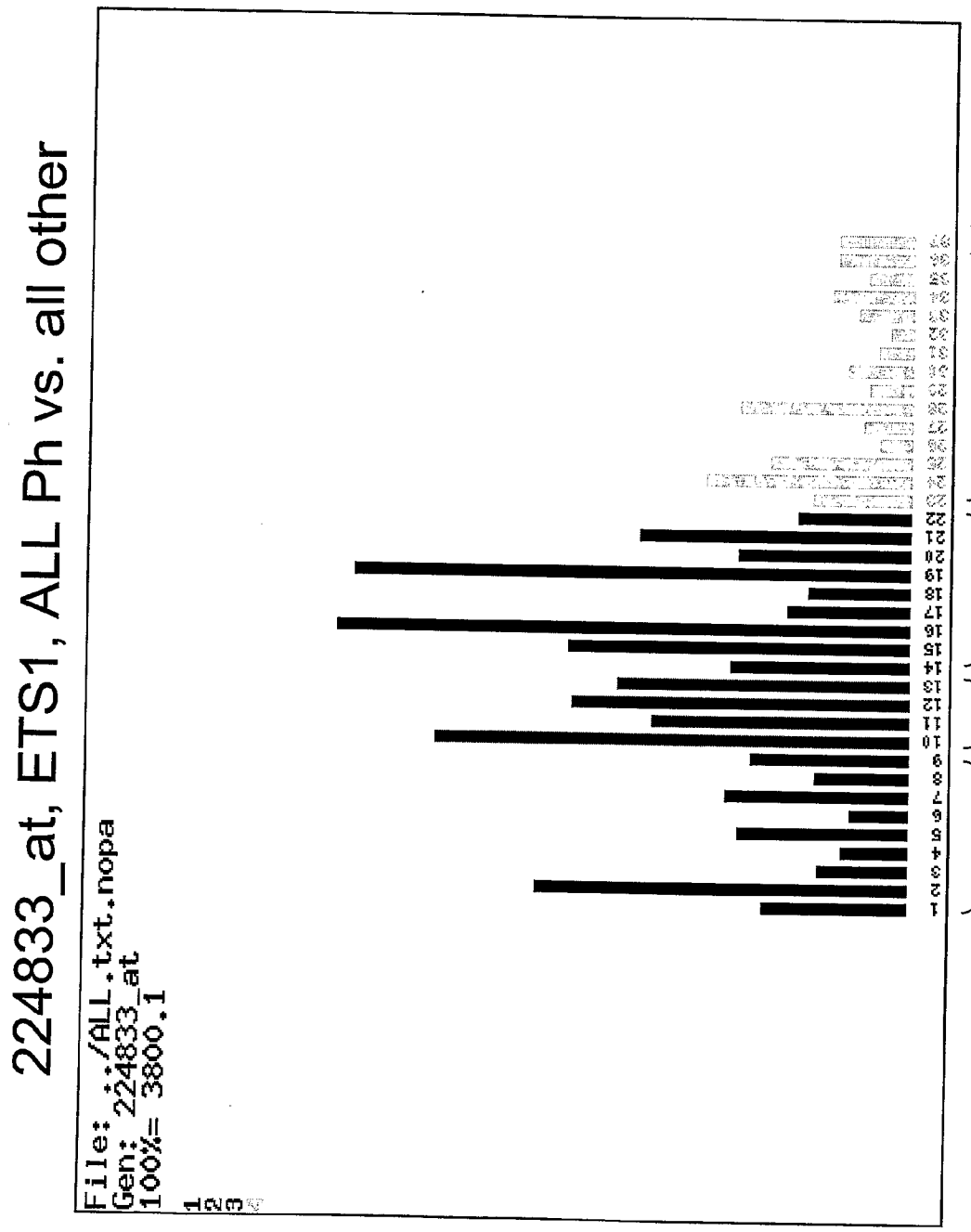

224833_at, ETS1, ALL Ph vs. all other
File: ../ALL.txt.nopa
Gen: 224833_at
100%= 3800.1
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 250

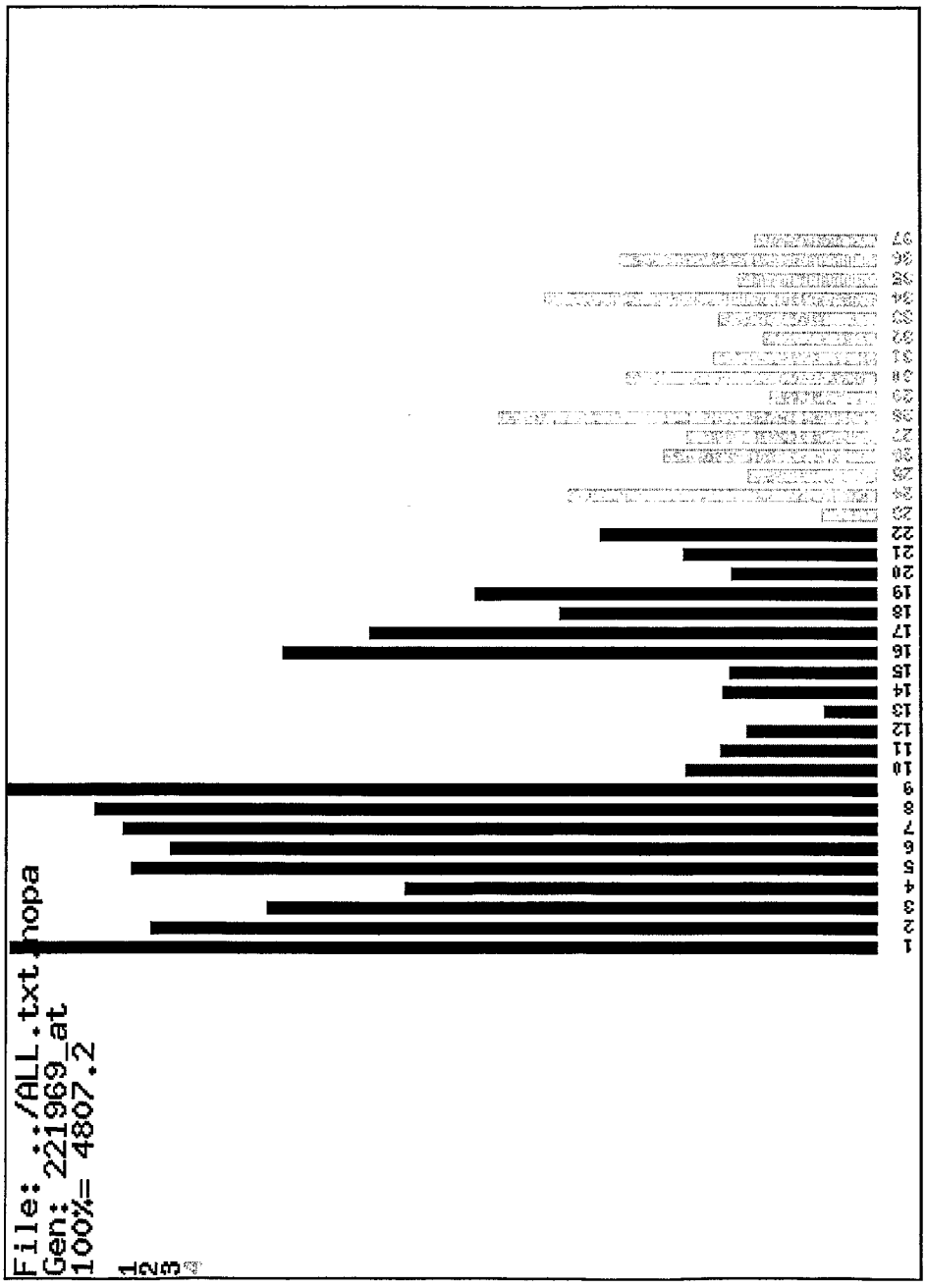

221969_at, PAX5, ALL Ph vs. T-ALL
File: .:/ALL.txt.hopa
Gen: 221969_at
100%= 4807.2
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 251

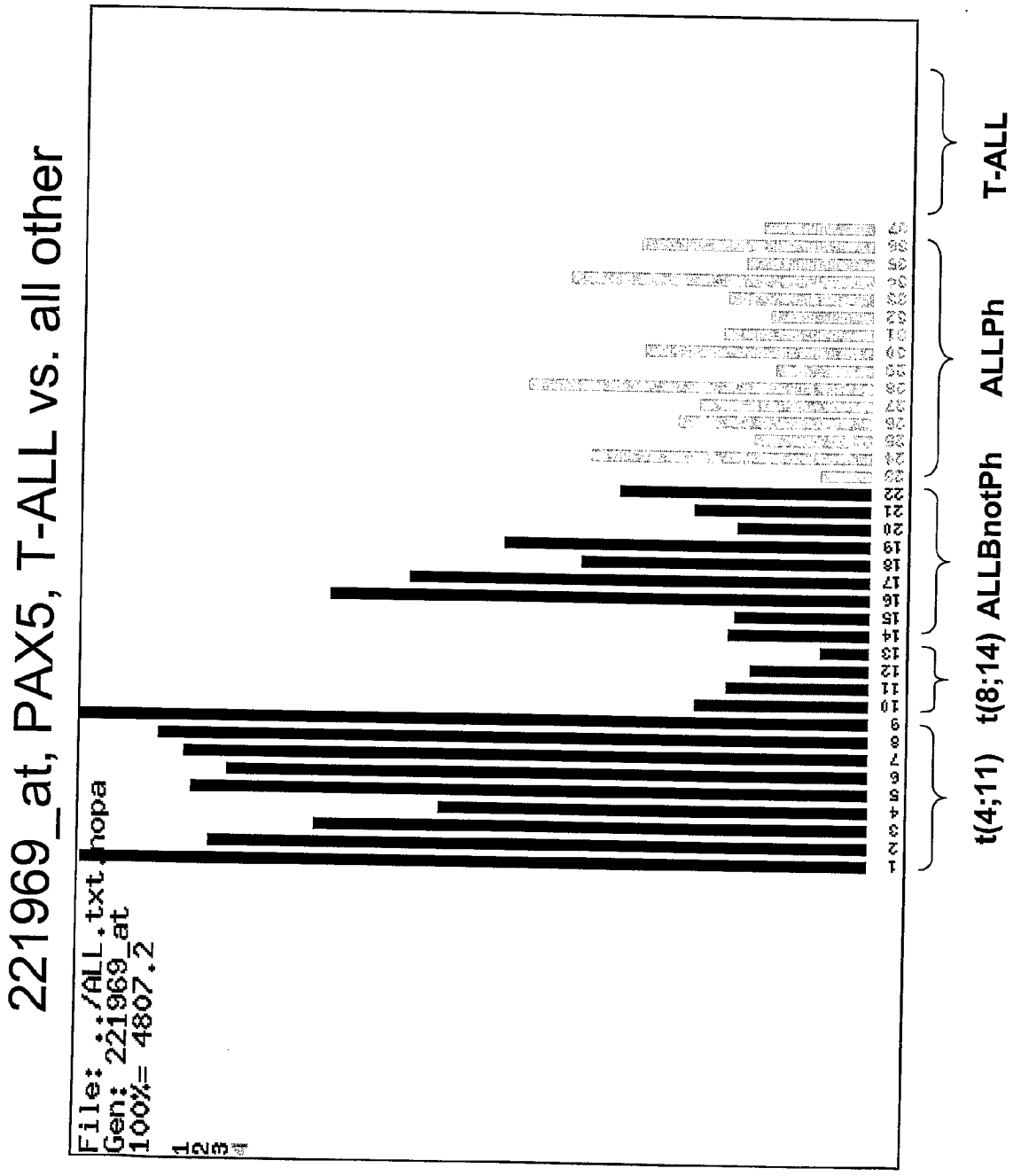

221969_at, PAX5, T-ALL vs. all other
File: ../ALL.txt hopa
Gen: 221969_at
100%= 4807.2
1 2 3
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 252

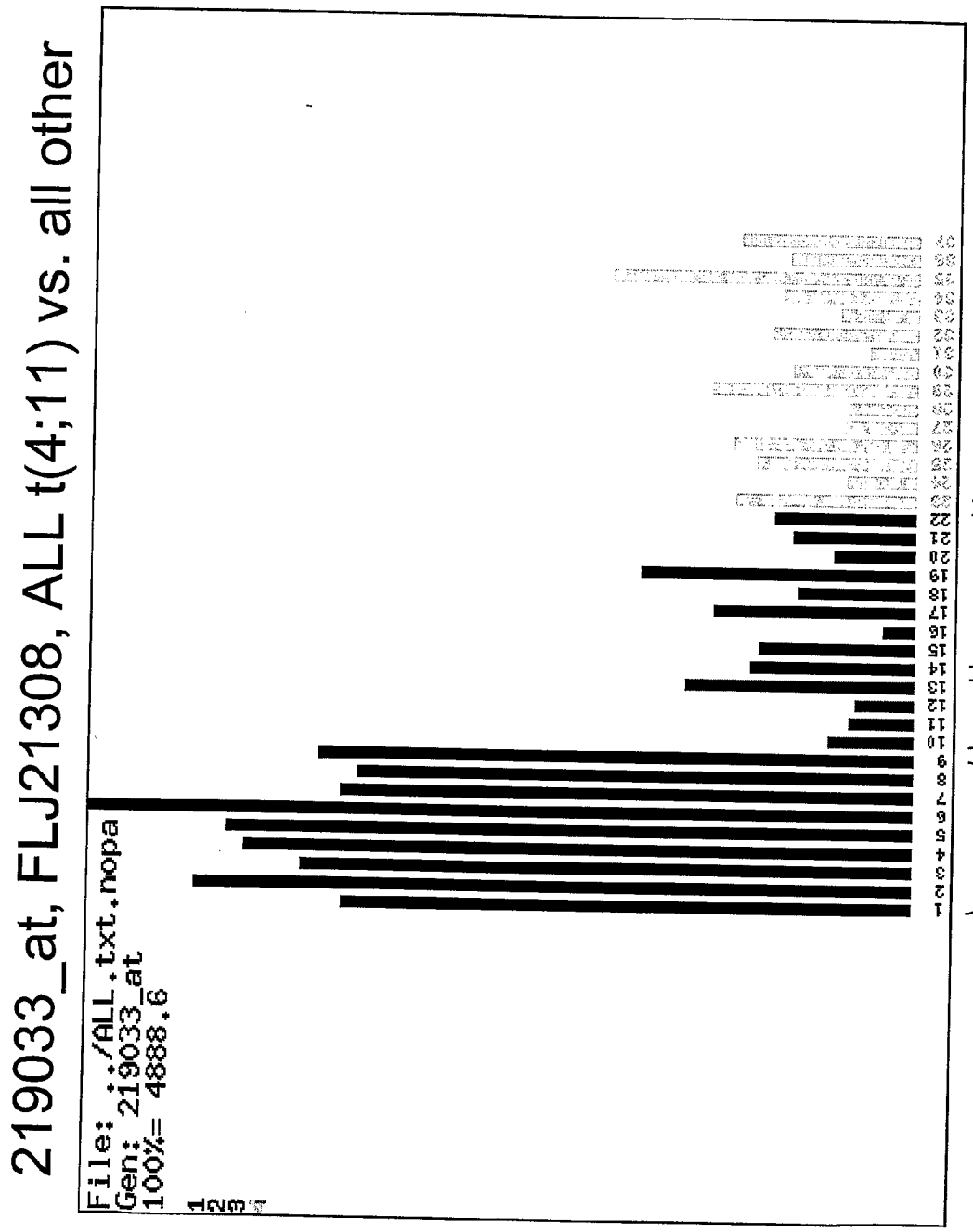

219033_at, FLJ21308, ALL t(4;11) vs. all other
File: ../ALL.txt.mopa
Gen: 219033_at
100%= 4888.6
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 253

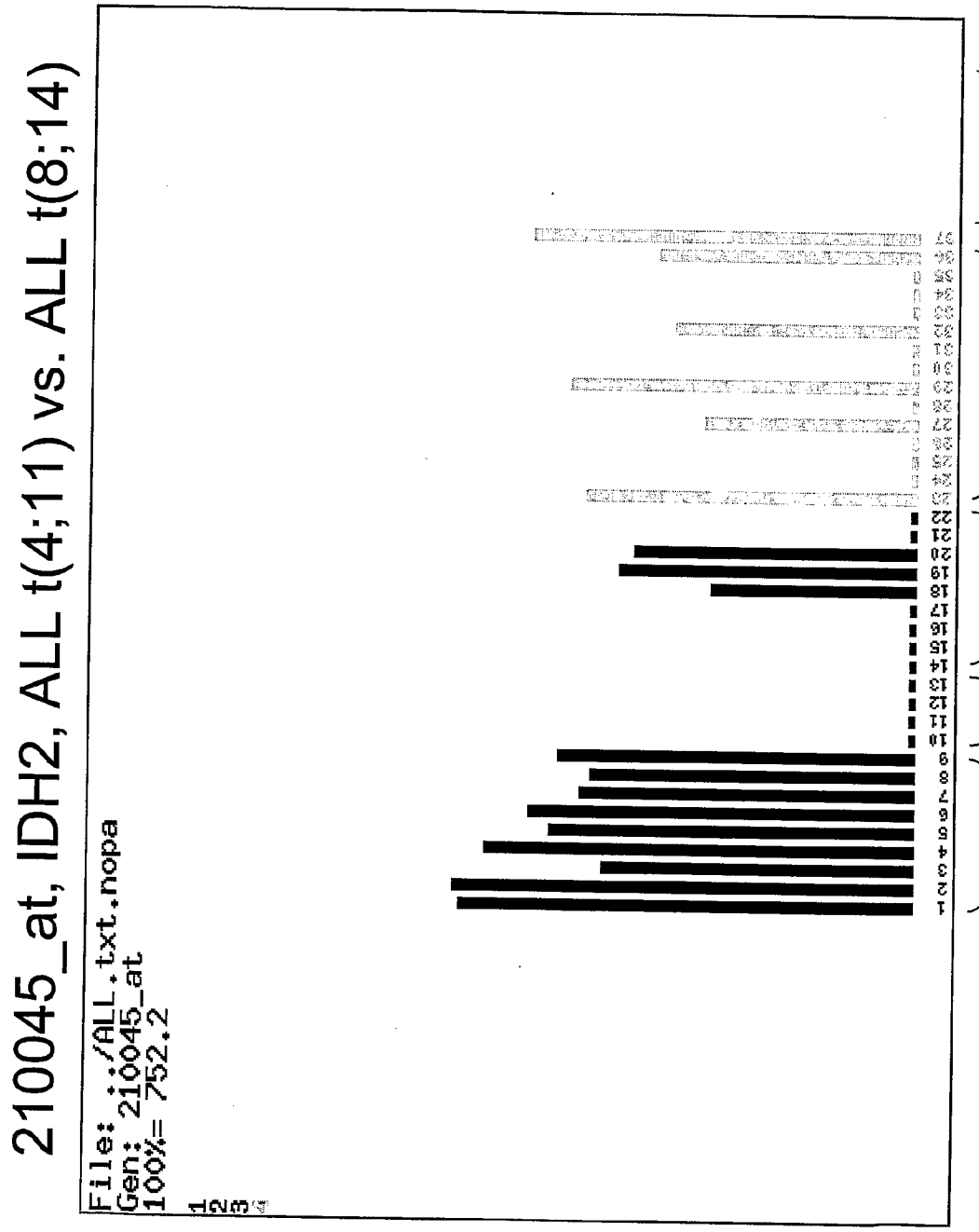

210045_at, IDH2, ALL t(4;11) vs. ALL t(8;14)
File: ../ALL.txt.nopa
Gen: 210045_at
100%= 752.2
1 2 3 4
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 254

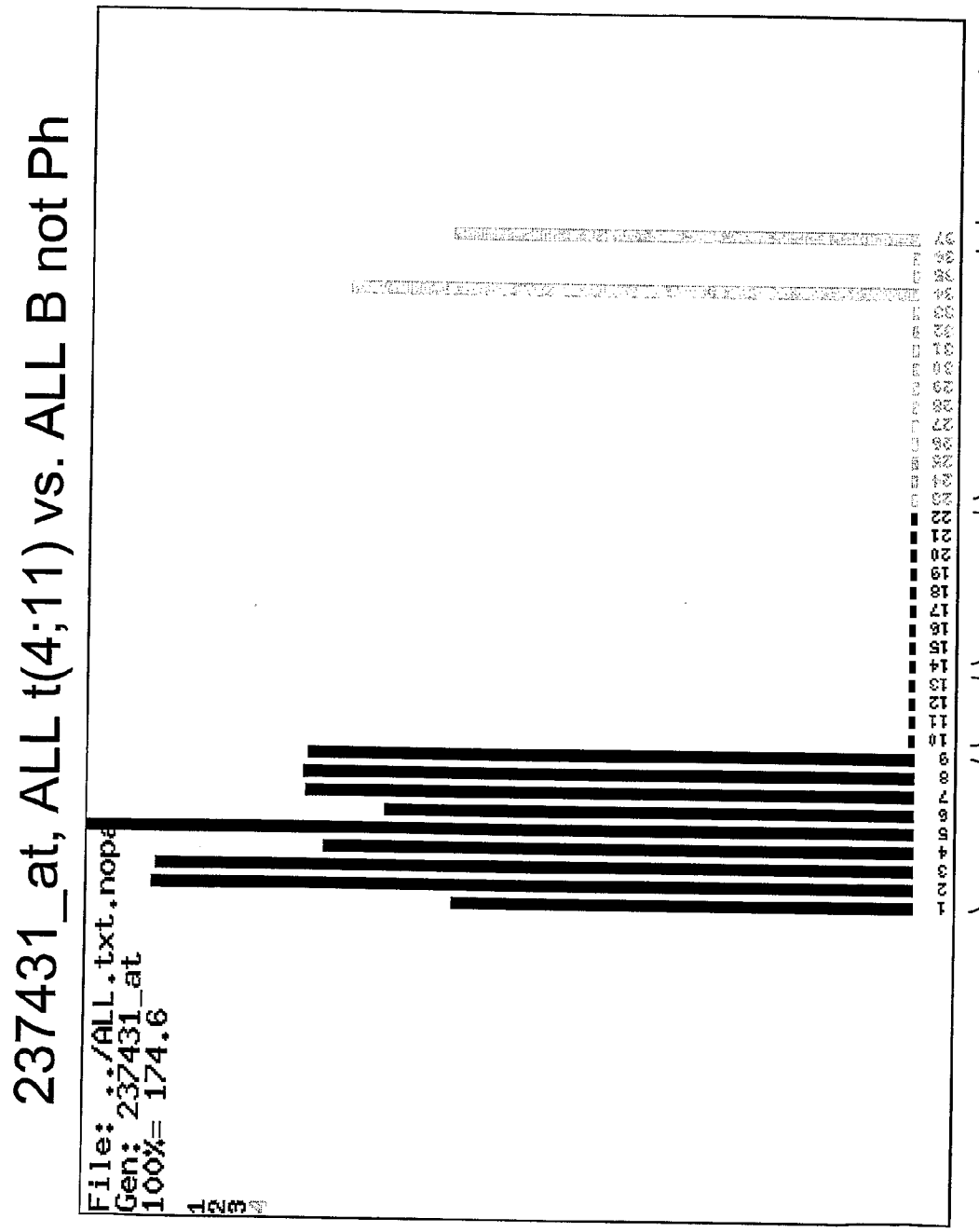

237431_at, ALL t(4;11) vs. ALL B not Ph
File: ...\ALL.txt.nopa
Gen: 237431_at
100%= 174.6
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 255

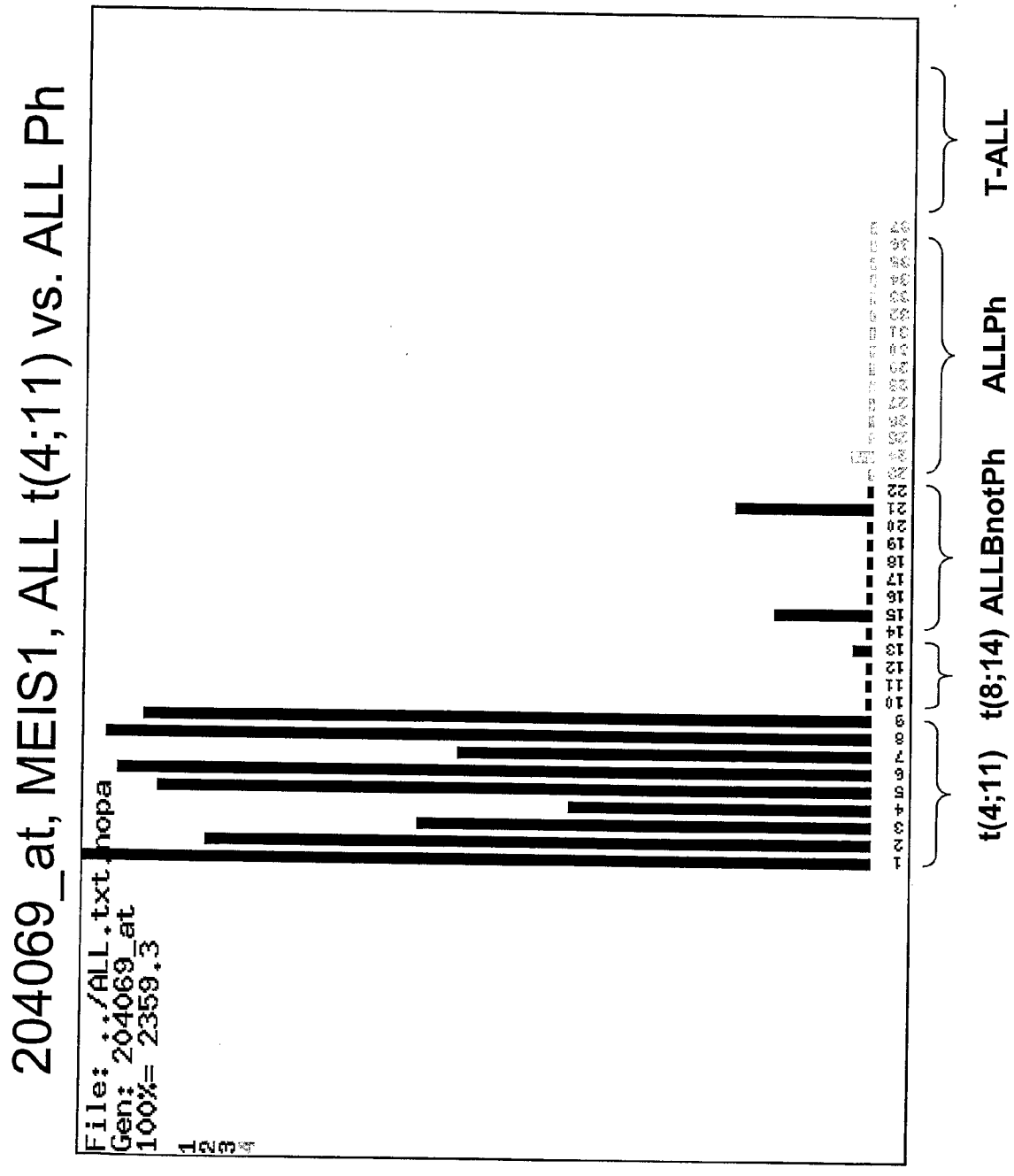

204069_at, MEIS1, ALL t(4;11) vs. ALL Ph
File: ../ALL.txt.hopa
Gen: 204069_at
100%= 2359.3
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 256

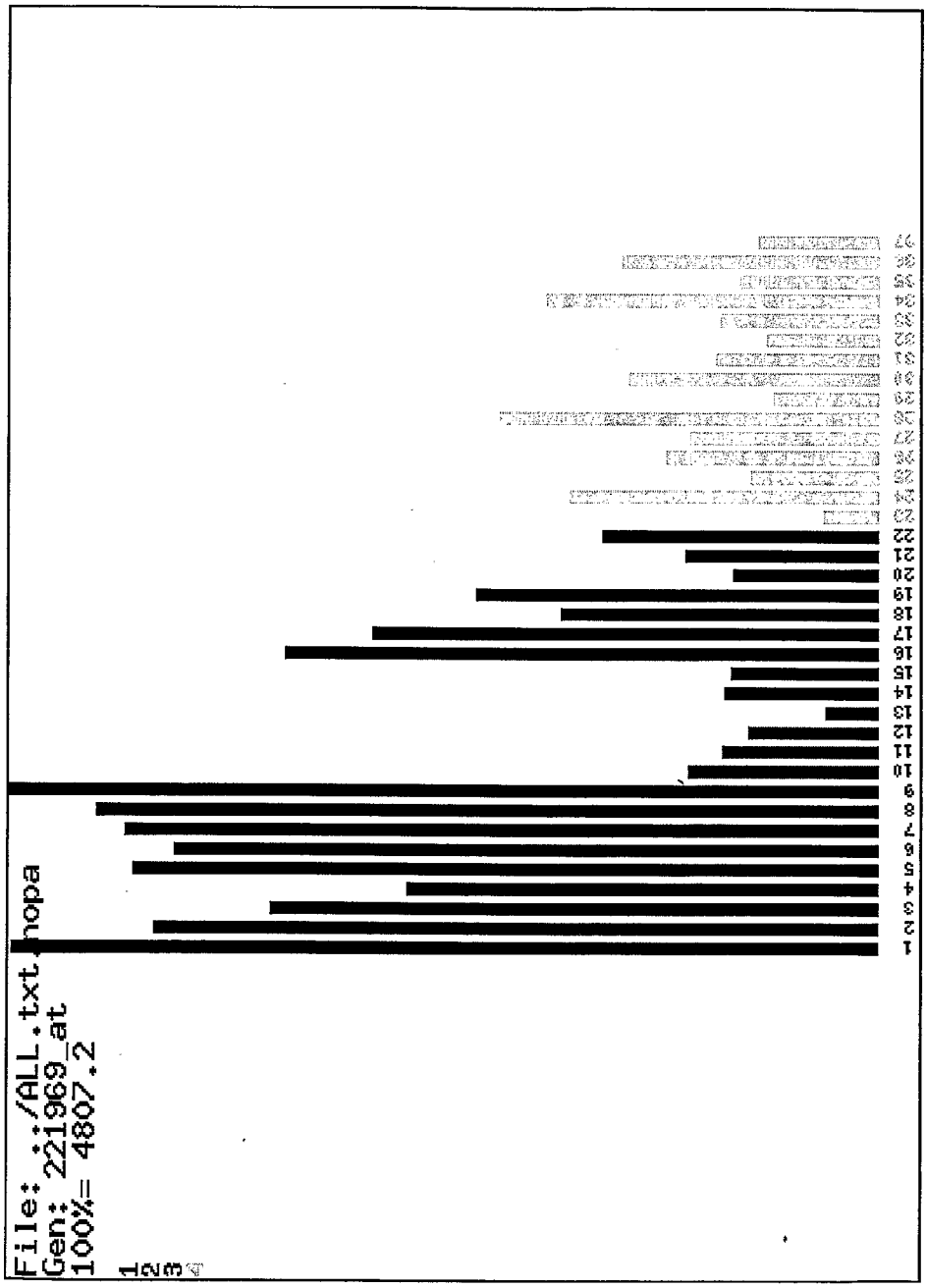

221969_at, PAX5, ALL t(4;11) vs. T-ALL
File: ../ALL.txt
Gen: 221969_at
100%= 4807.2
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 257

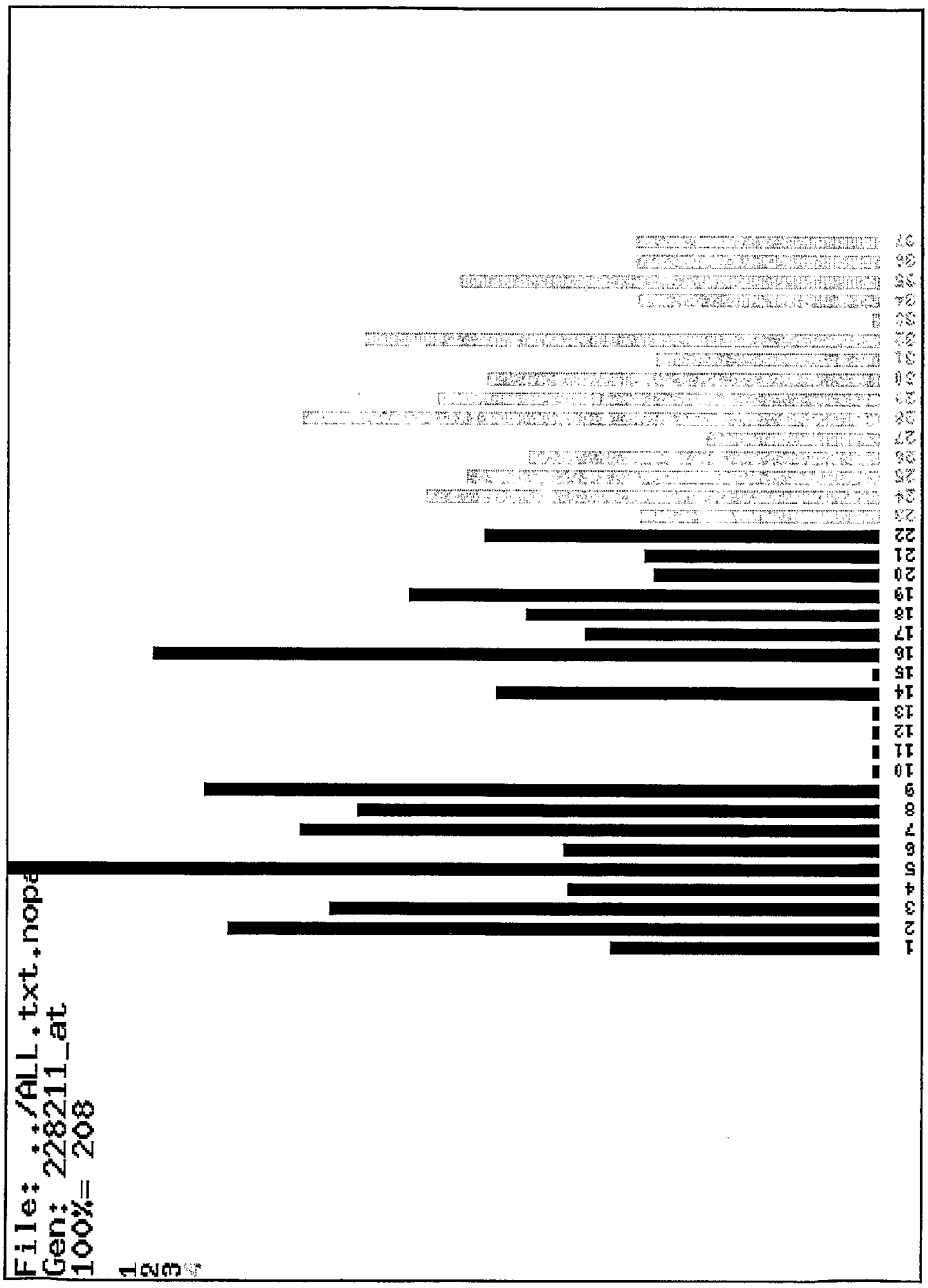

228211_at, ALL t(8;14) vs. all other
File: ../ALL.txt.nopa
Gen: 228211_at
100%= 208
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 258

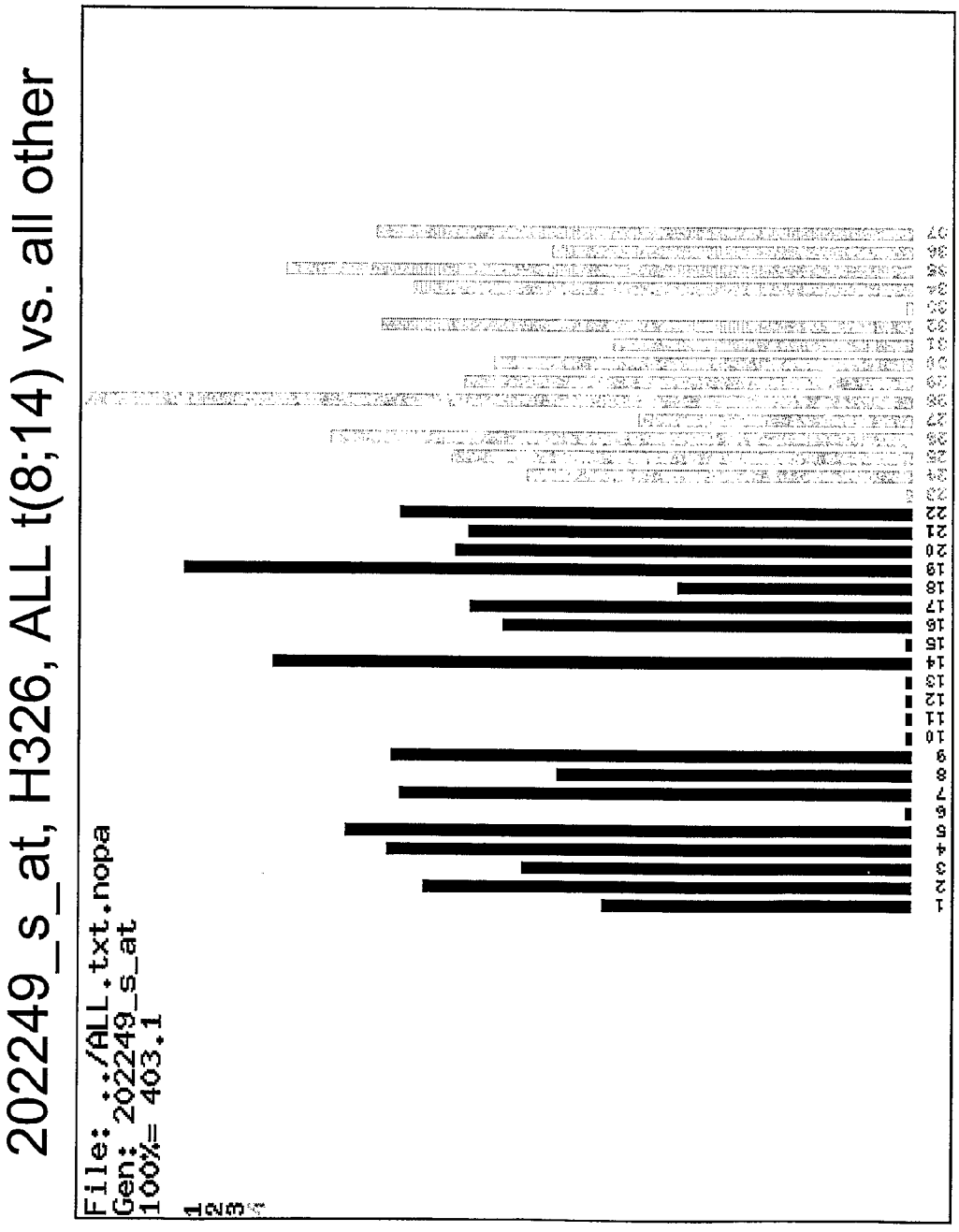

202249_s_at, H326, ALL t(8;14) vs. all other
File: ../ALL.txt.nopa
Gen: 202249_s_at
100%= 403.1
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 259

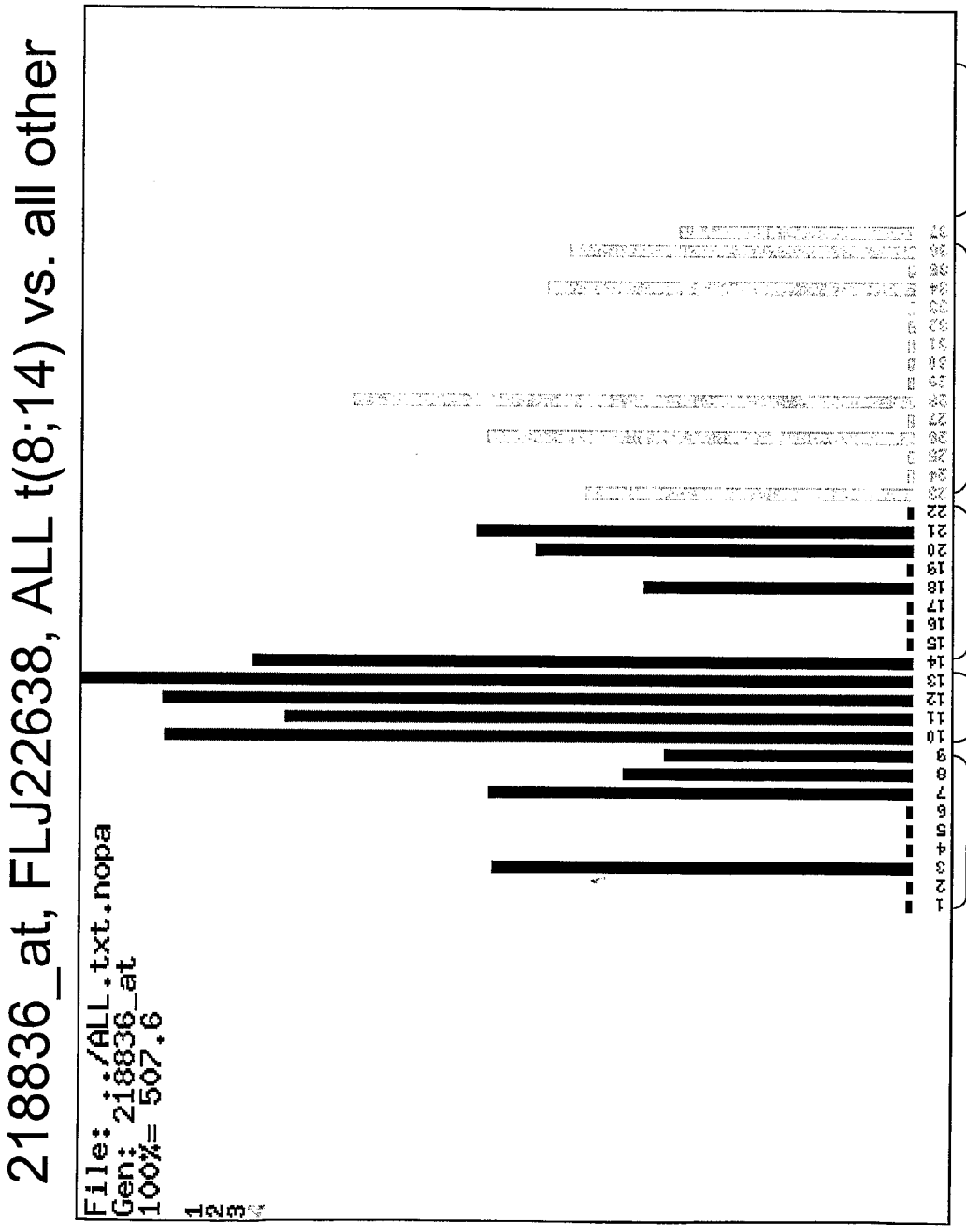

218836_at, FLJ22638, ALL t(8;14) vs. all other
File: ../ALL.txt.nopa
Gen: 218836_at
100%= 507.6
123
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 260

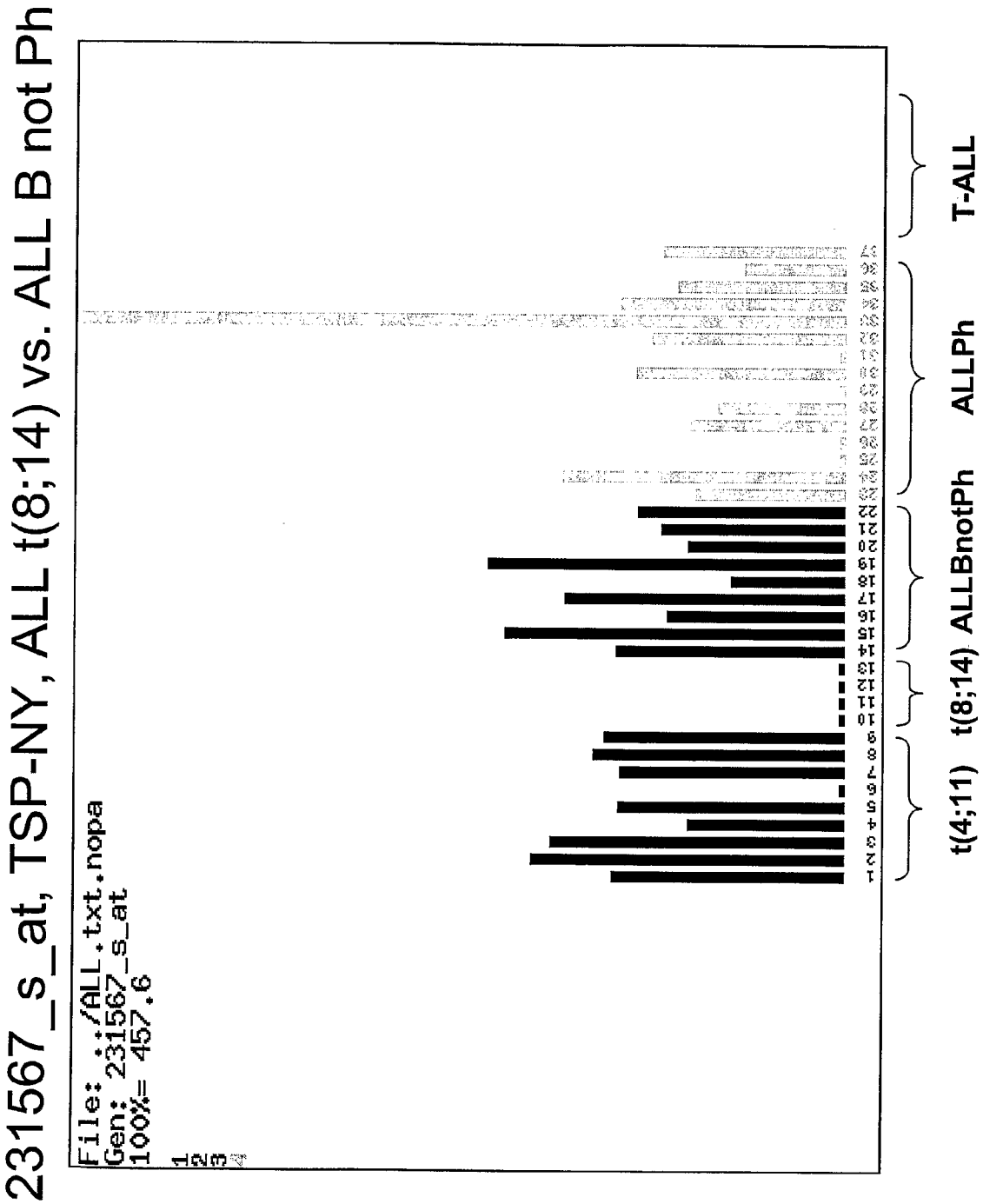

231567_s_at, TSP-NY, ALL t(8;14) vs. ALL B not Ph
File: ../ALL.txt.nopa
Gen: 231567_s_at
100%= 457.6
1
2
3
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 261

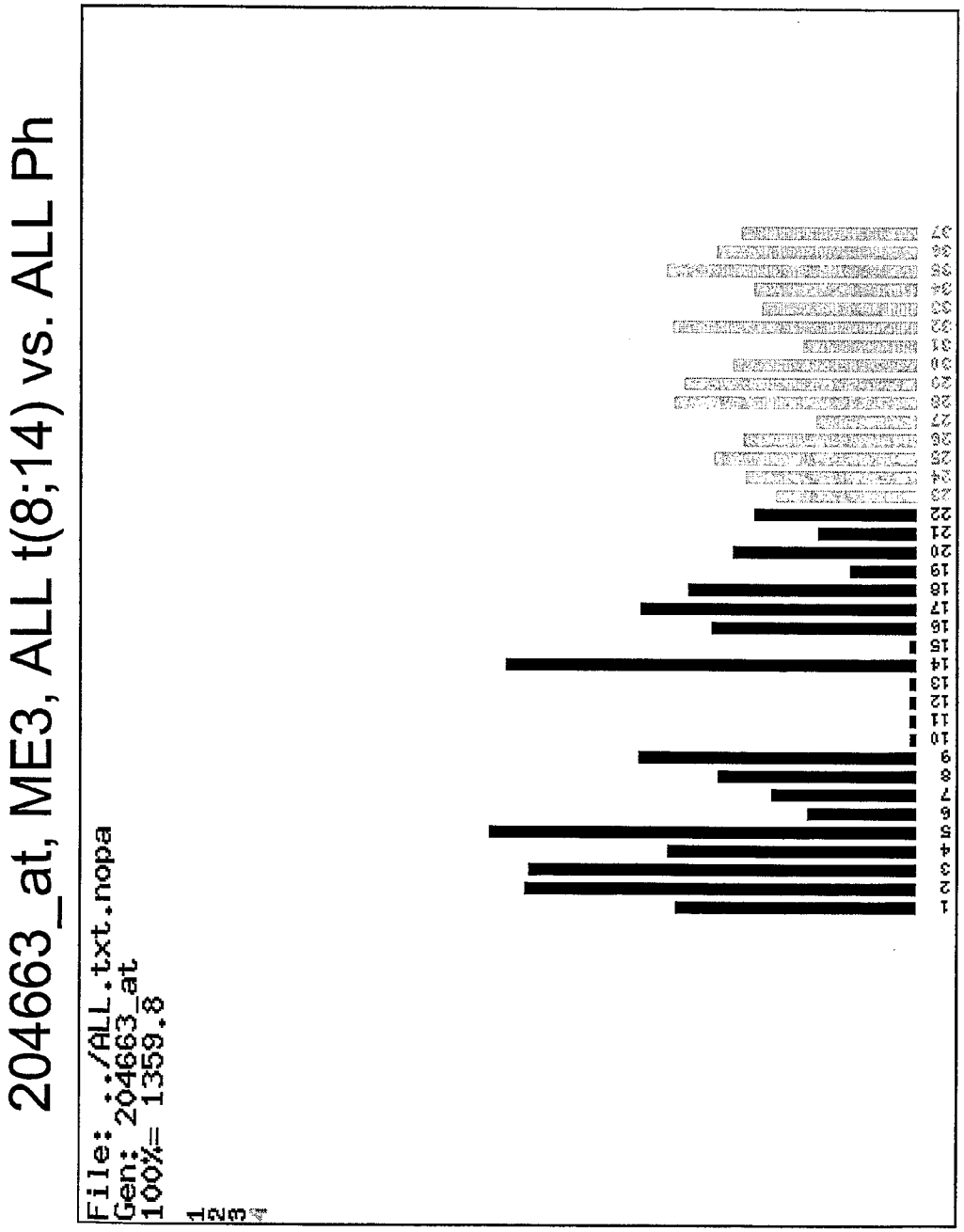

204663_at, ME3, ALL t(8;14) vs. ALL Ph
File: ../ALL.txt.nopa
Gen: 204663_at
100%= 1359.8
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 262

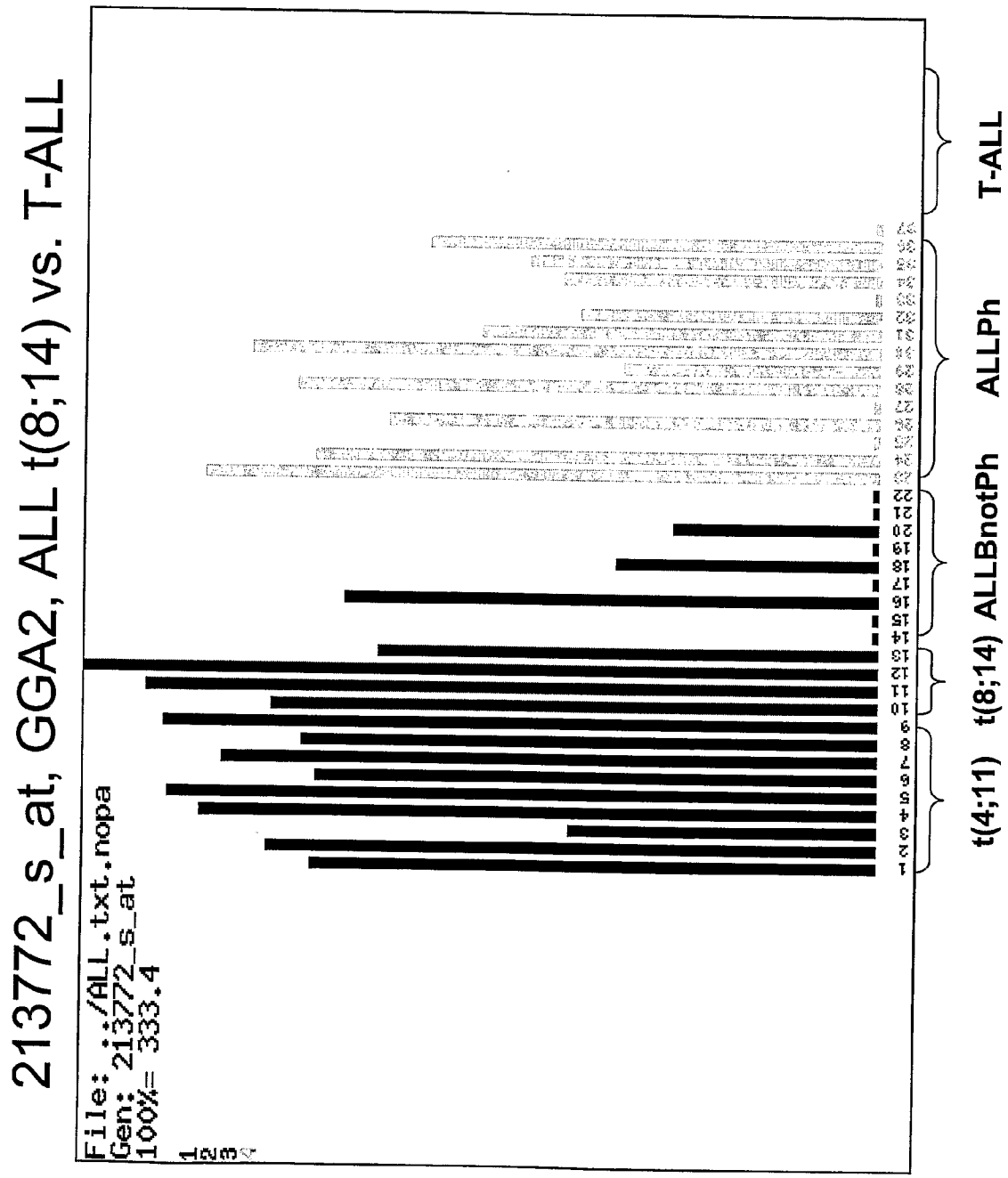

213772_s_at, GGA2, ALL t(8;14) vs. T-ALL
File: ../ALL.txt.nopa
Gen: 213772_s_at
100%= 333.4
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 263

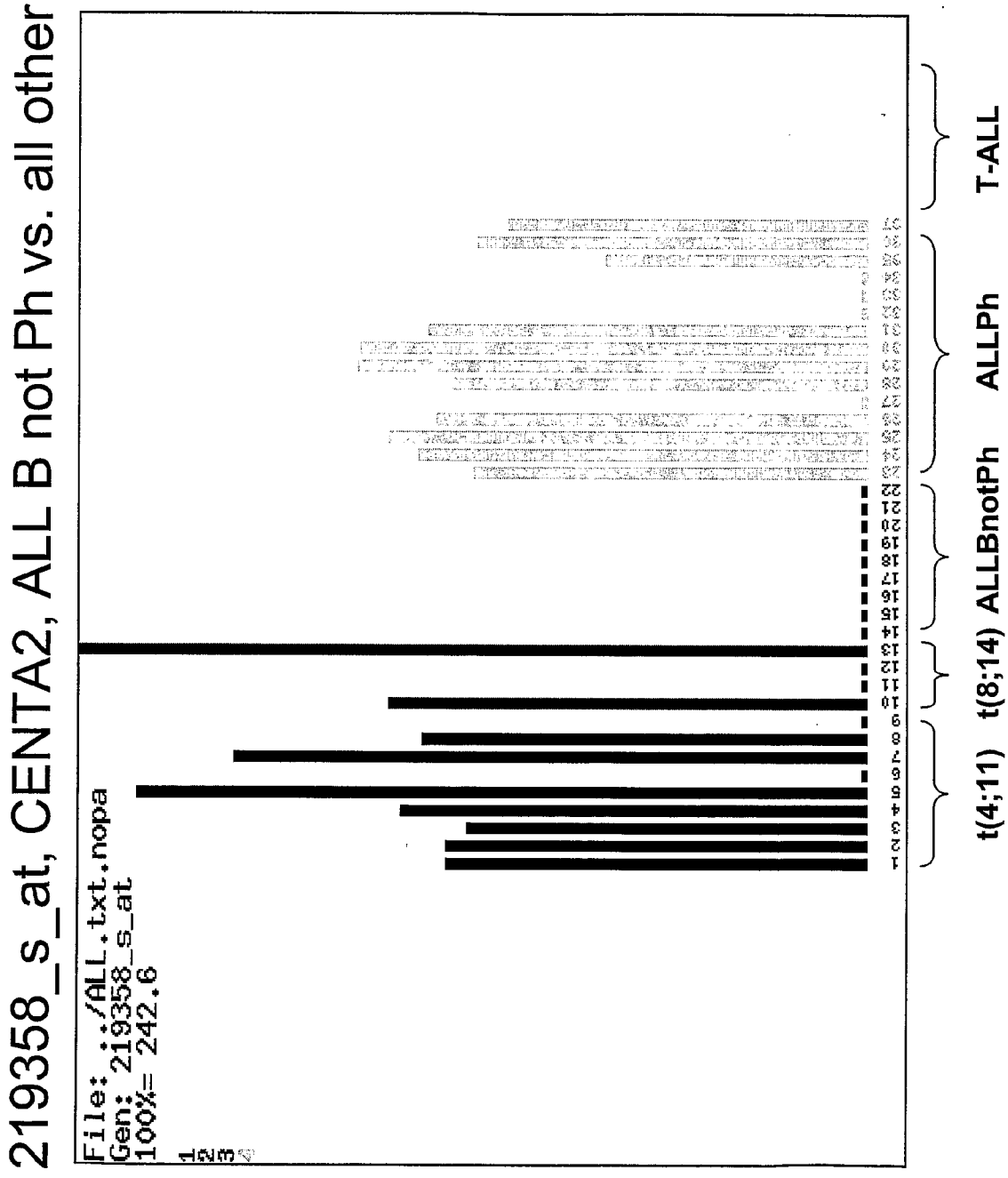

219358_s_at, CENTA2, ALL B not Ph vs. all other
File: ../ALL.txt.nopa
Gen: 219358_s_at
100%= 242.6
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 264

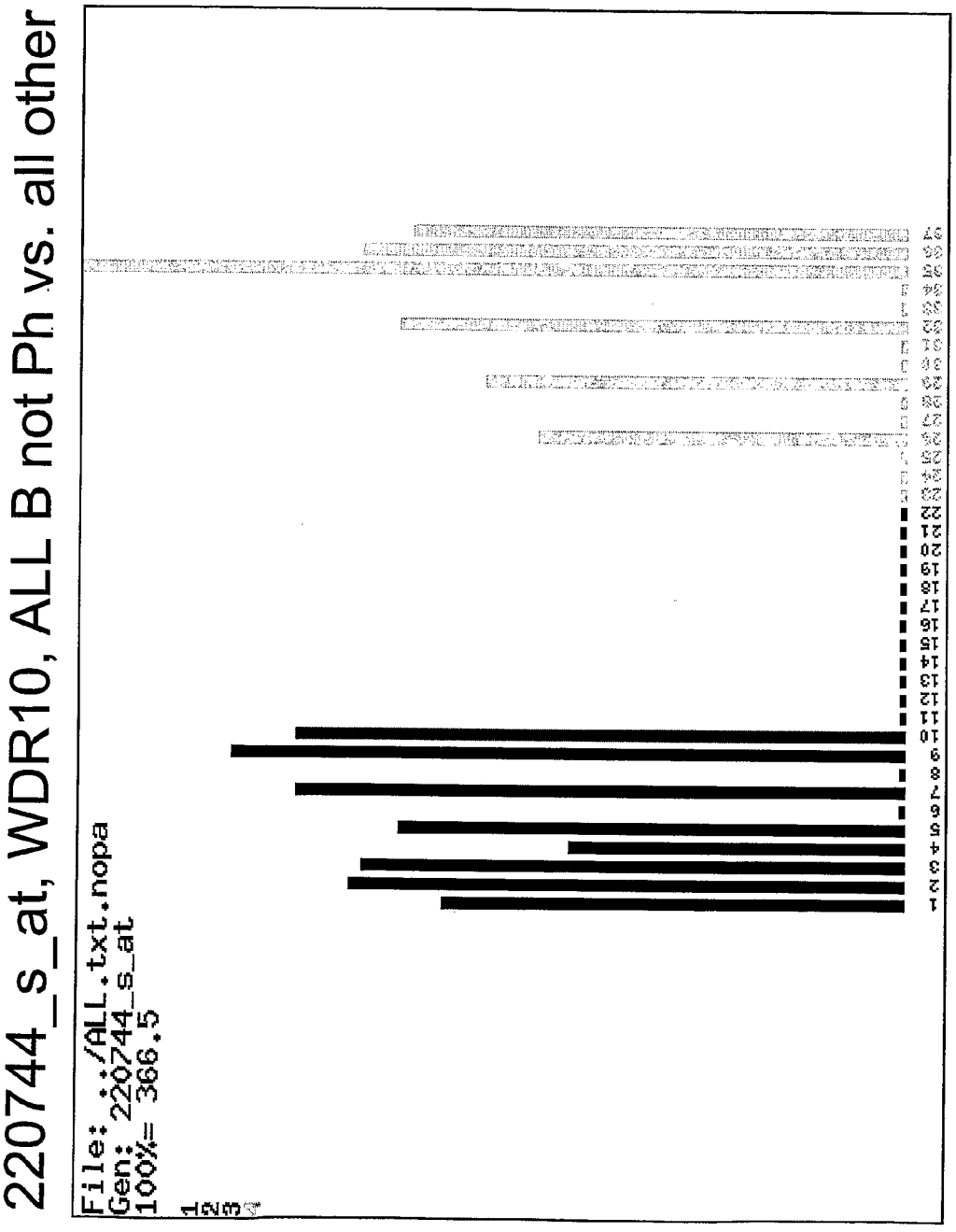

220744_s_at, WDR10, ALL B not Ph vs. all other
File: ../ALL.txt.nopa
Gen: 220744_s_at
100%= 366.5
t(4;11)
t(8;14) ALLBnotPh
ALLPh
T-ALL

Figure 265

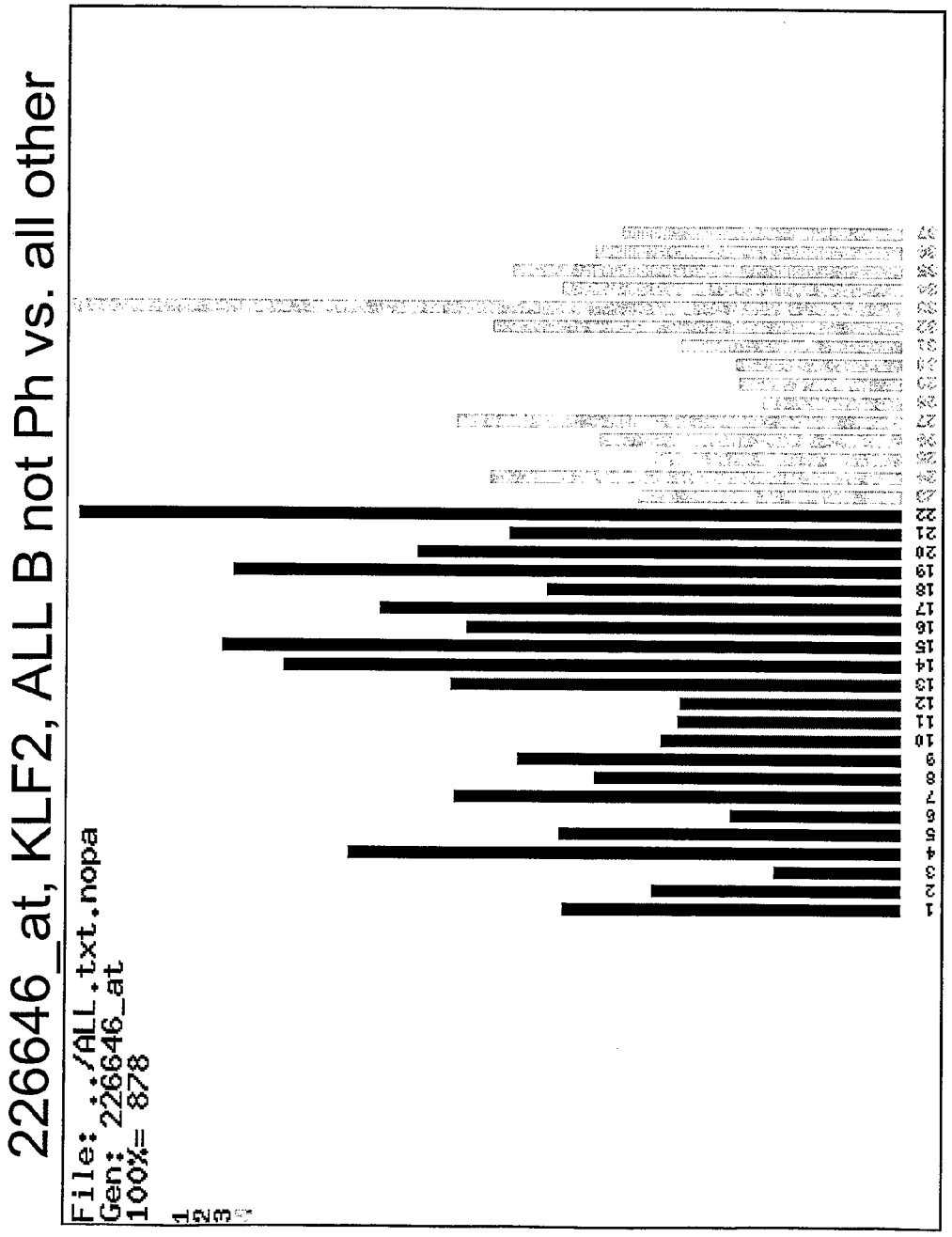

226646_at, KLF2, ALL B not Ph vs. all other
File: ../ALL.txt.nopa
Gen: 226646_at
100%= 878
1 2 3
t(4;11) t(8;14) ALLBnotPh ALLPh T-ALL

Figure 266

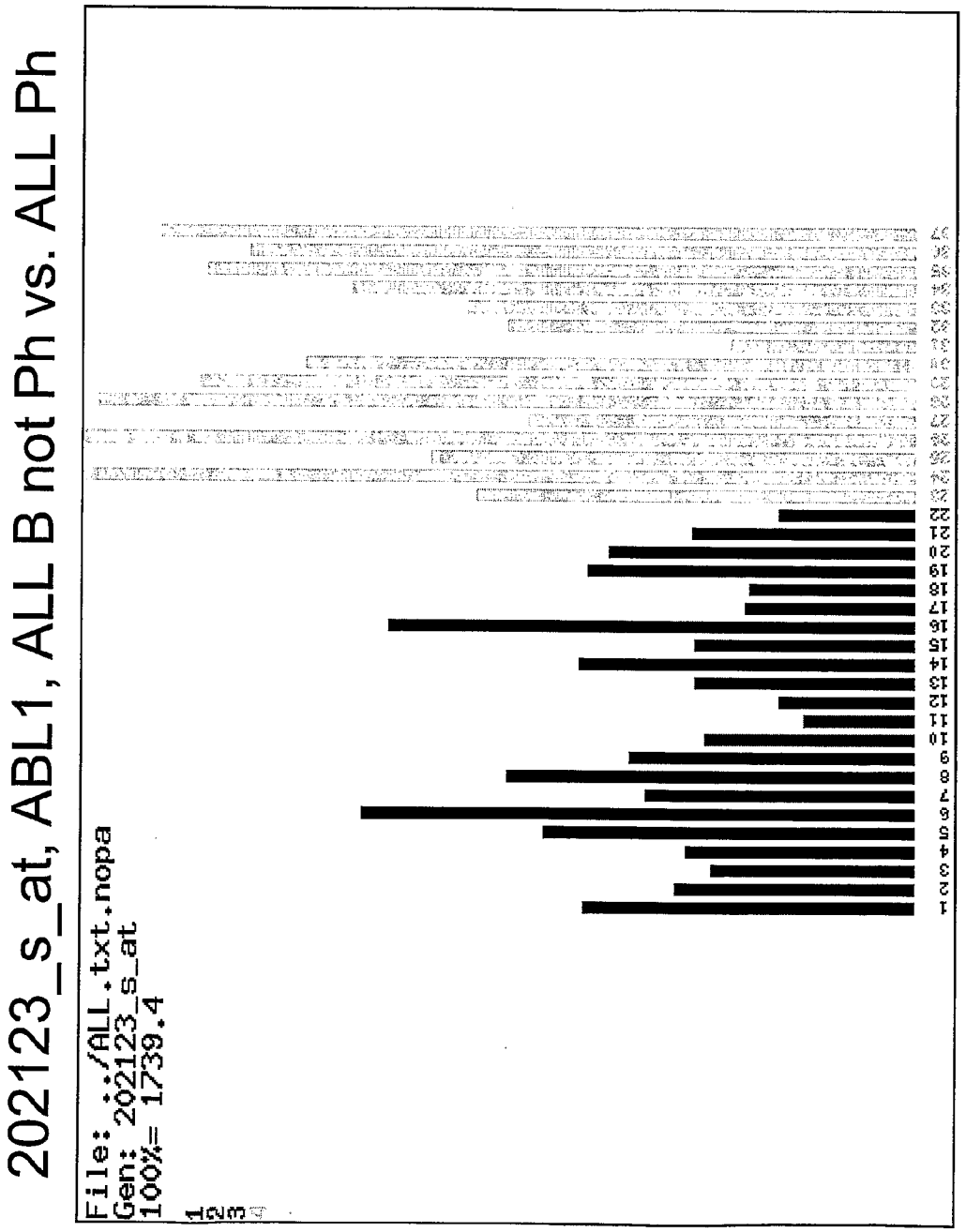

202123_s_at, ABL1, ALL B not Ph vs. ALL Ph
File: ../ALL.txt.nopa
Gen: 202123_s_at
100%= 1739.4
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 267

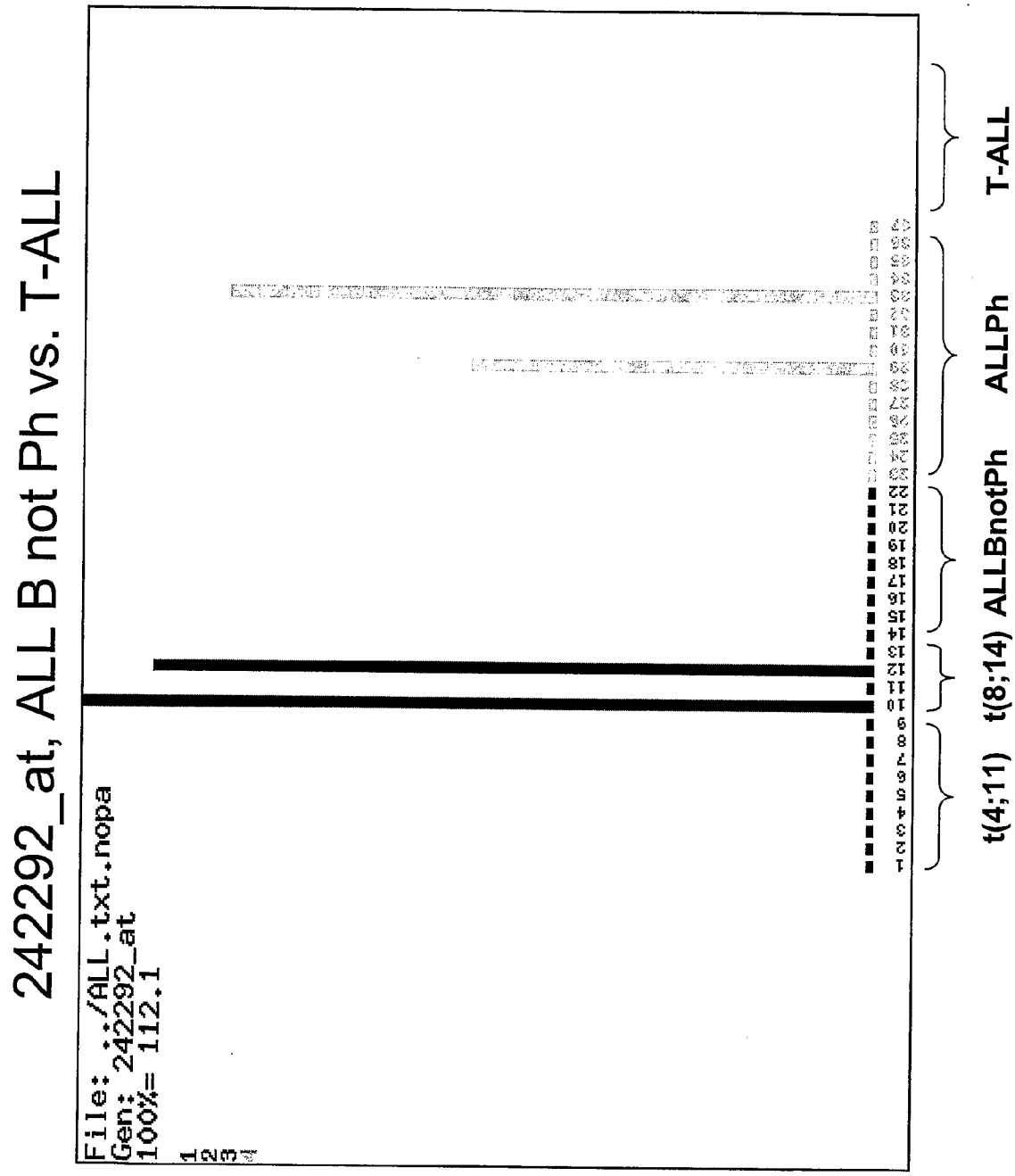

242292_at, ALL B not Ph vs. T-ALL
File: ../ALL.txt.nopa
Gen: 242292_at
100%= 112.1
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 268

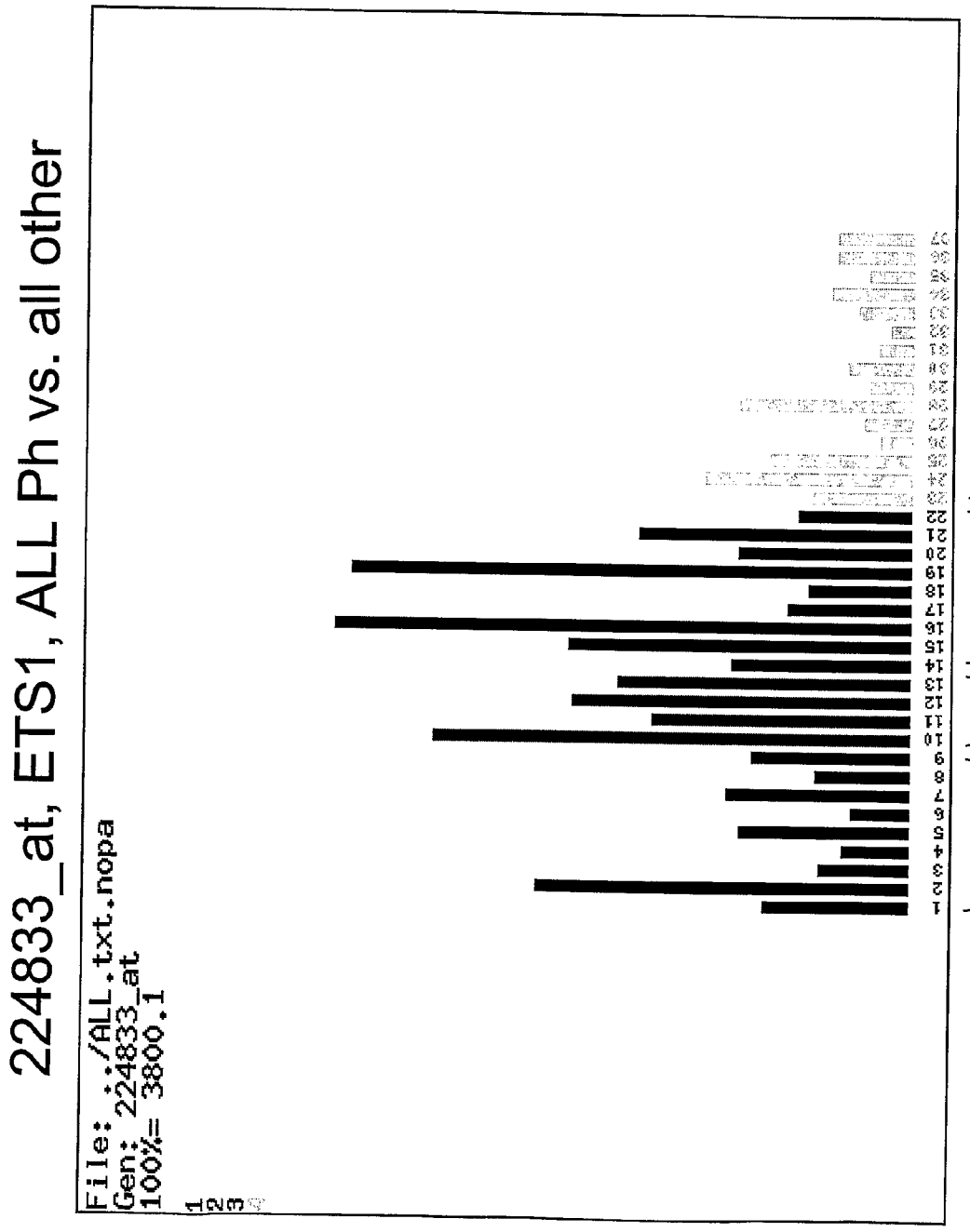

224833_at, ETS1, ALL Ph vs. all other
File: ../ALL.txt.nopa
Gen: 224833_at
100%= 3800.1
1
2
3
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 269

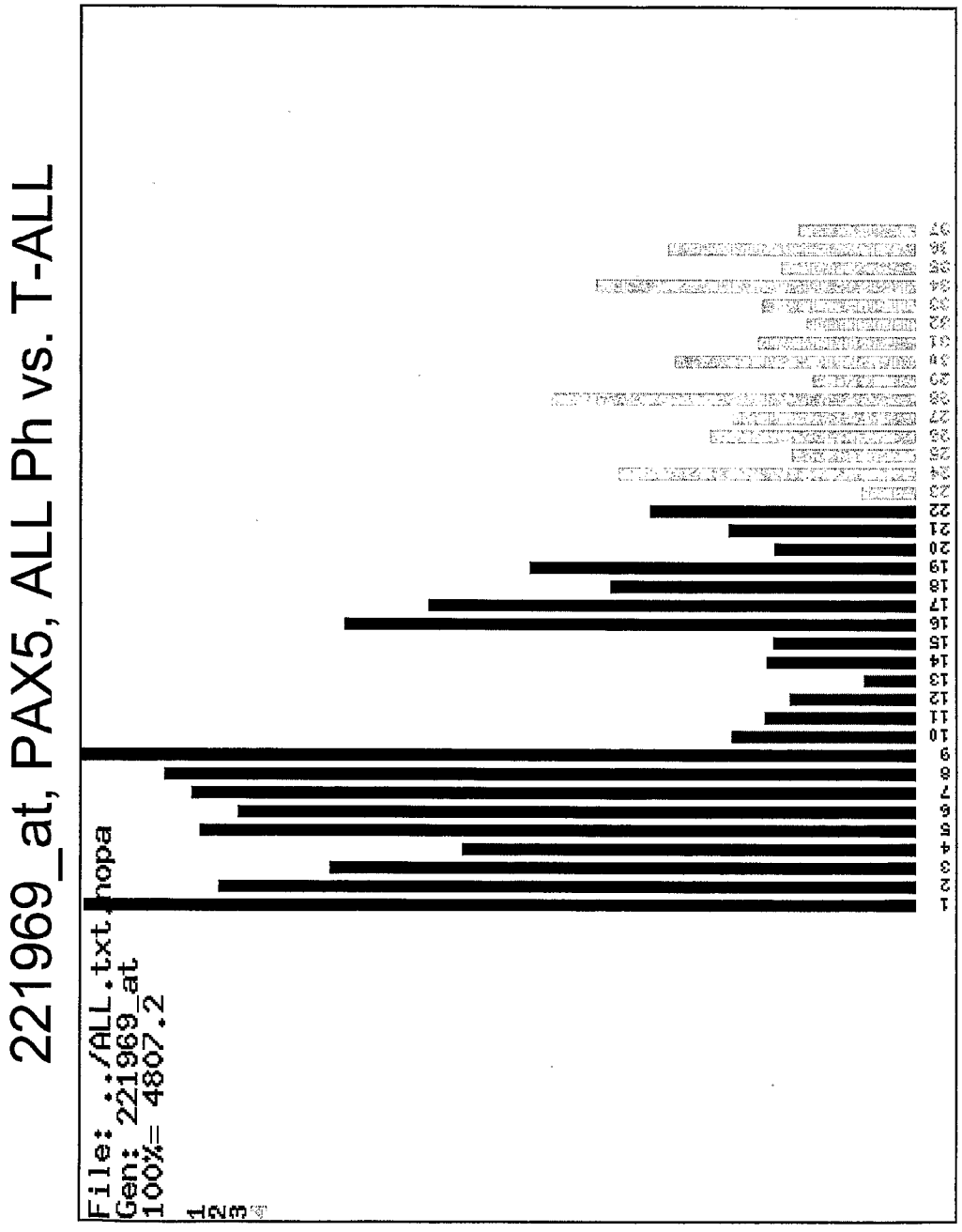

221969_at, PAX5, ALL Ph vs. T-ALL
File: ../ALL.txt.hopa
Gen: 221969_at
100%= 4807.2
t(4;11)
t(8;14)
ALLBnotPh
ALLPh
T-ALL

Figure 270

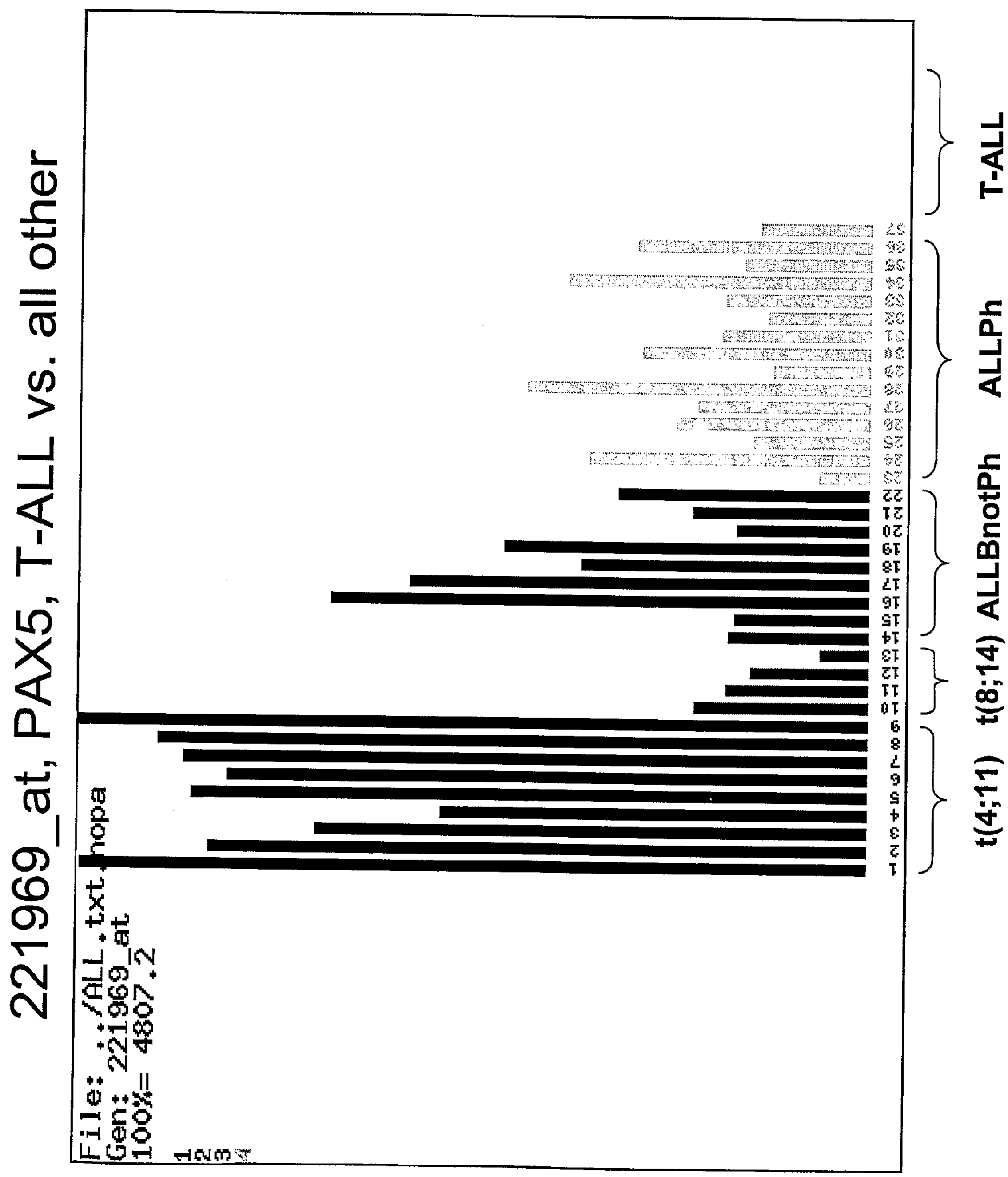

221969_at, PAX5, T-ALL vs. all other
File: ..:/ALL.txt.nopa
Gen: 221969_at
100%= 4807.2
T-ALL
ALLPh
ALLBnotPh
t(8;14)
t(4;11)

Figure 271

218549_s_at, LOC51115, trisomy 8 vs. other aberrant

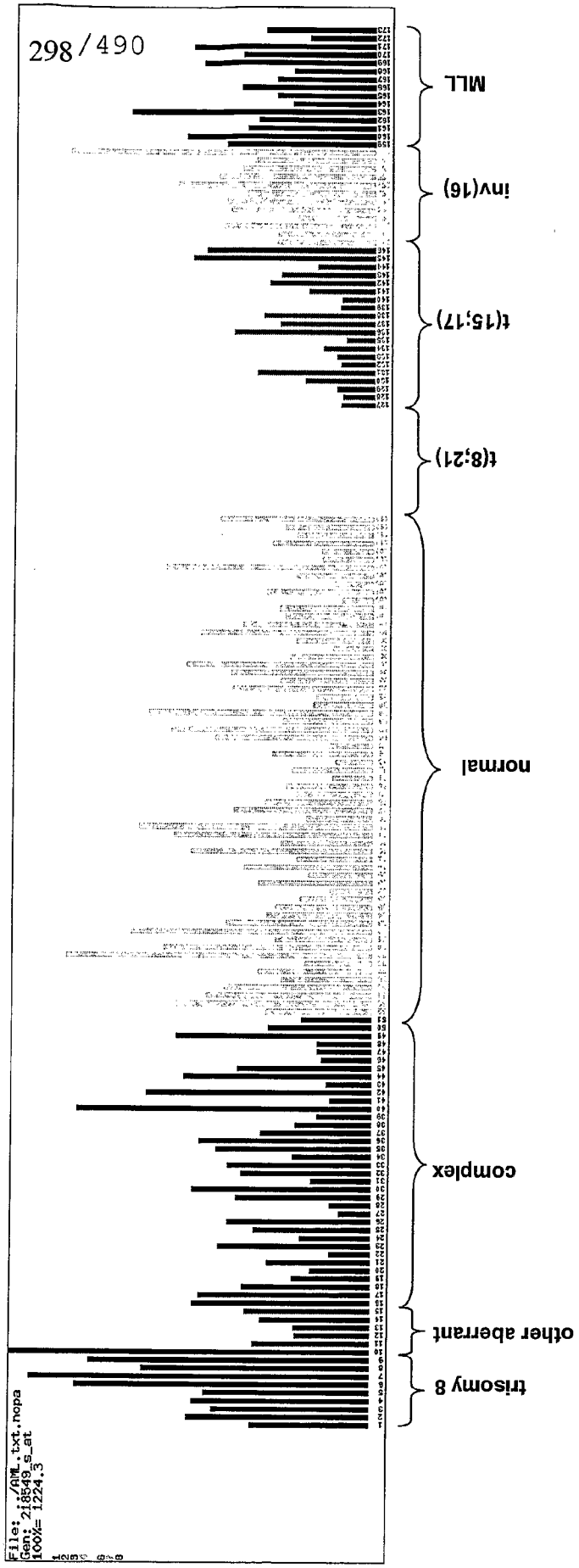


Figure 272

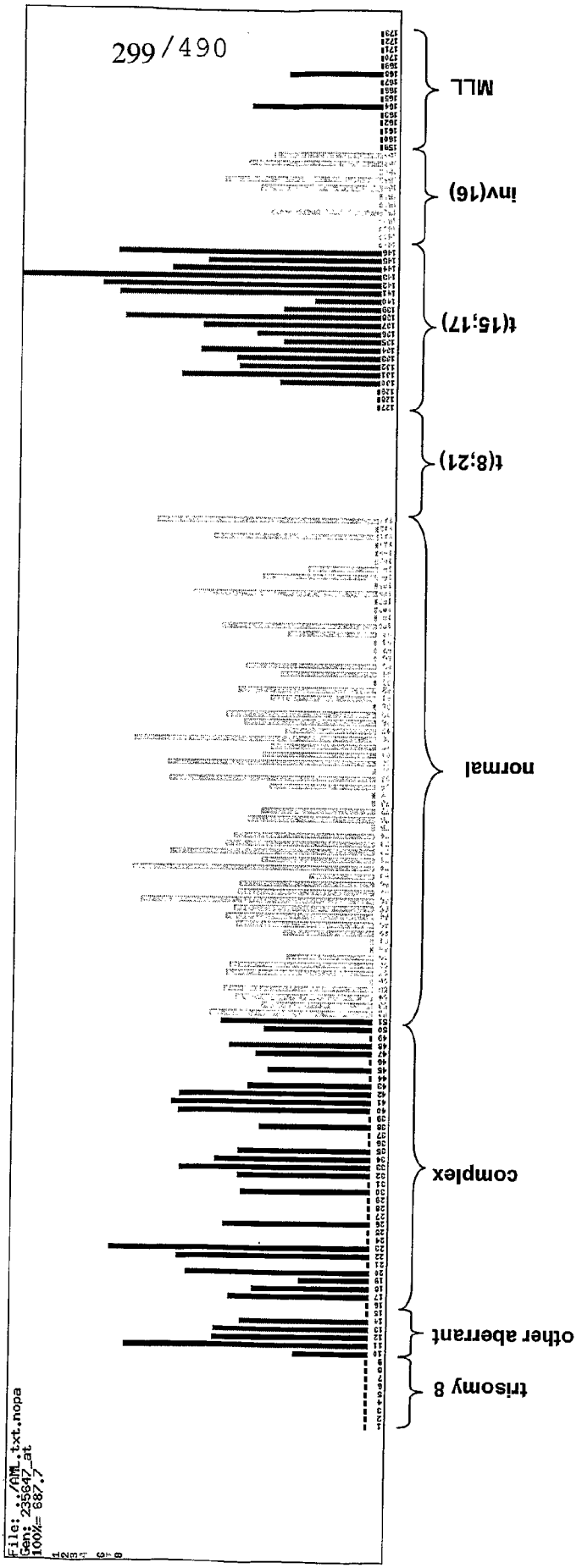

235647_at, trisomy 8 vs. all other AML
File: ../AML.txt.nopa
Gen: 235647_at
100%= 687.7
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 273

231981_at, trisomy 8 vs. all other AML

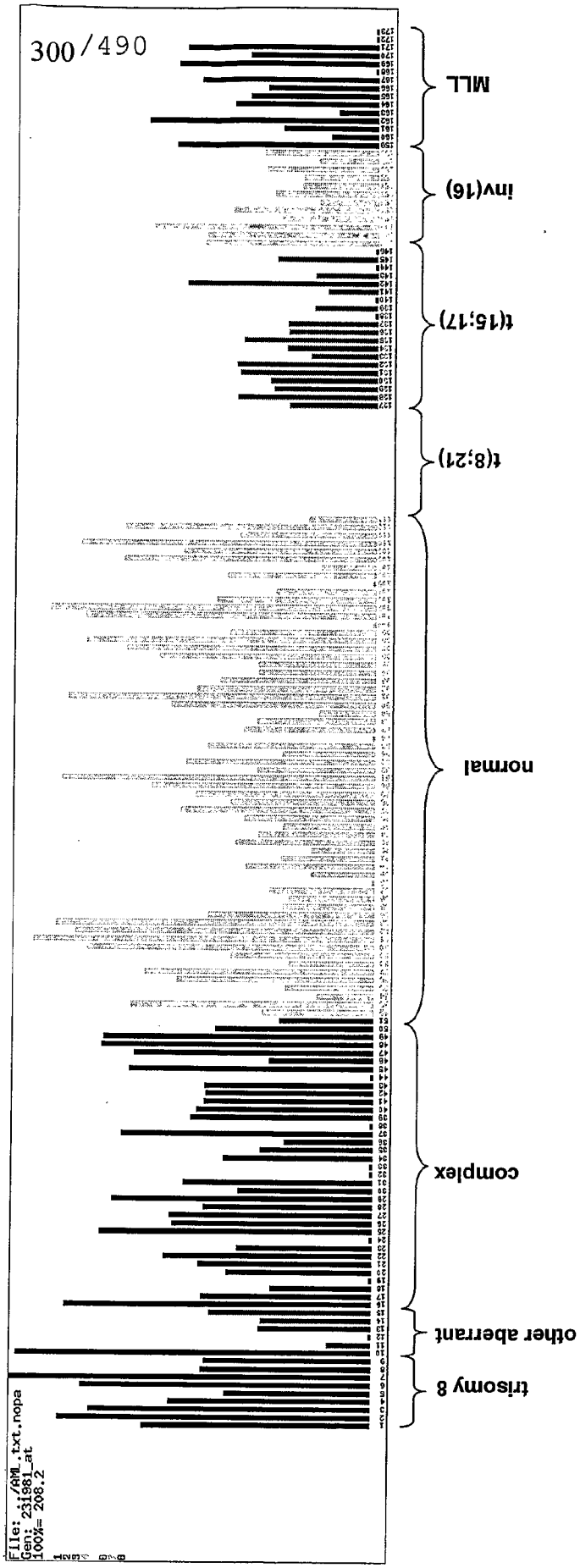


Figure 274

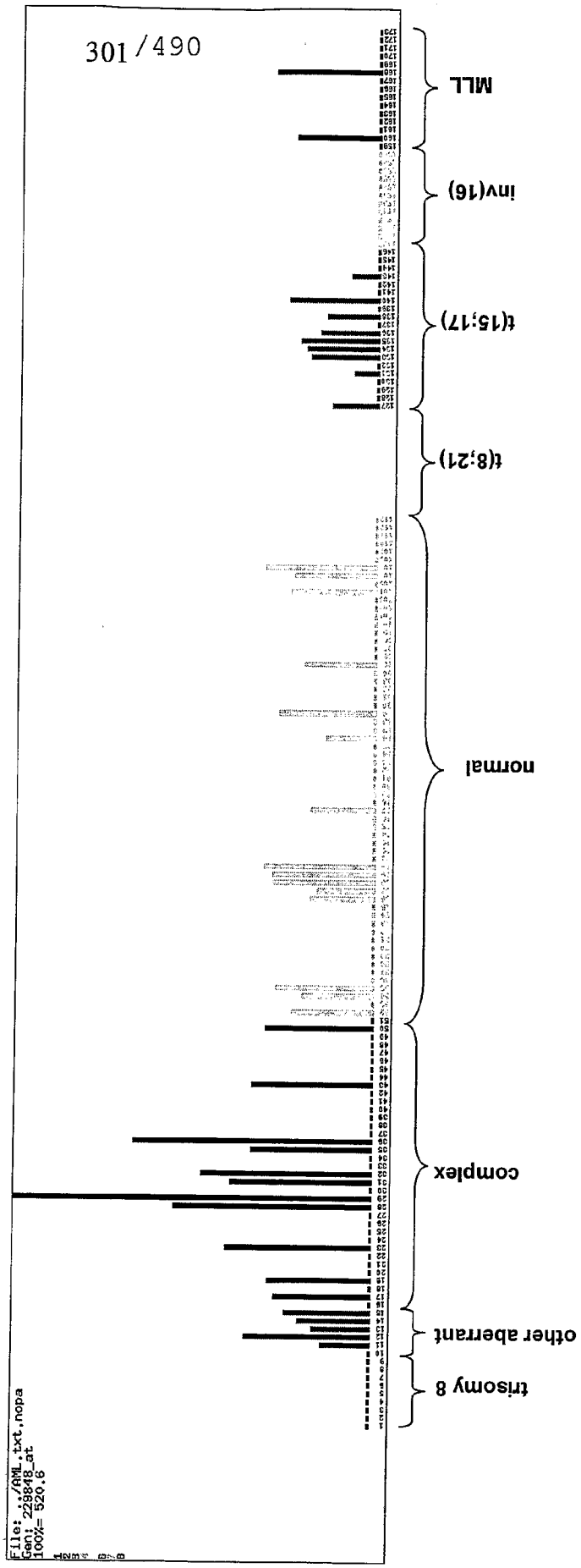

229848_at, ZNF10, trisomy 8 vs. ather aberrant
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML.txt.nopa
Gen: 229848_at
100%= 520.6

Figure 275

212586_at, ARTS-1, trisomy 8 vs. complex

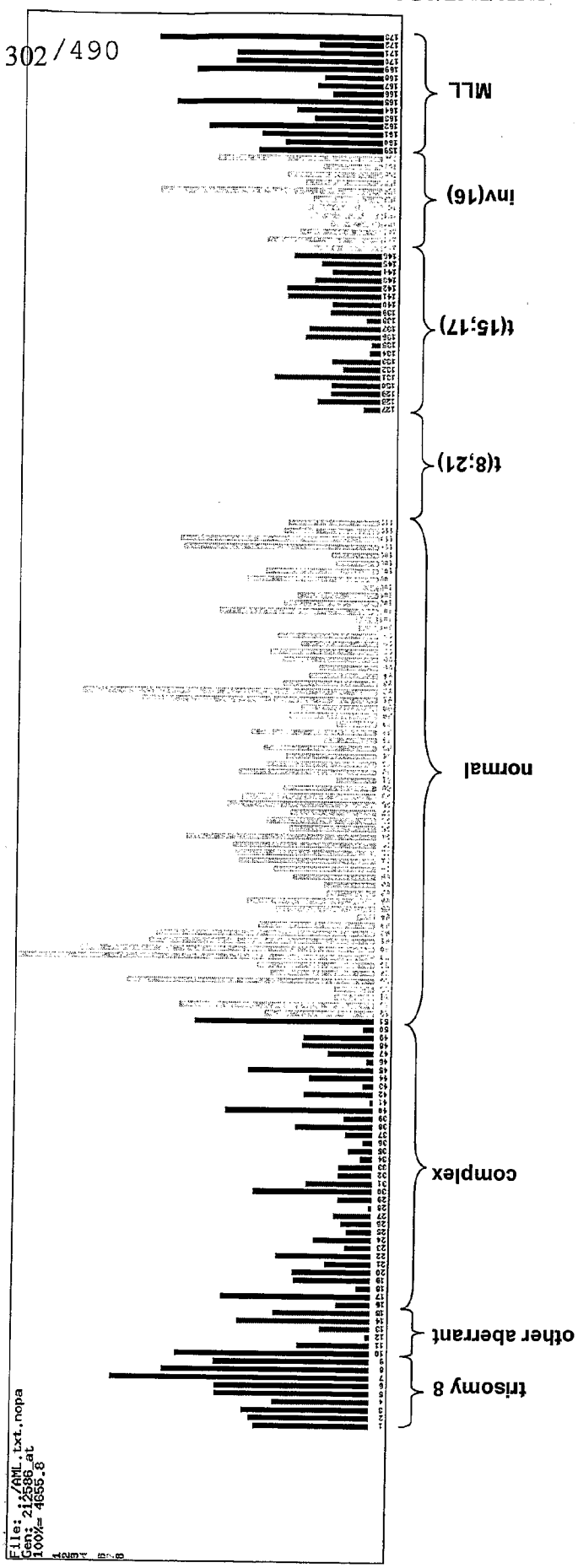


Figure 276

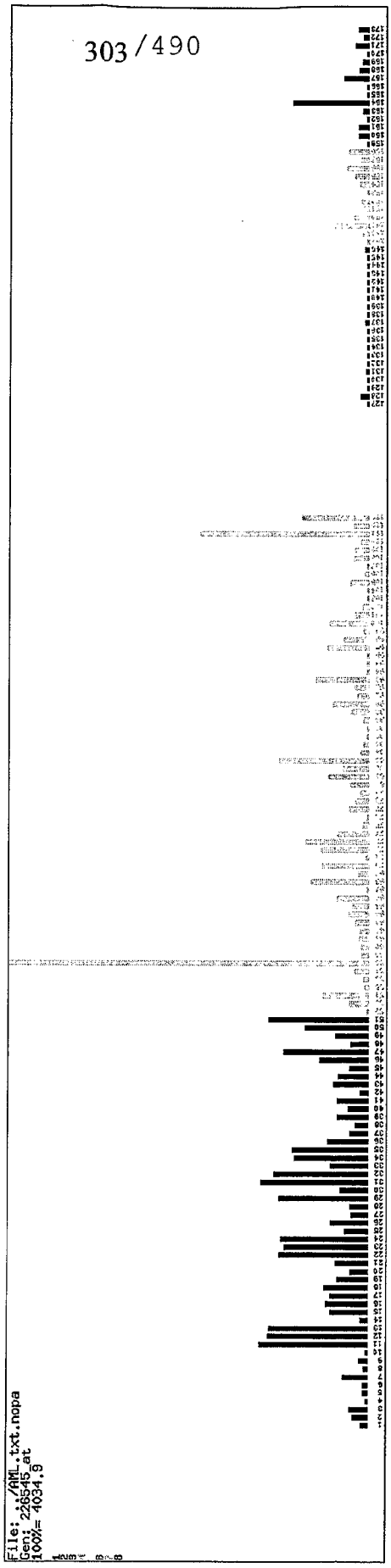

226545_at, trisomy 8 vs. complex
File: ../AML_txt.nopa
Gen: 226545_at
100%= 4034.9
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 277

222166_at, trisomy 8 vs. complex

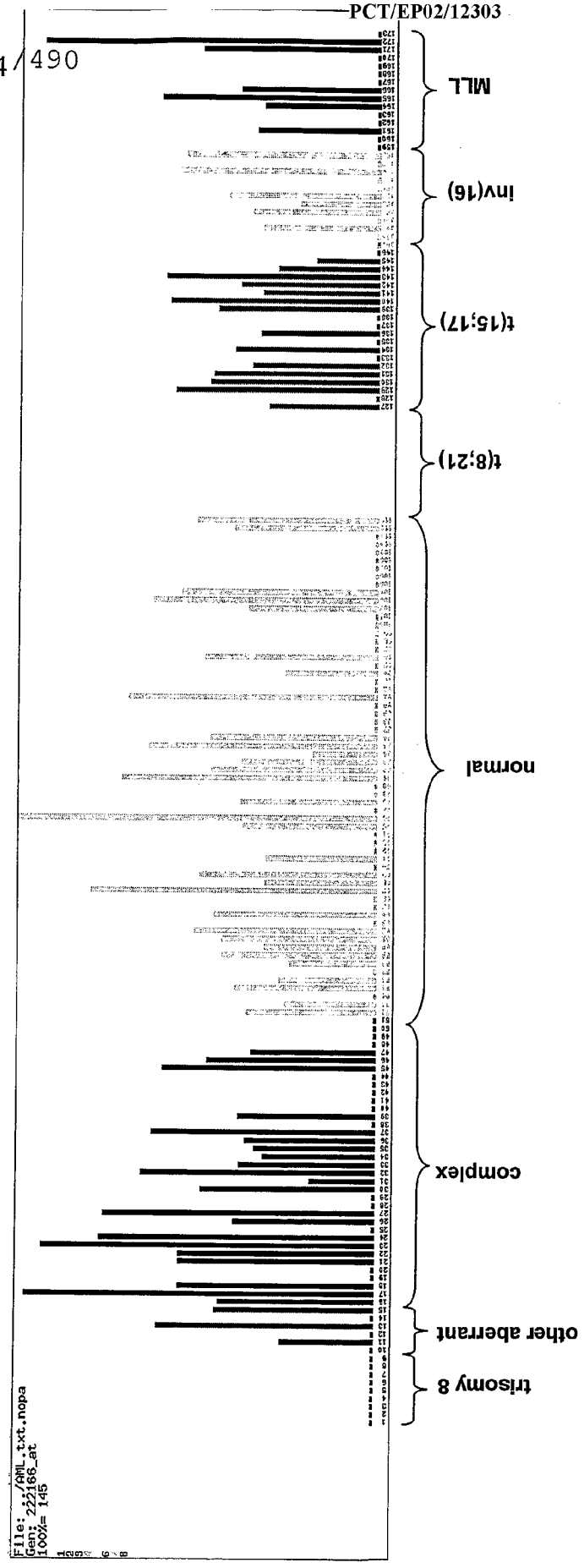


Figure 278

210715_s_at, SPINT2, trisomy 8 vs. complex

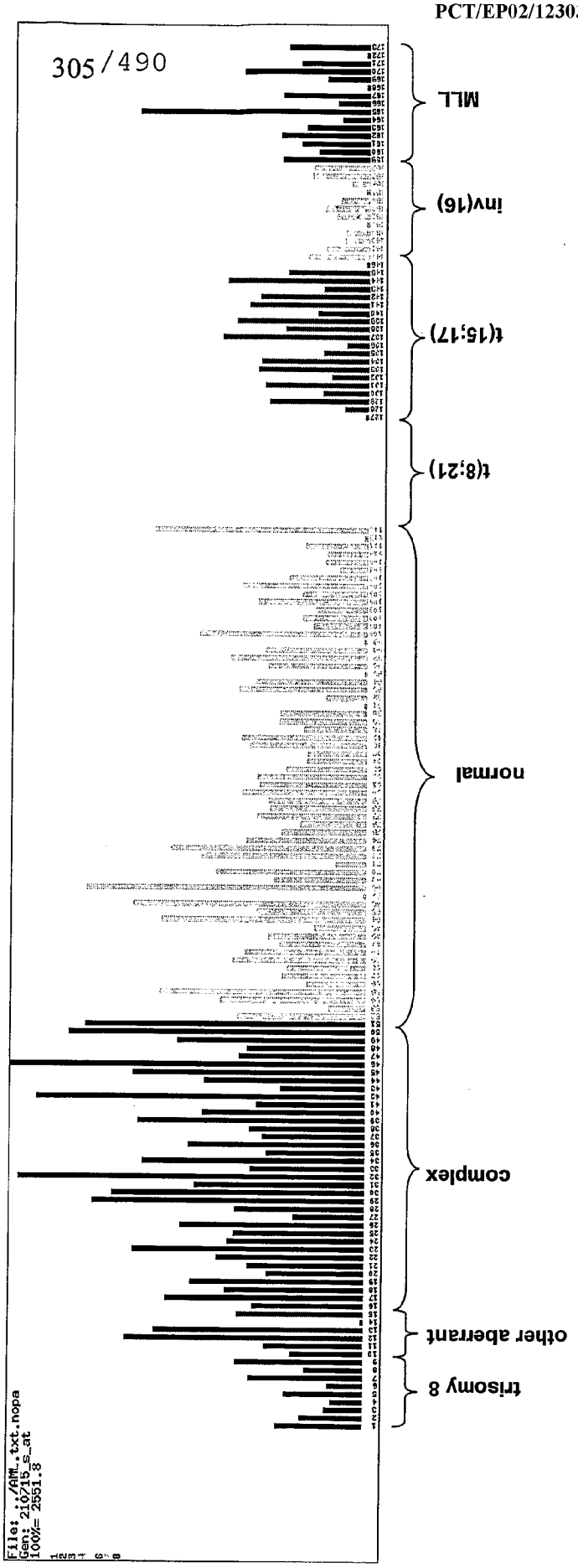


Figure 279

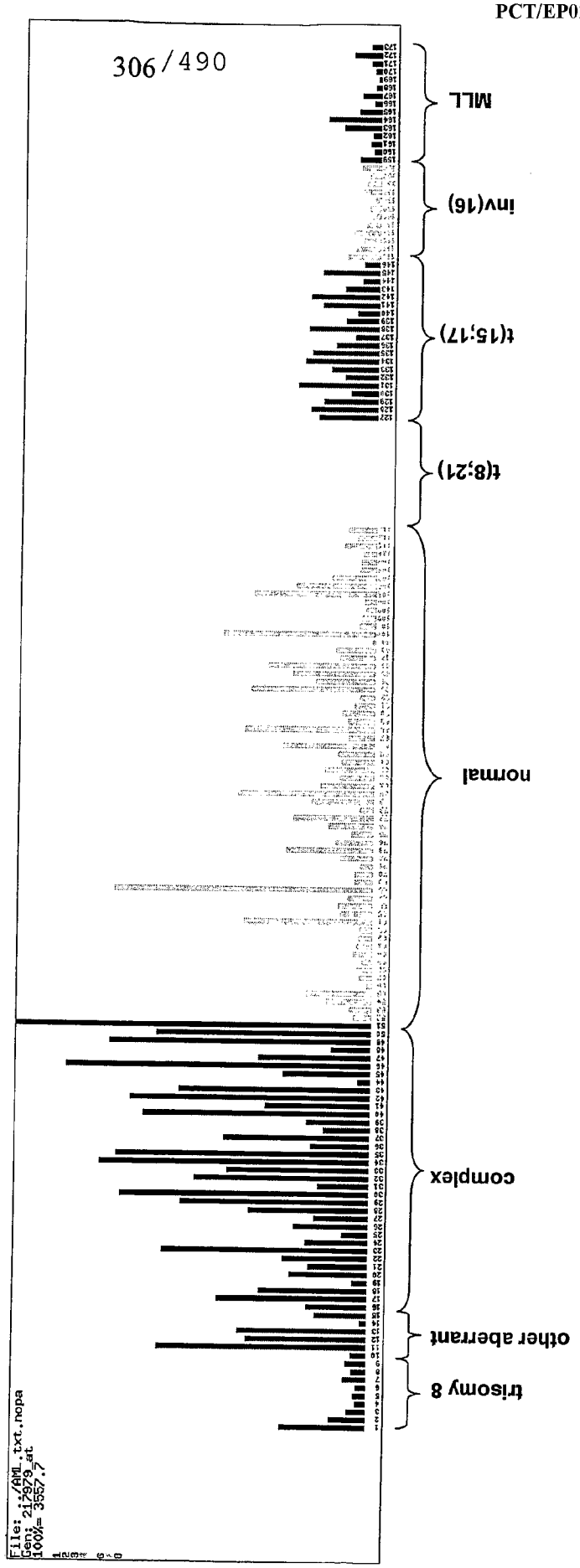

217979_at, NET-6, trisomy 8 vs. complex
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: i:/AML_txt.hopa
Gen: 217979_at
100%= 3557.7

Figure 280

201548_s_at, PLU-1, trisomy 8 vs. complex

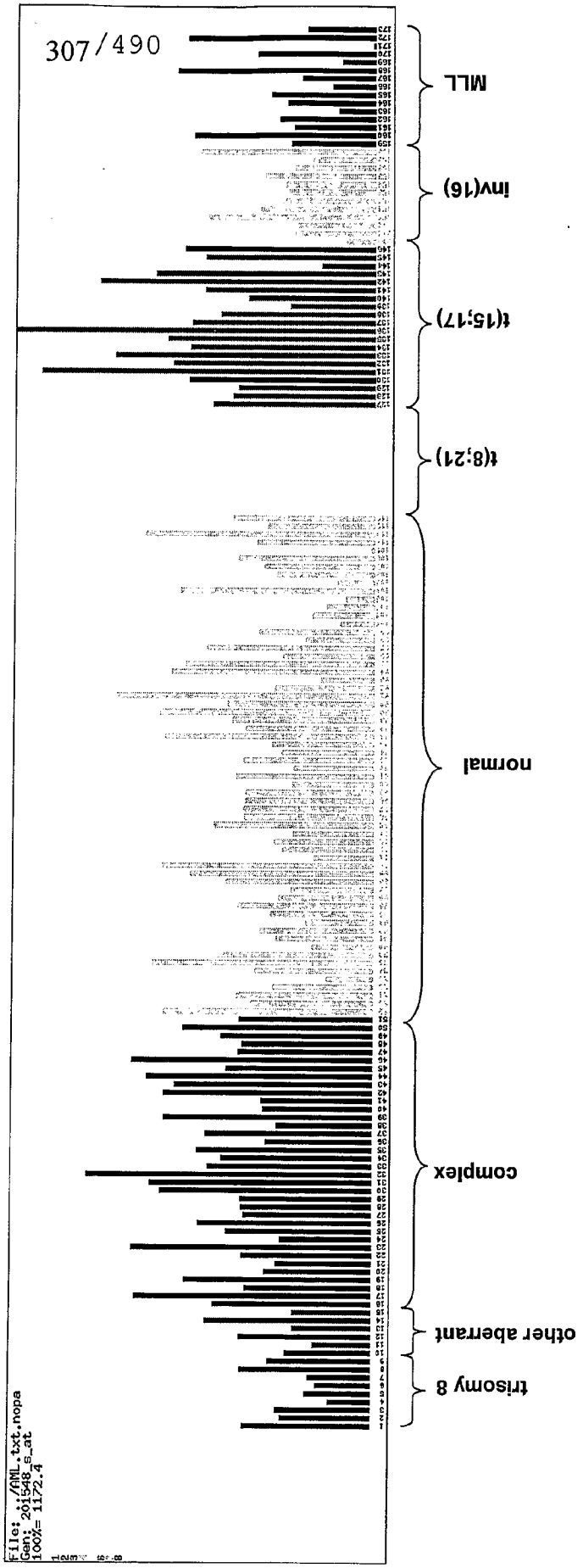
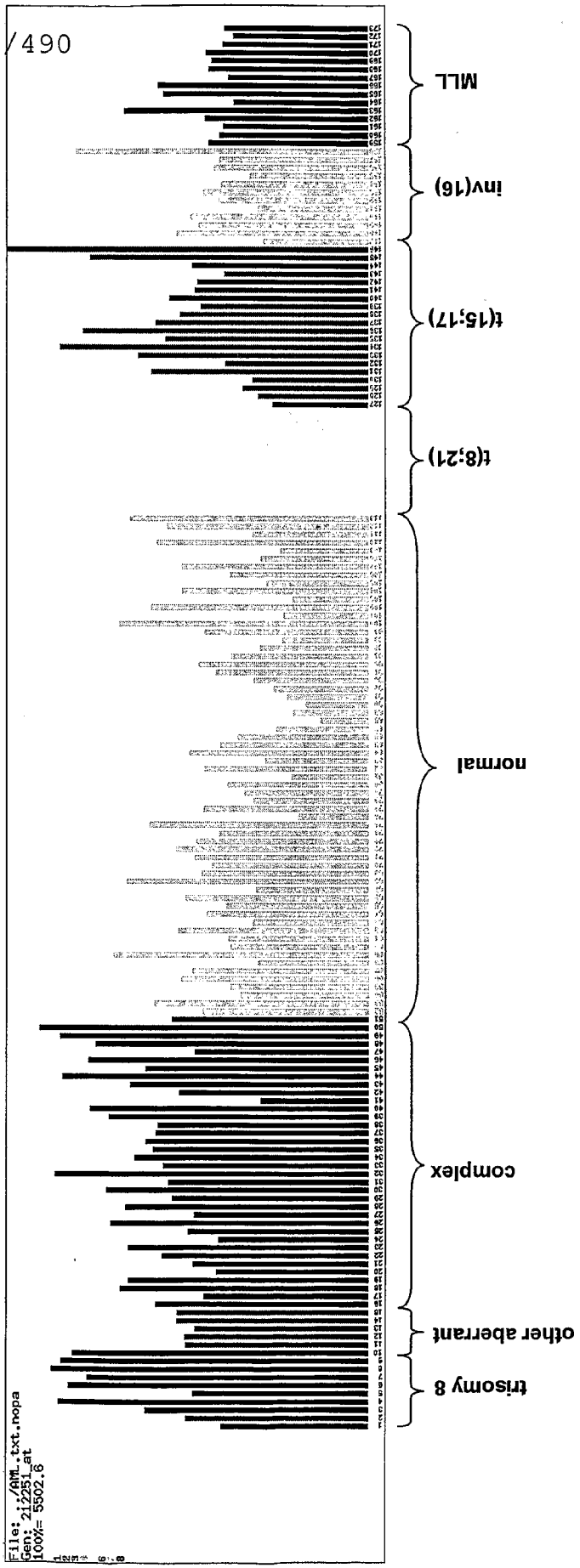


Figure 281

212251_at, trisomy 8 vs. normal

Figure 282



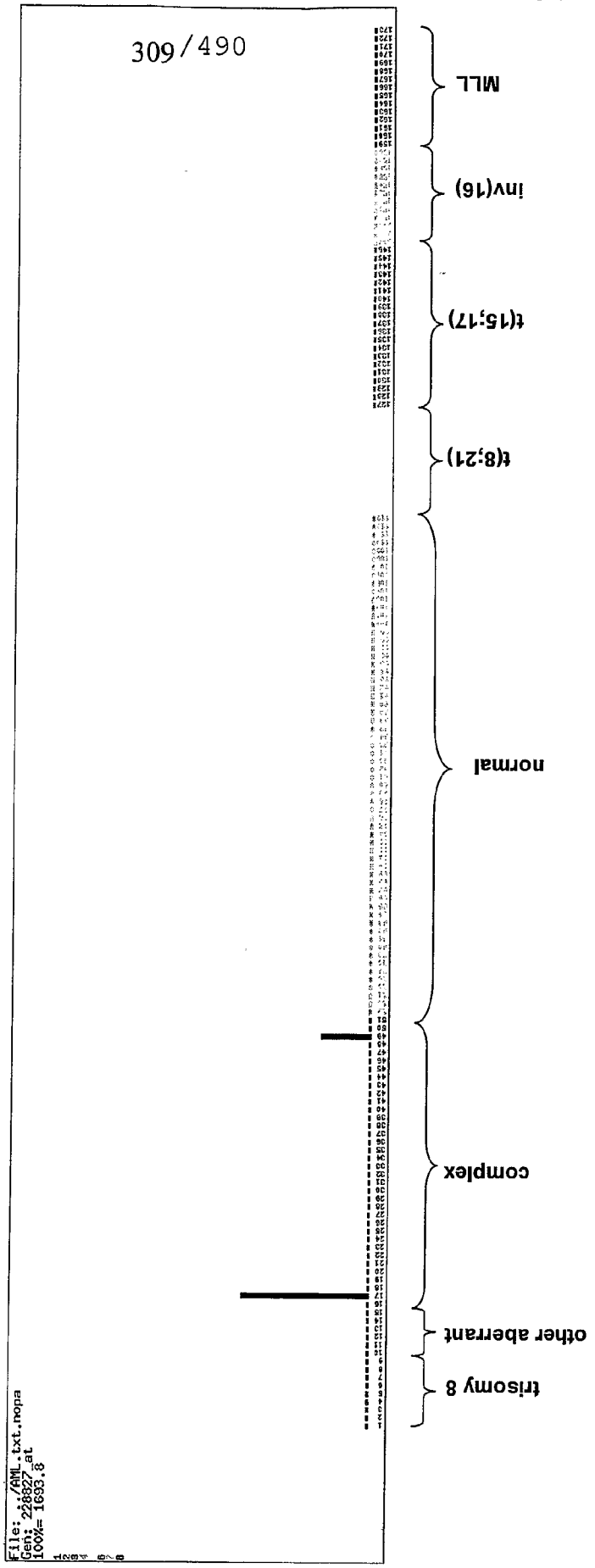

228827_at, trisomy 8 vs. t(8;21)
File: /AML.txt.nopa
Gen: 228827_at
100%= 1693.8
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 283

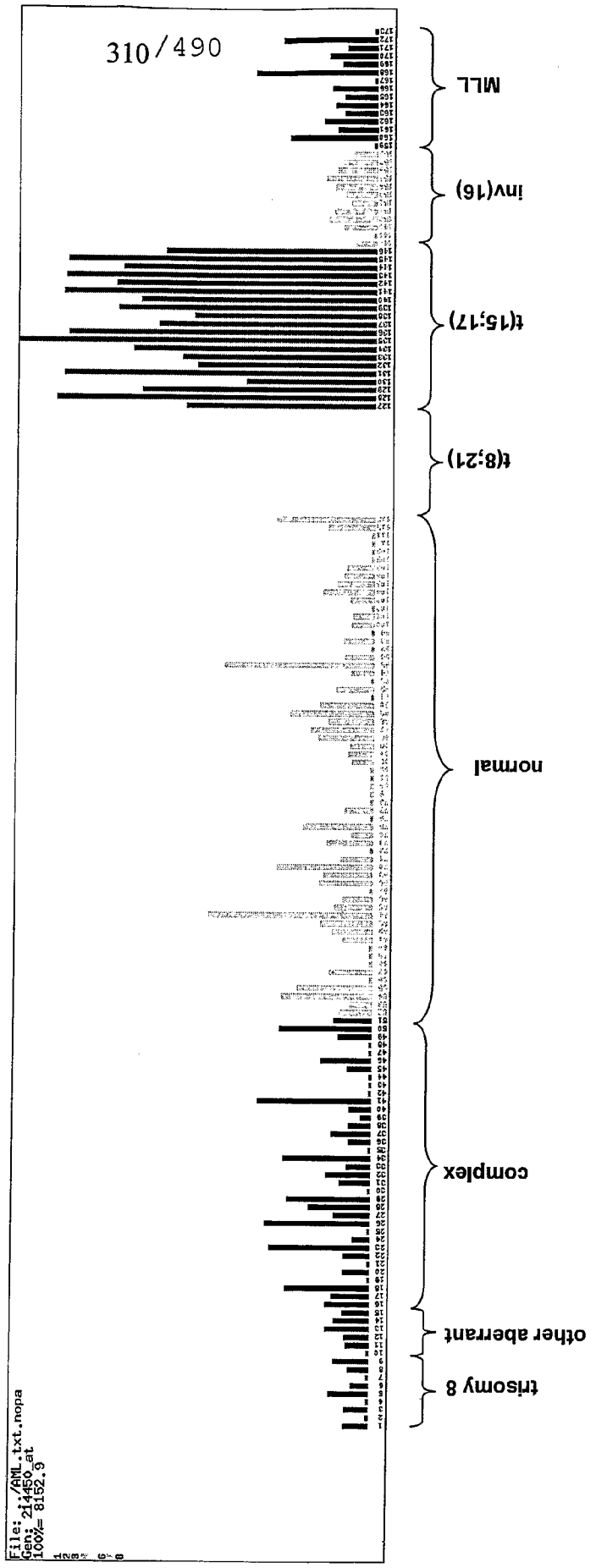

214450_at, CTSW, trisomy 8 vs. t(15;17)
File: /AML.txt.nopa
Gen: 214450_at
100%= 8152.9
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 284

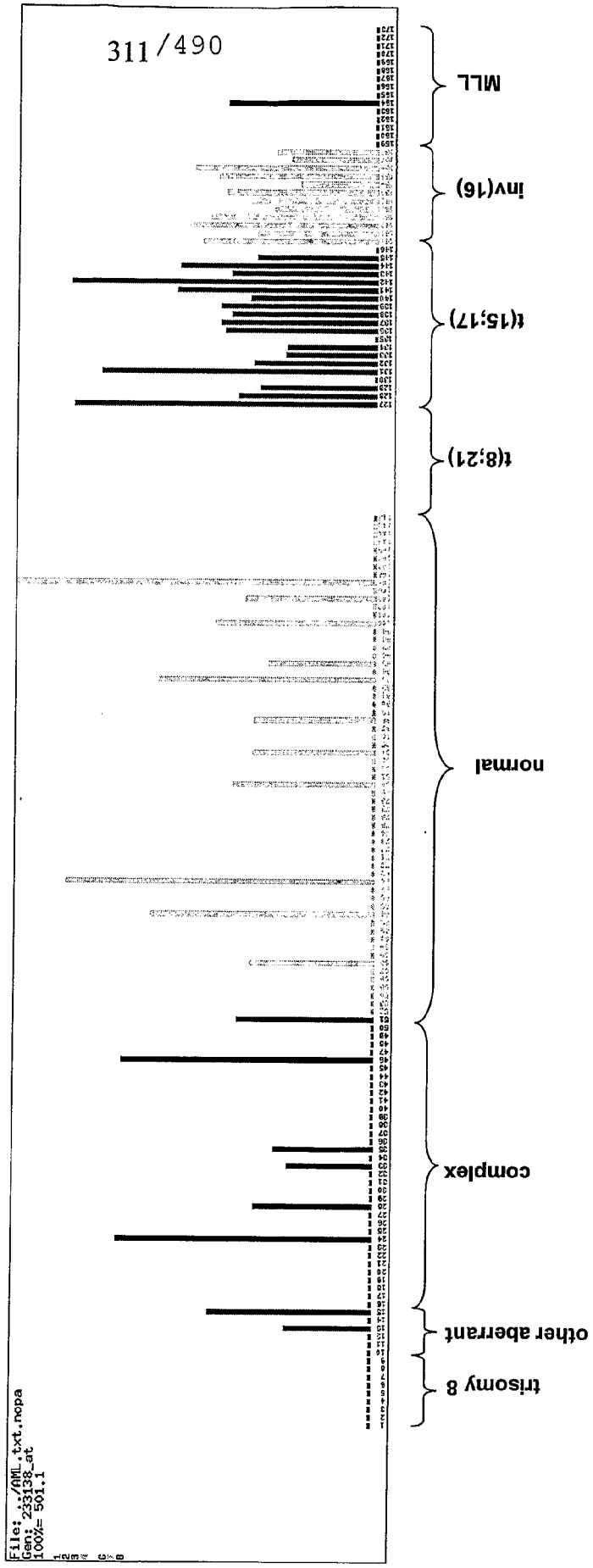

233138_at, trisomy 8 vs. inv(16)
File: .../AML.txt.nopa
Gen: 233138_at
100%= 501.1
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8

Figure 285

212479_s_at, FLJ13910, trisomy 8 vs. MLL

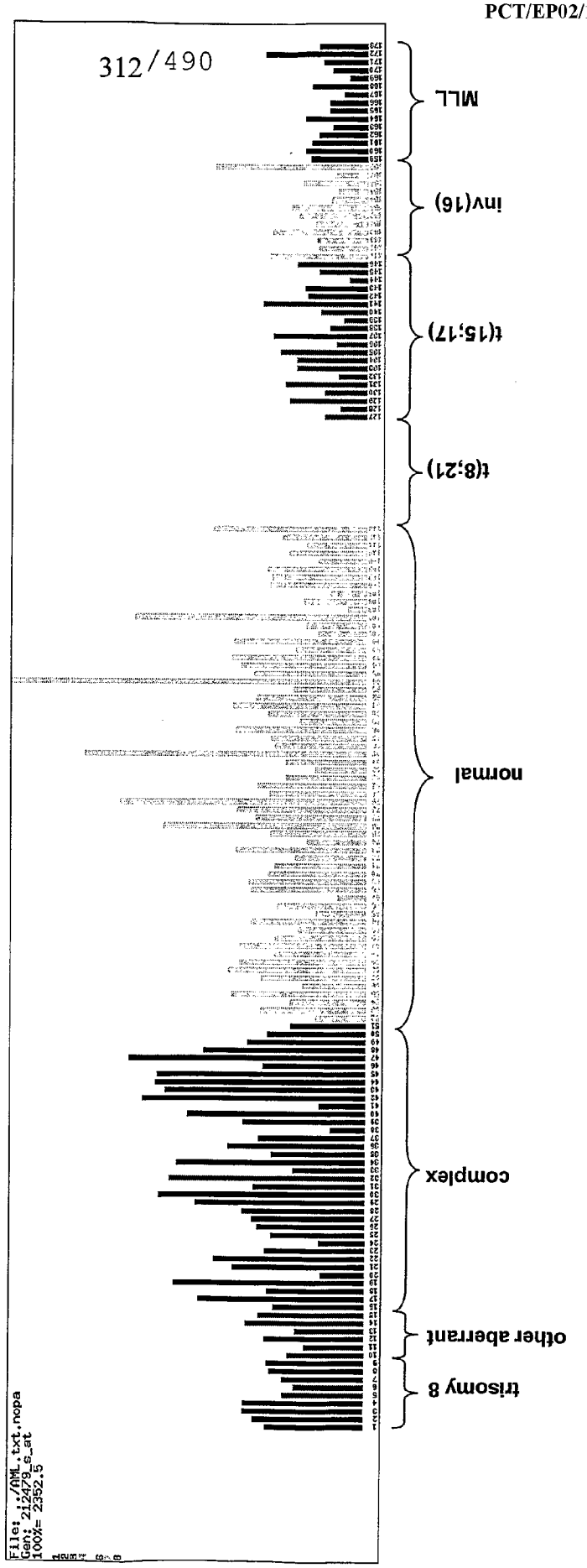


Figure 286

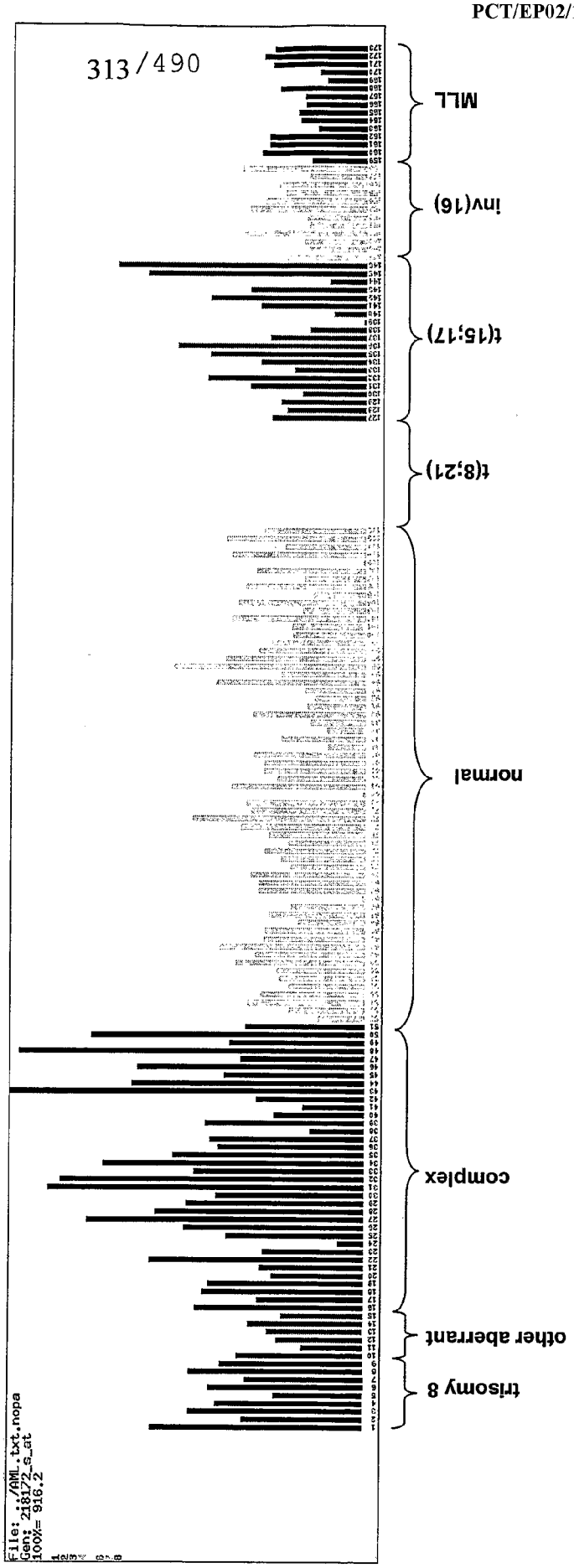
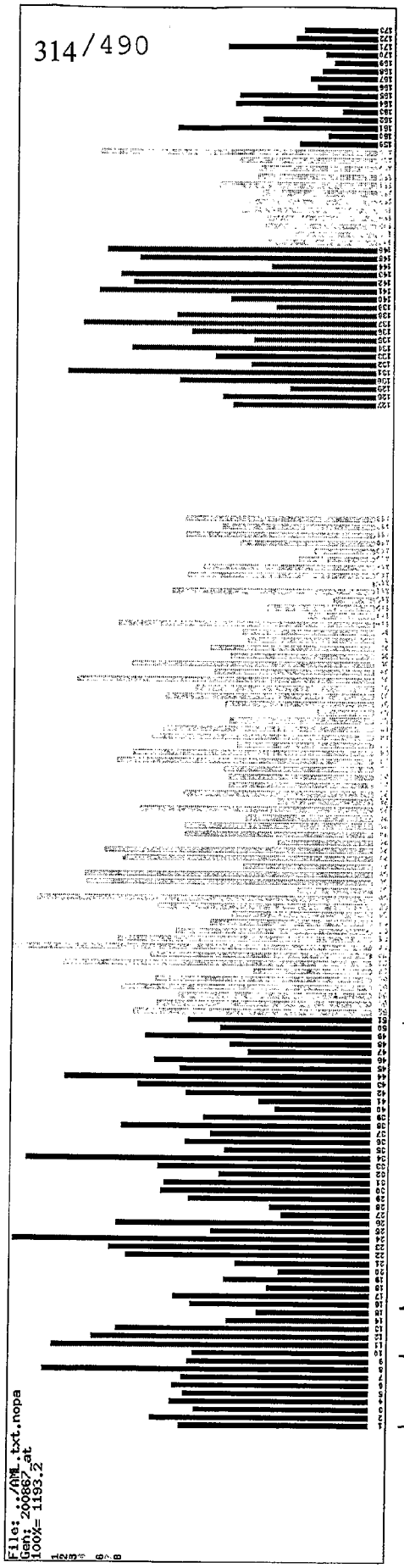

218172_s_at, PRO2577, trisomy 8 vs. MLL
File: ../AML.txt,nopa
Gen: 218172_s_at
100%= 916.2
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 287



200867_at, trisomy 8 vs. MLL

Figure 288

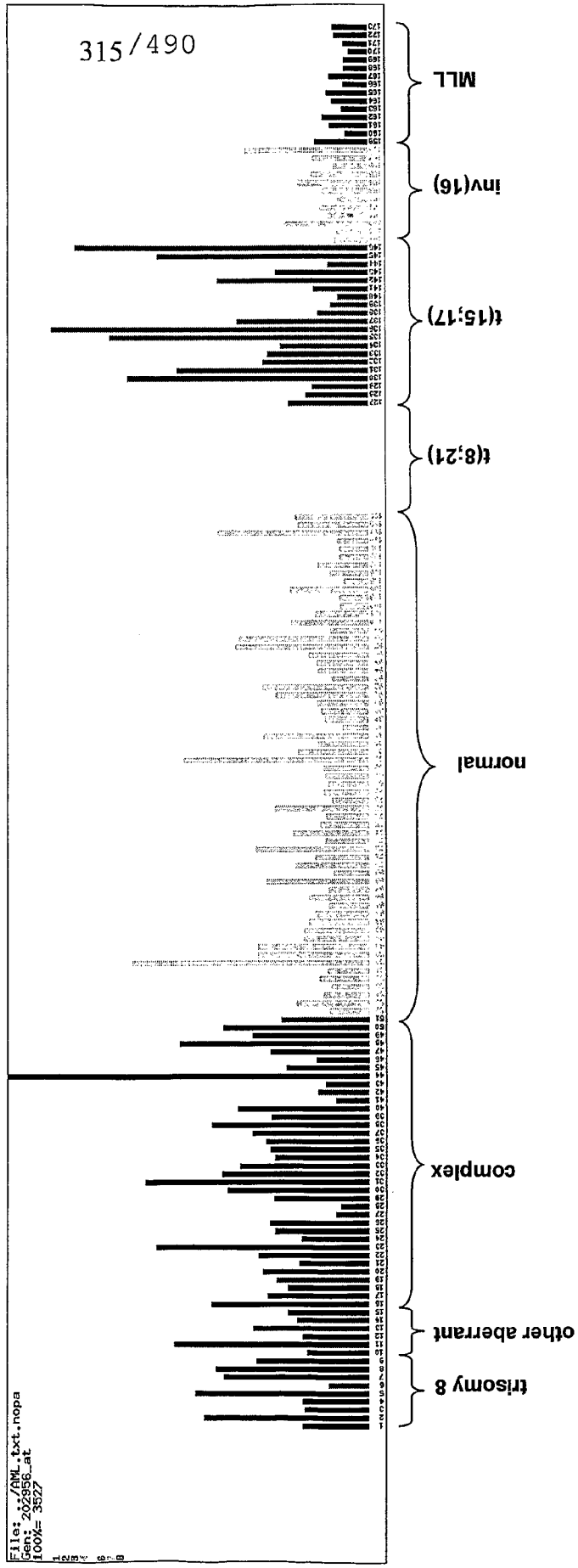

202956_at, BIG1, trisomy 8 vs. MLL
File: ../AML_txt.nopa
Gen: 202956_at
100%= 3527
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 289

236648_at, other aberrant vs. all other AML

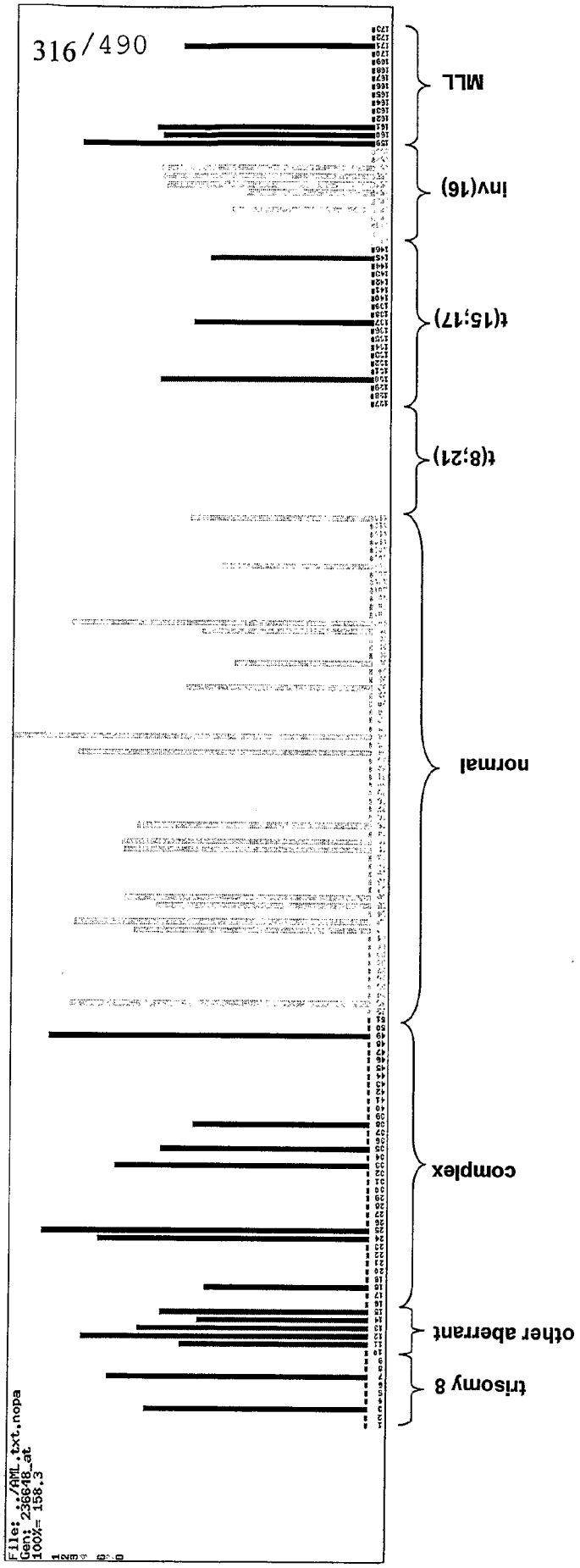


Figure 290

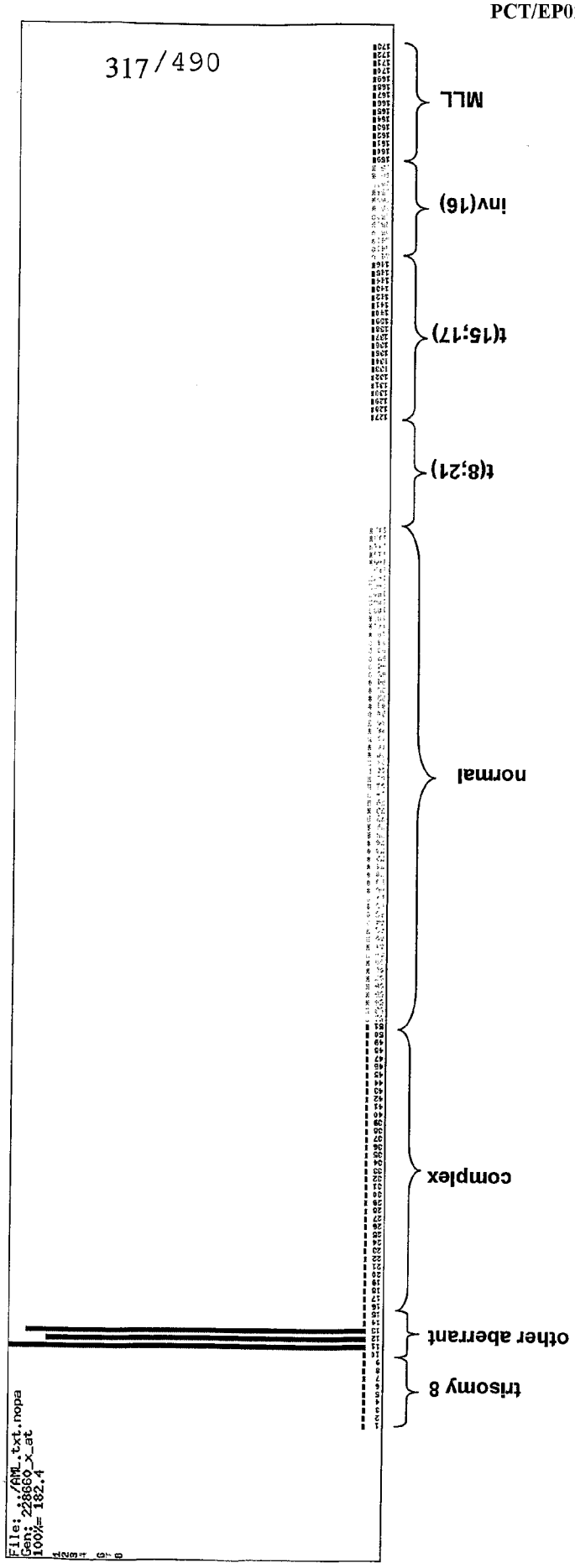
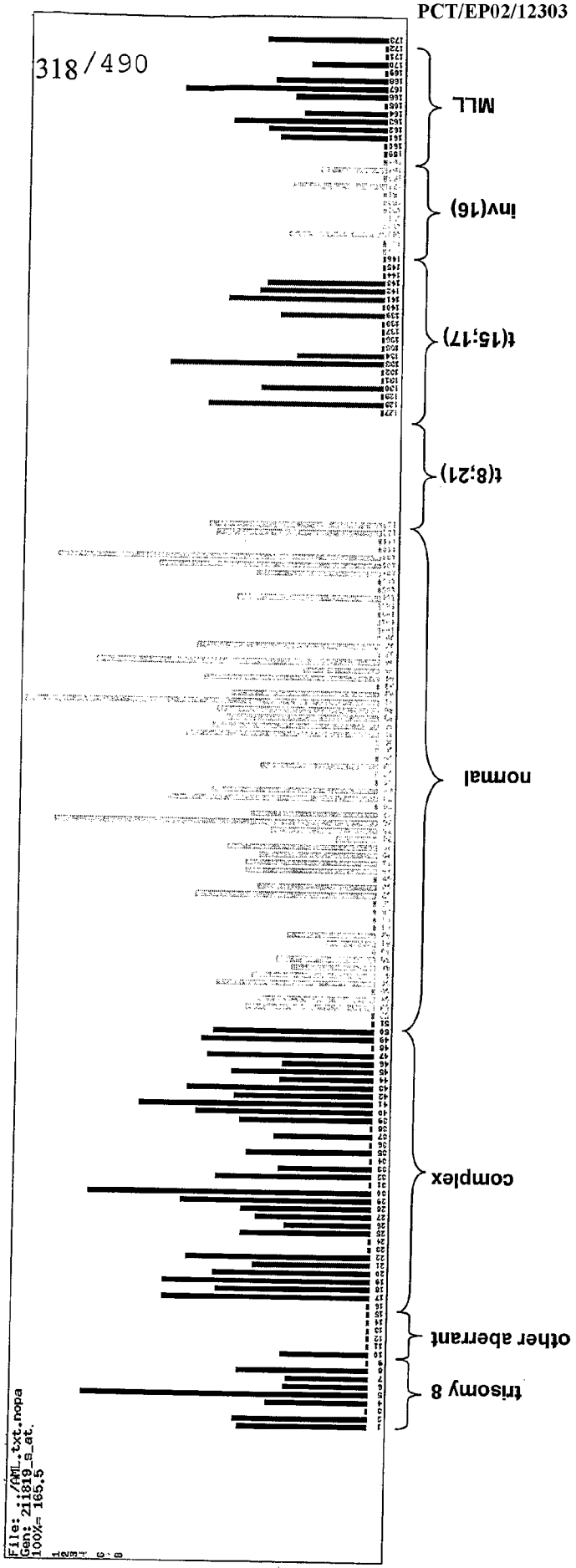

228660_x_at, SEMA4F, other aberrant vs. all other AML
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML.txt.nopa
Gen: 228660_x_at
100%= 182.4

Figure 291

211819_s_at, SH3D5, other aberrant vs. complex

Figure 292



233328_x_at, other aberrant vs. complex

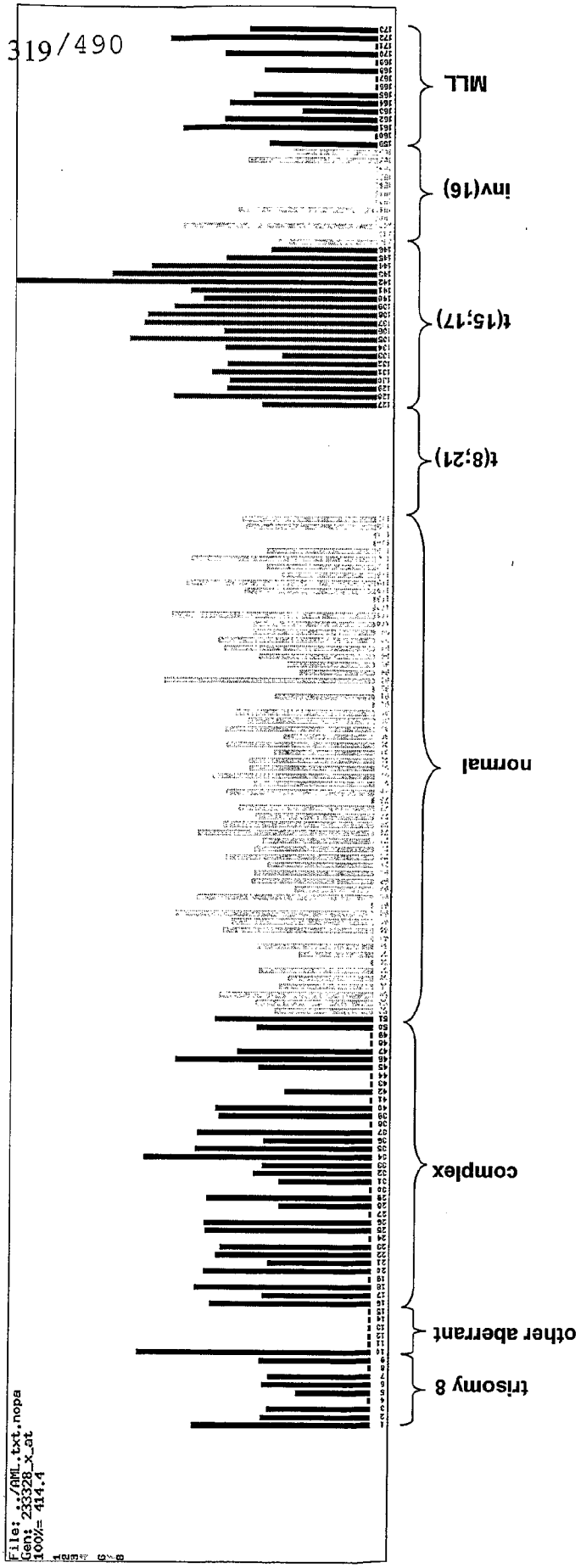


Figure 293

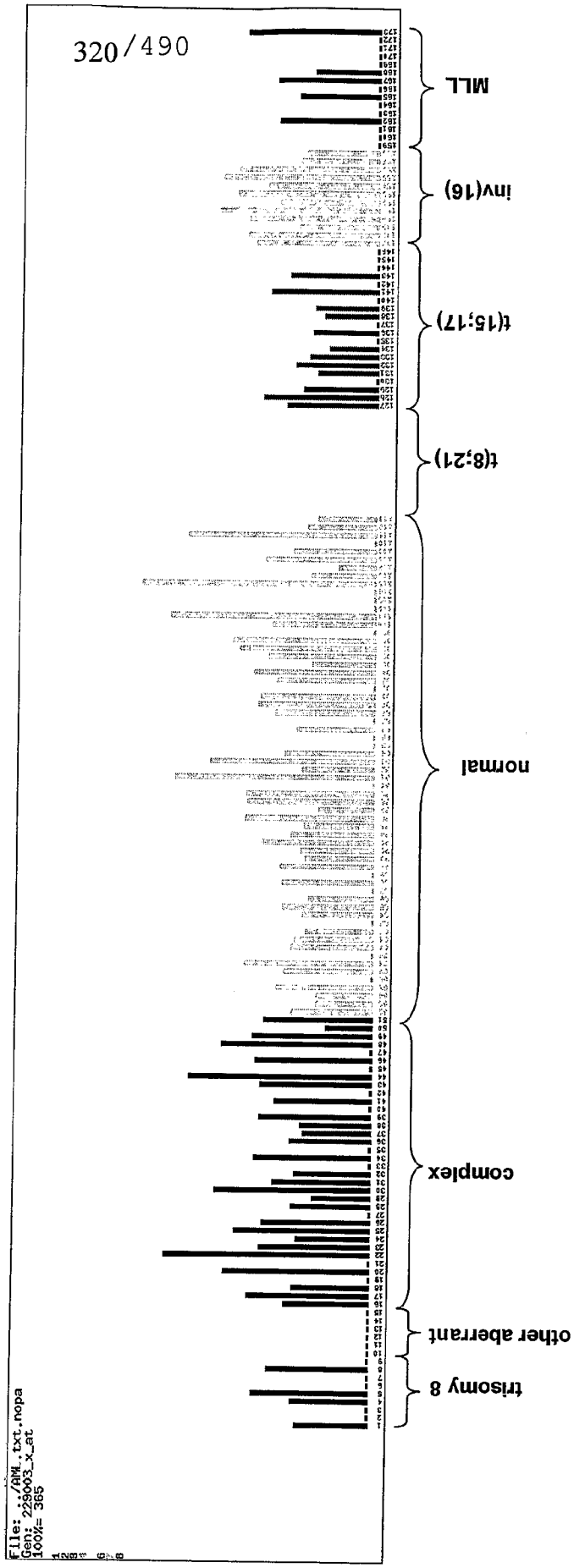

229003_x_at, other aberrant vs. complex
File: ../AML.txt.nopa
Gen: 229003_x_at
100%= 365
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 294

233328_x_at, other aberrant vs. normal

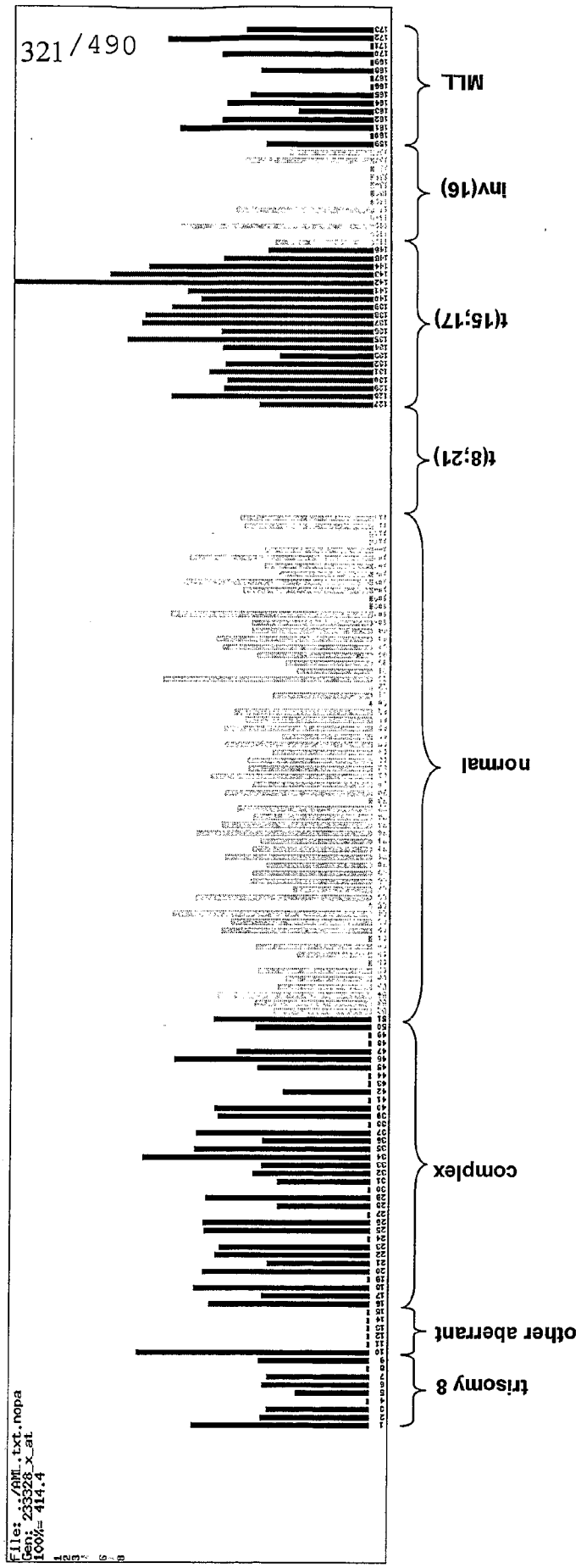
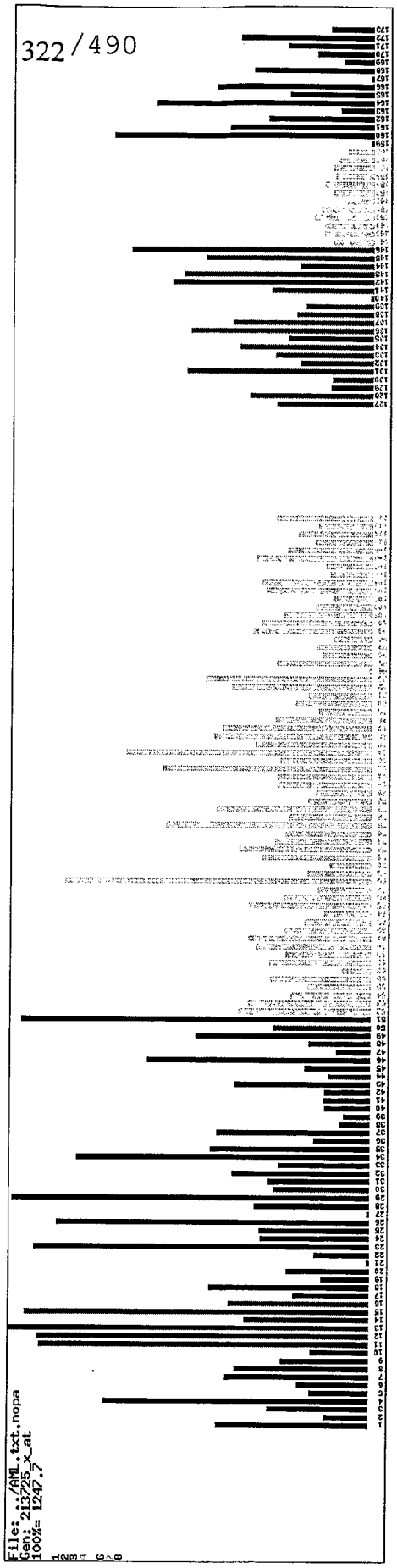


Figure 295



213725_x_at, other aberrant vs. normal

Figure 296

221770_at, RPE, other aberrant vs. t(8;21)

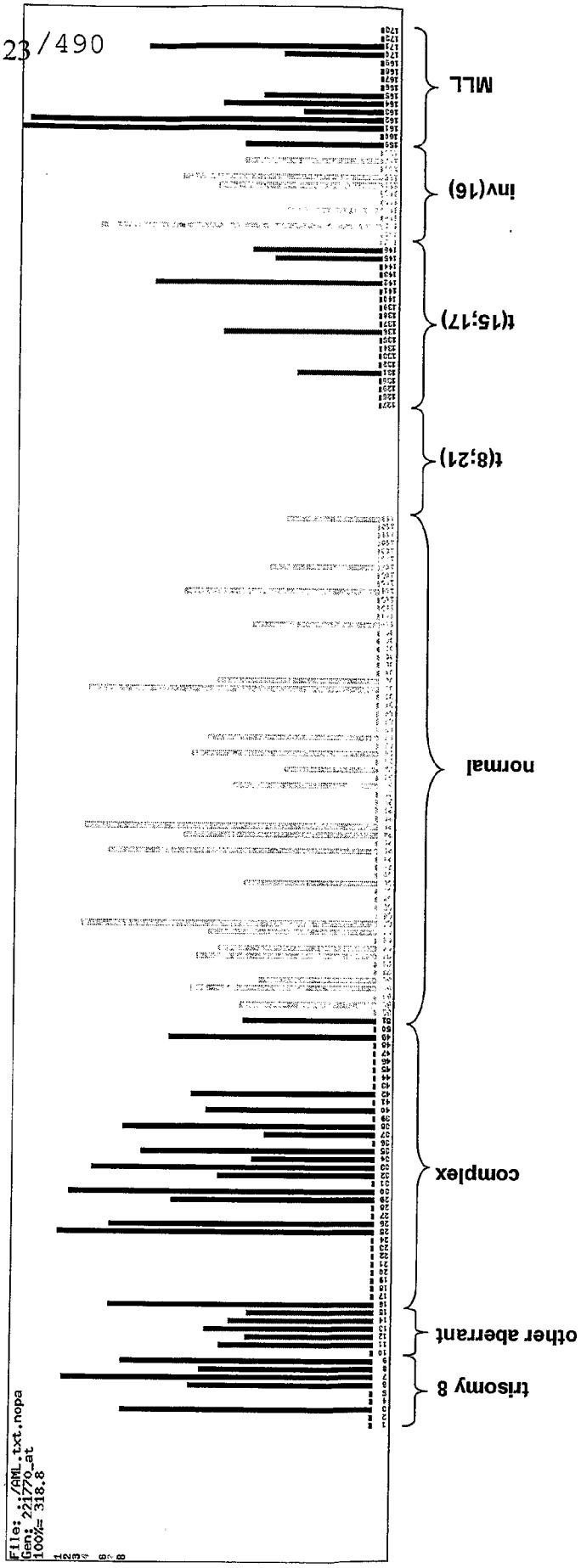


Figure 297

213716_s_at, SECTM1, other aberrant vs. t(15;17)

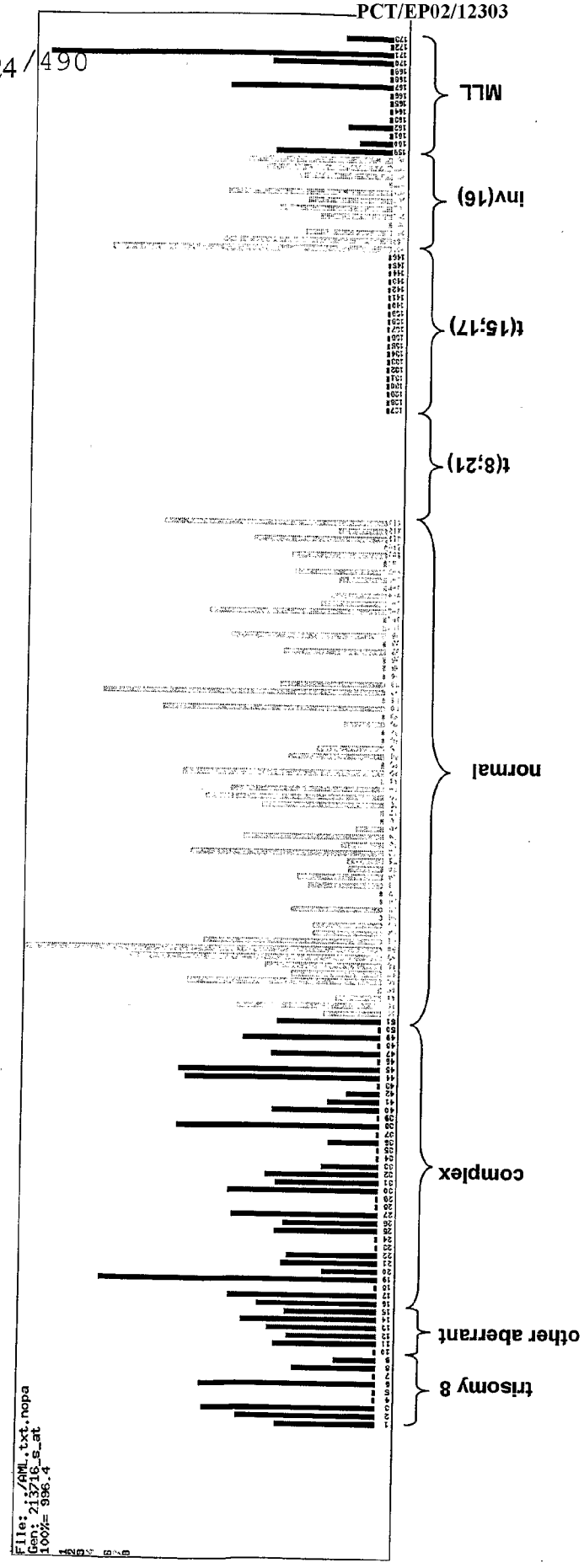
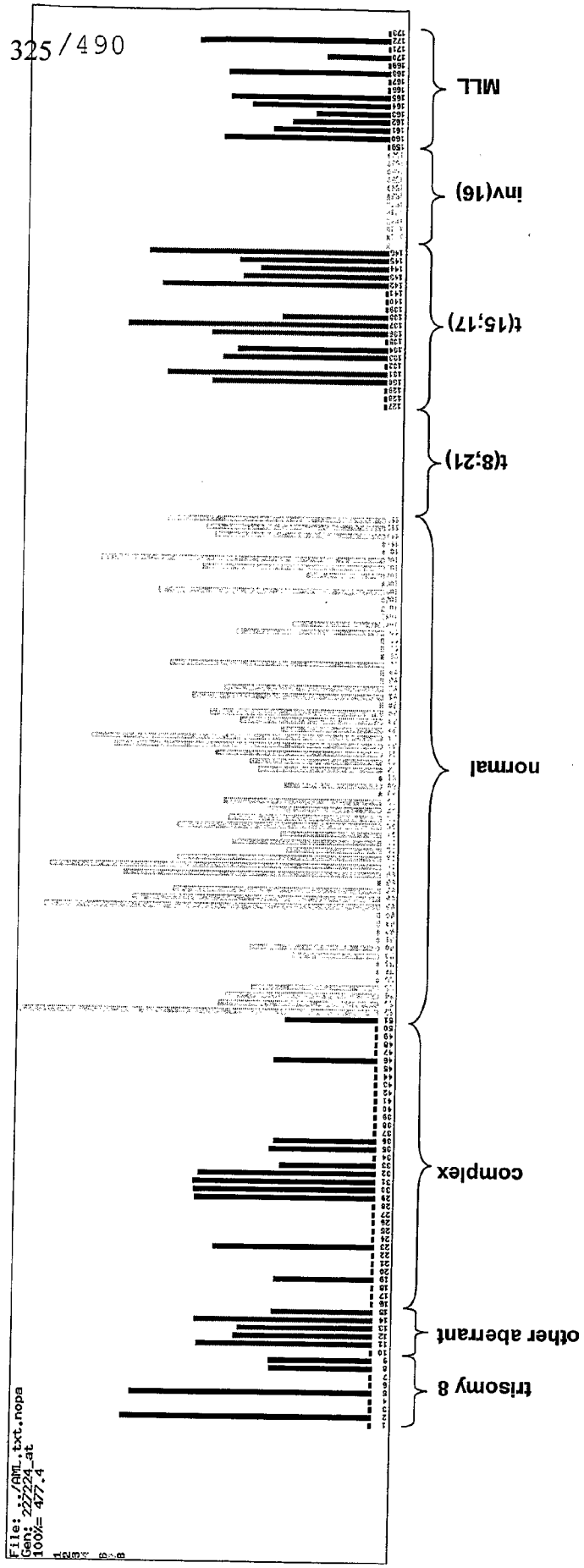


Figure 298

227224_at, other aberrant vs. inv(16)

Figure 299



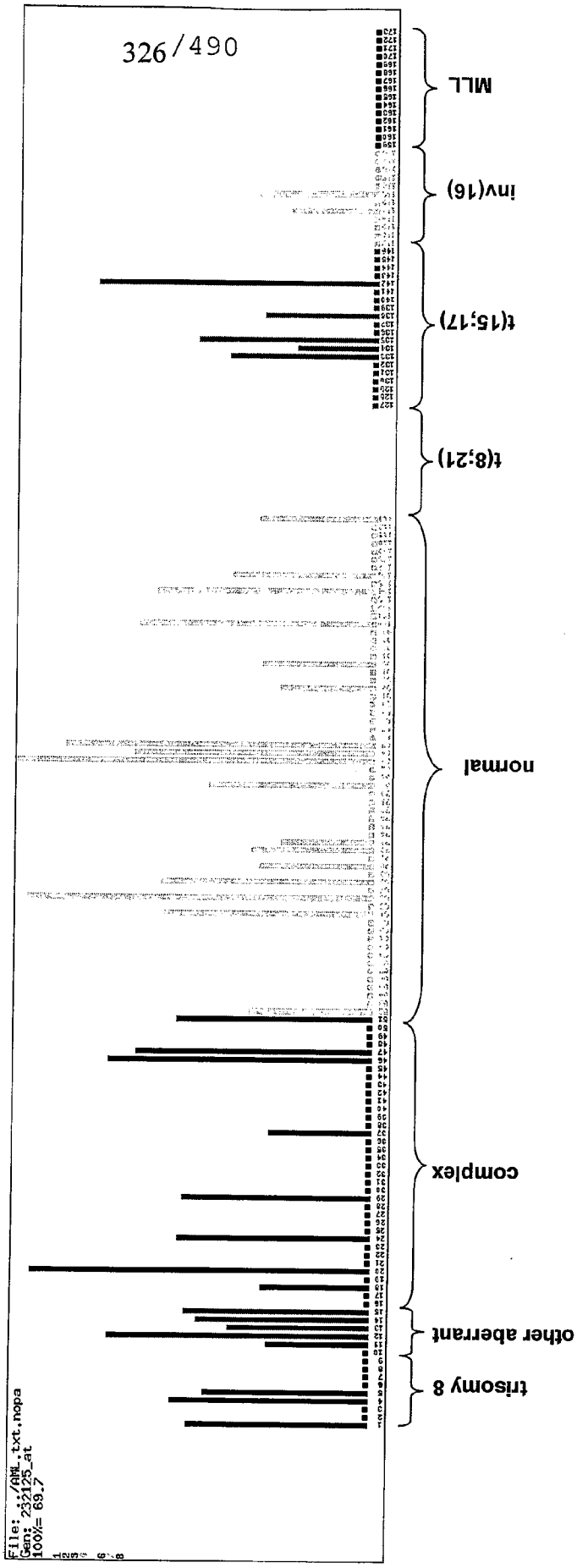

232125_at, other aberrant vs. MLL
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML_txt.nopa
Gen: 232125_at
100%= 69.7

Figure 300

200608_s_at, RAD21, complex vs. all other AML

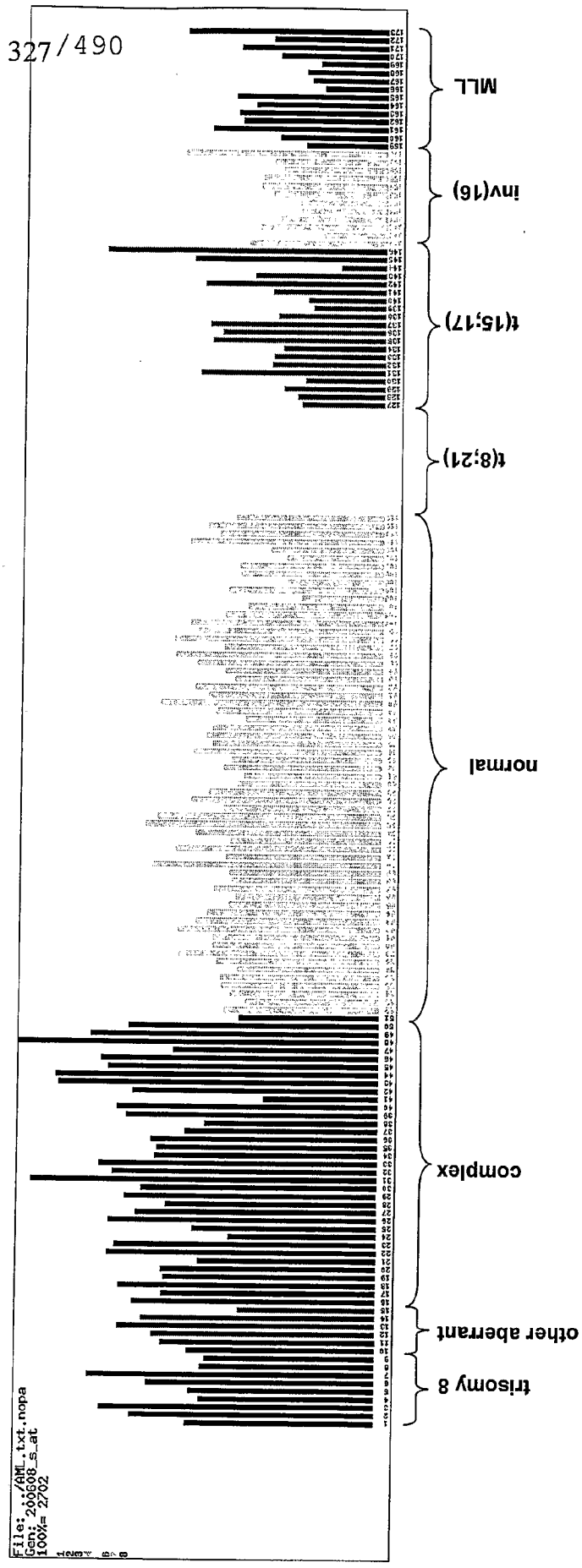


Figure 301

209085_x_at, RFC1, complex vs. all other AML

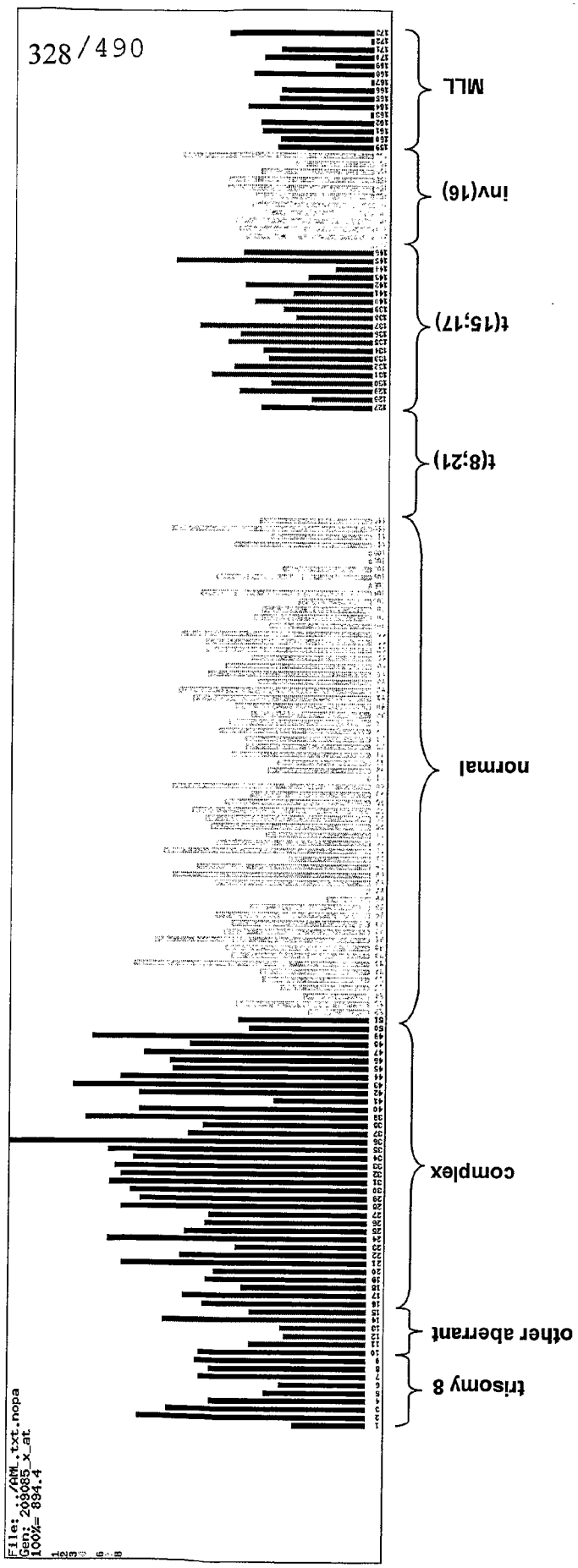


Figure 302

201922_at, YR-29, complex vs. normal

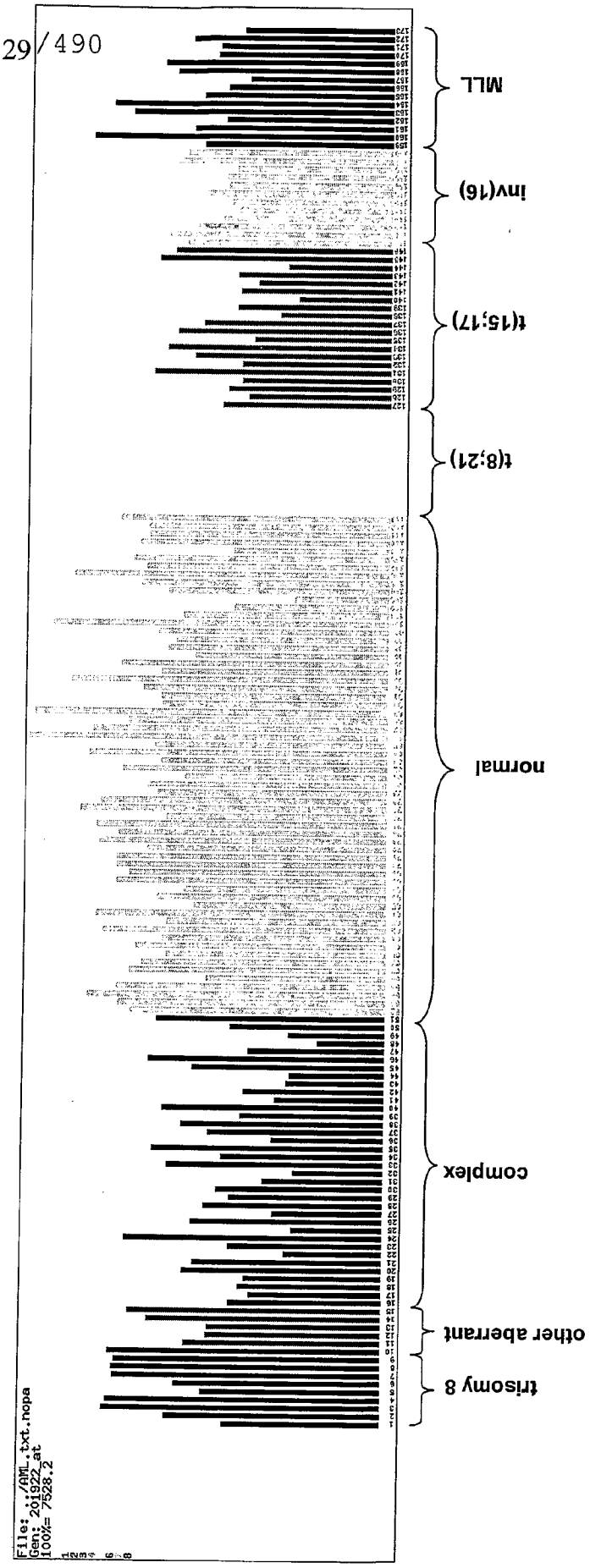


Figure 303

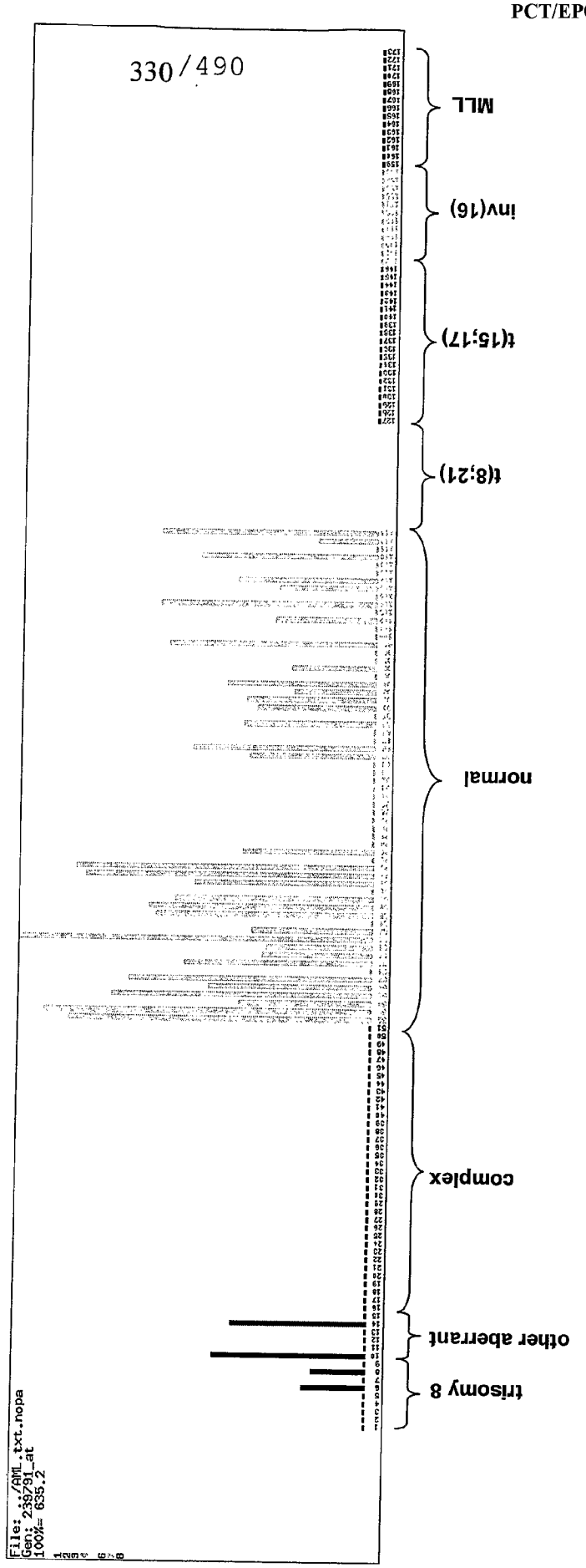

239791_at, HOXB6, complex vs. normal
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML.txt.nopa
Gen: 239791_at
100%= 635.2

Figure 304

200608_s_at, RAD21, complex vs. normal

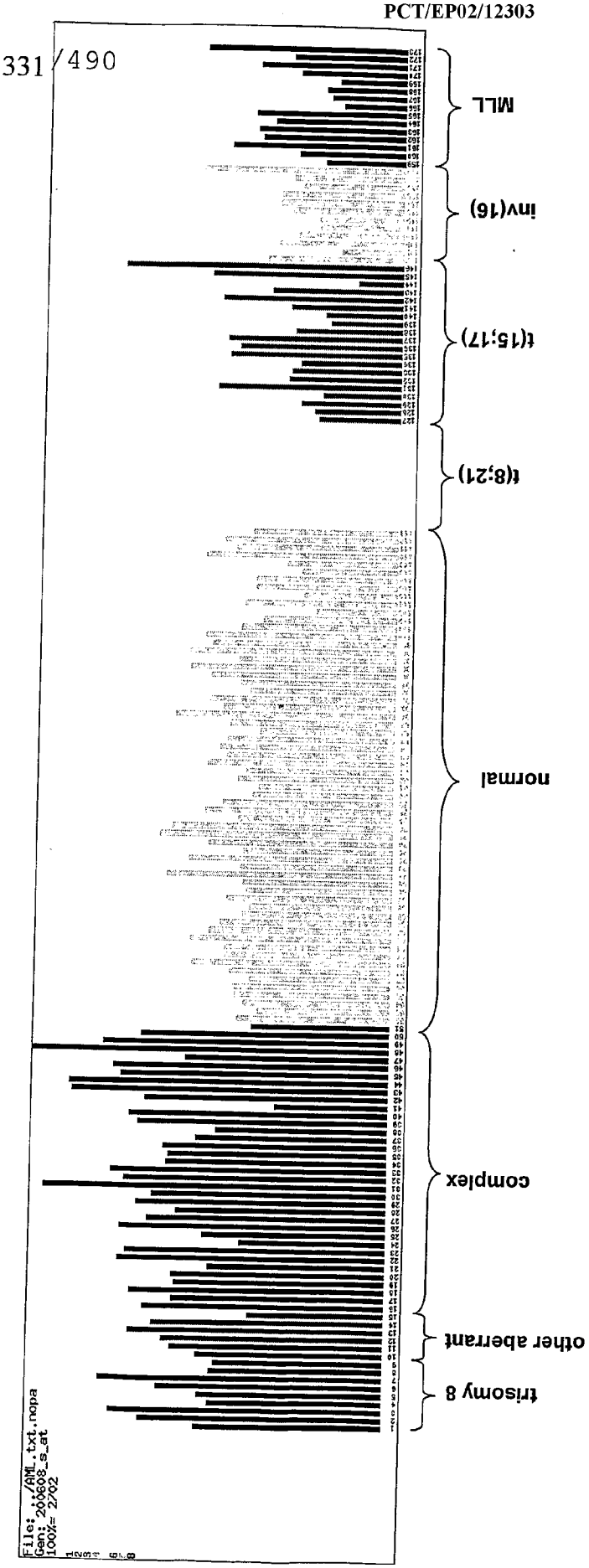


Figure 305

211950_at, RBAF600, complex vs. normal

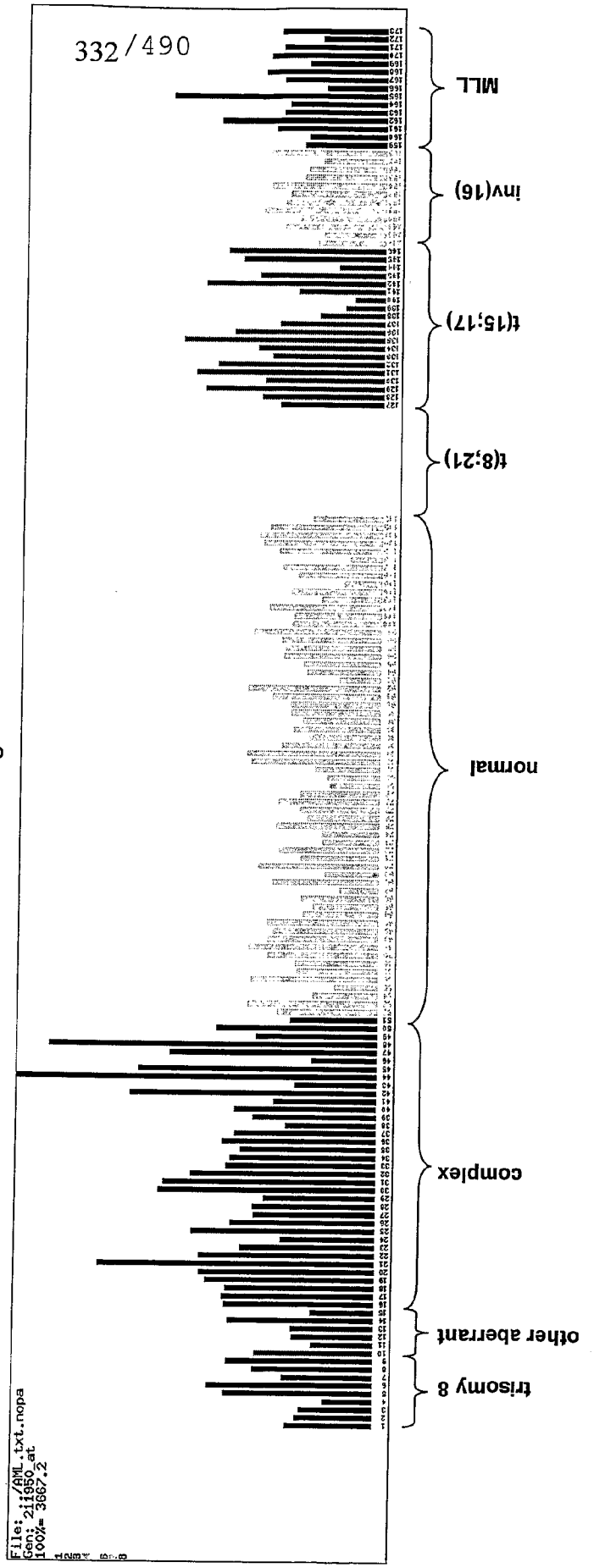


Figure 306

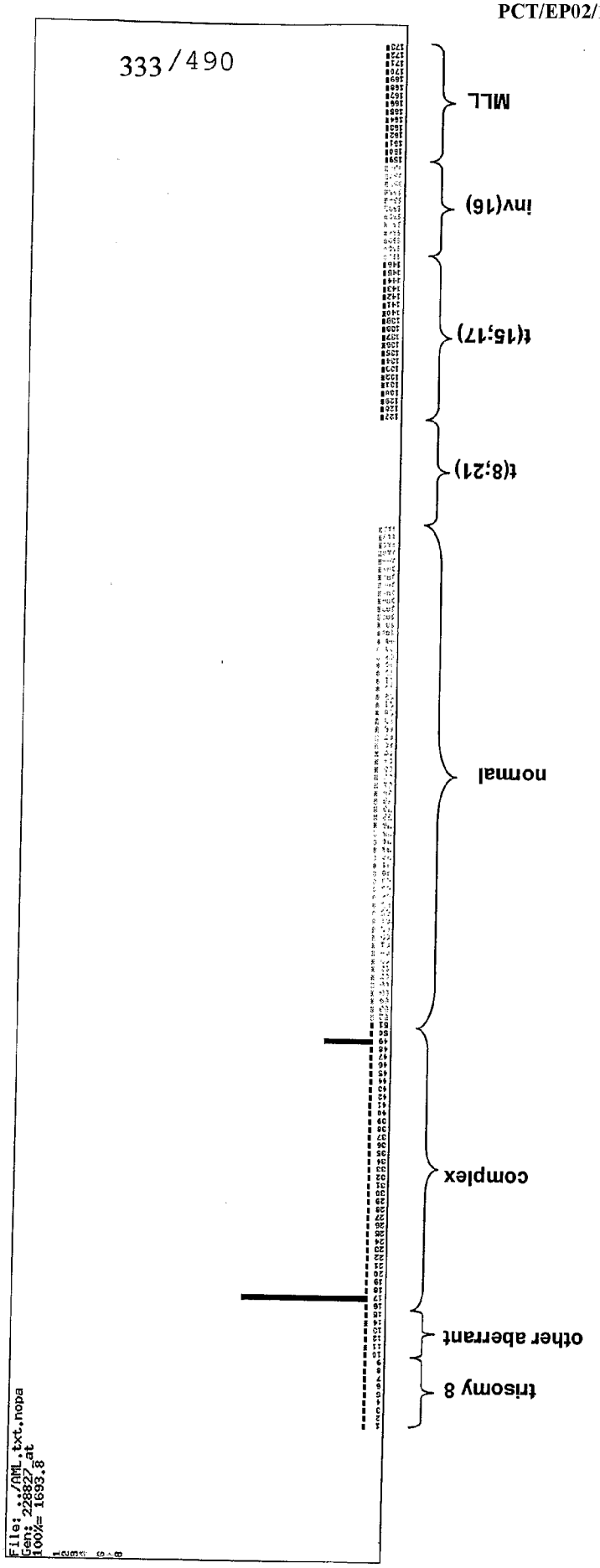

228827_at, complex vs. t(8;21)
File: .../AML.txt.nopa
Gen: 228827_at
100%= 1693.8
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 307

204249_s_at, LMO2, complex vs. t(8;21)

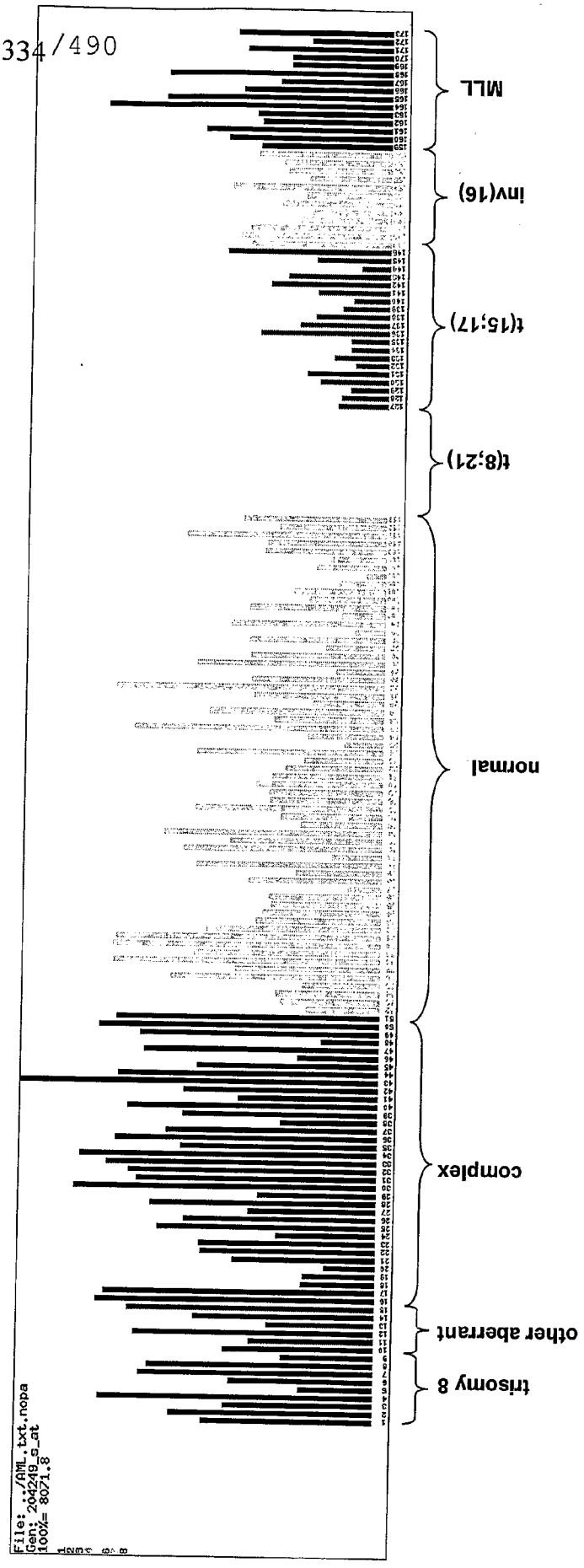


Figure 308

212953_x_at, CALR, complex vs. t(15;17)

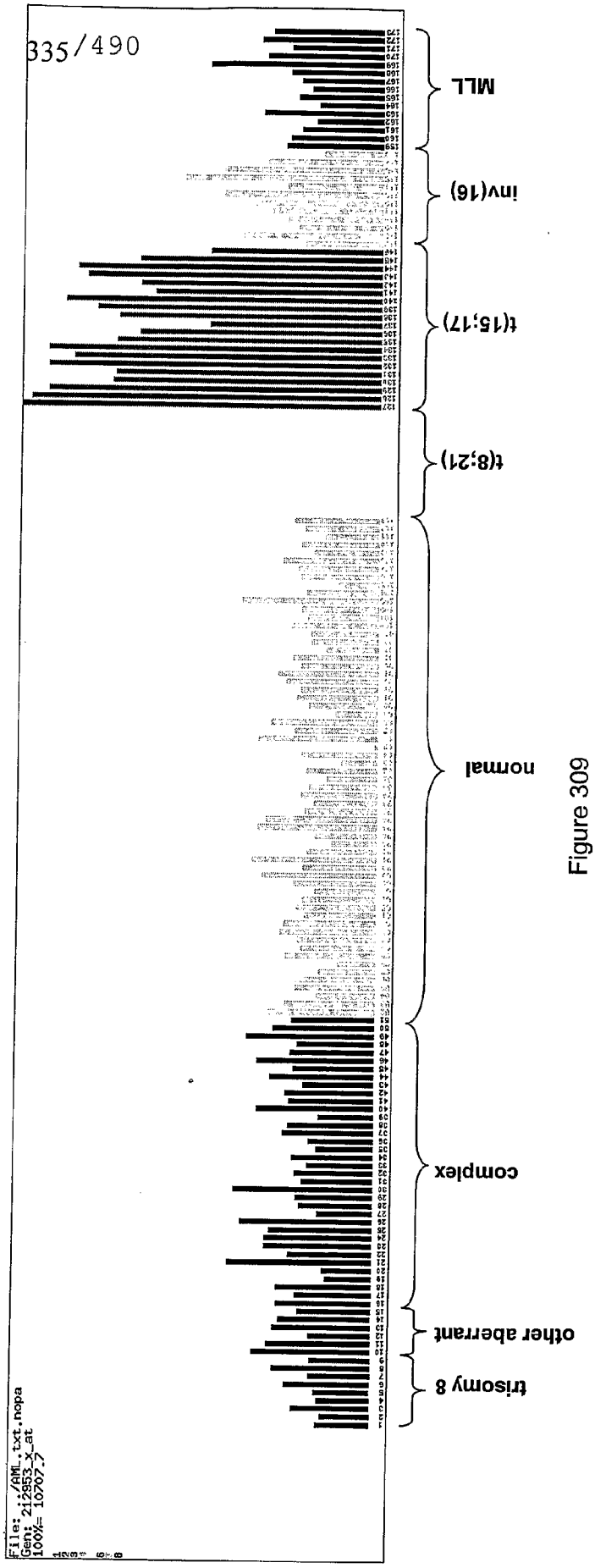


Figure 309

209190_s_at, DIAPH1, complex vs. inv(16)

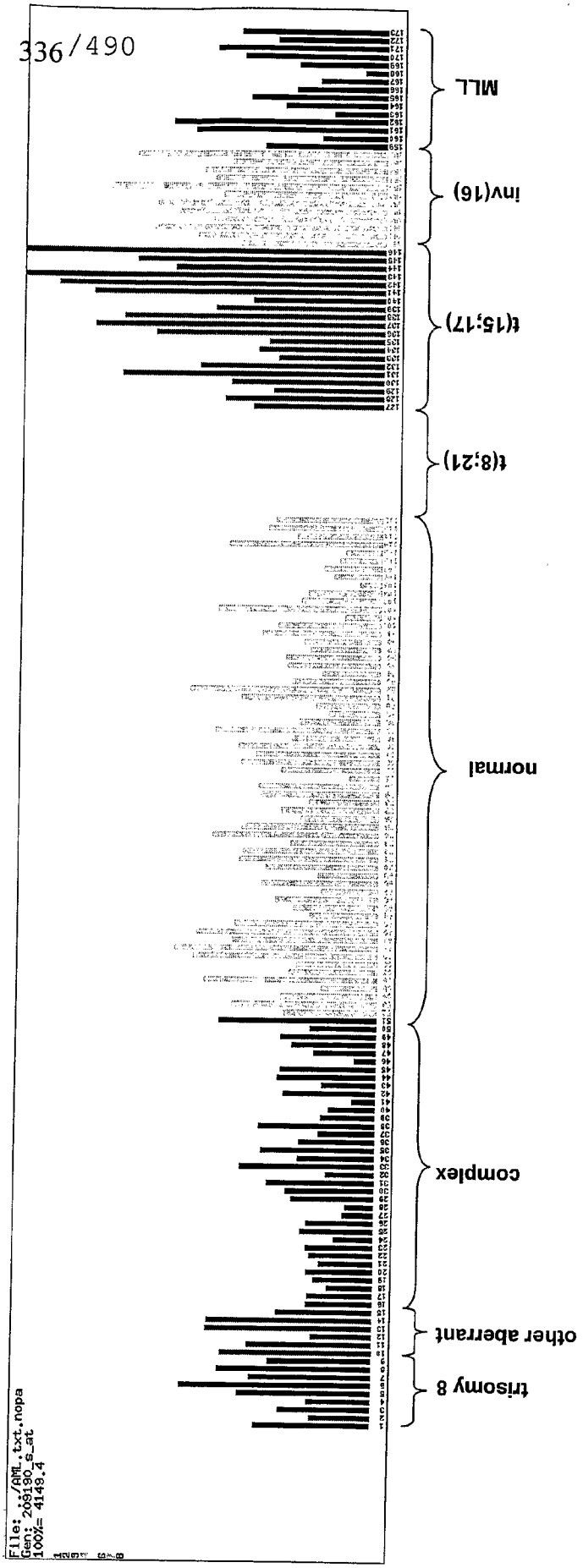


Figure 310

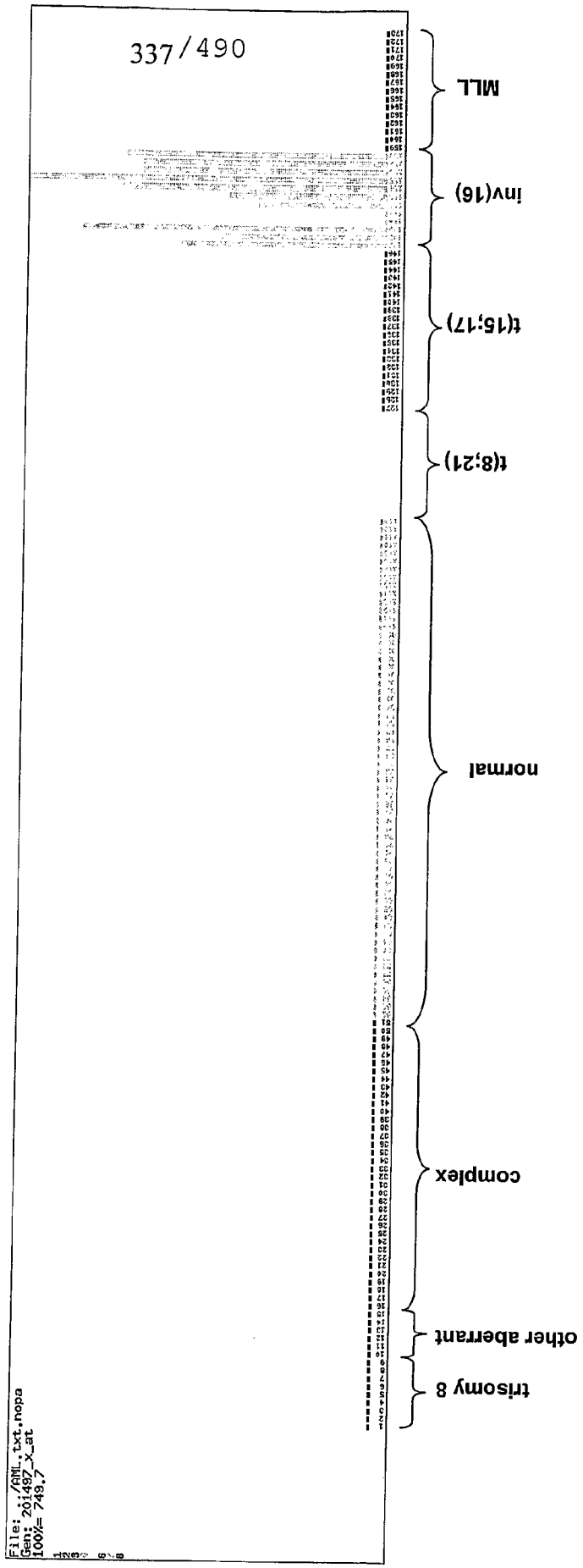
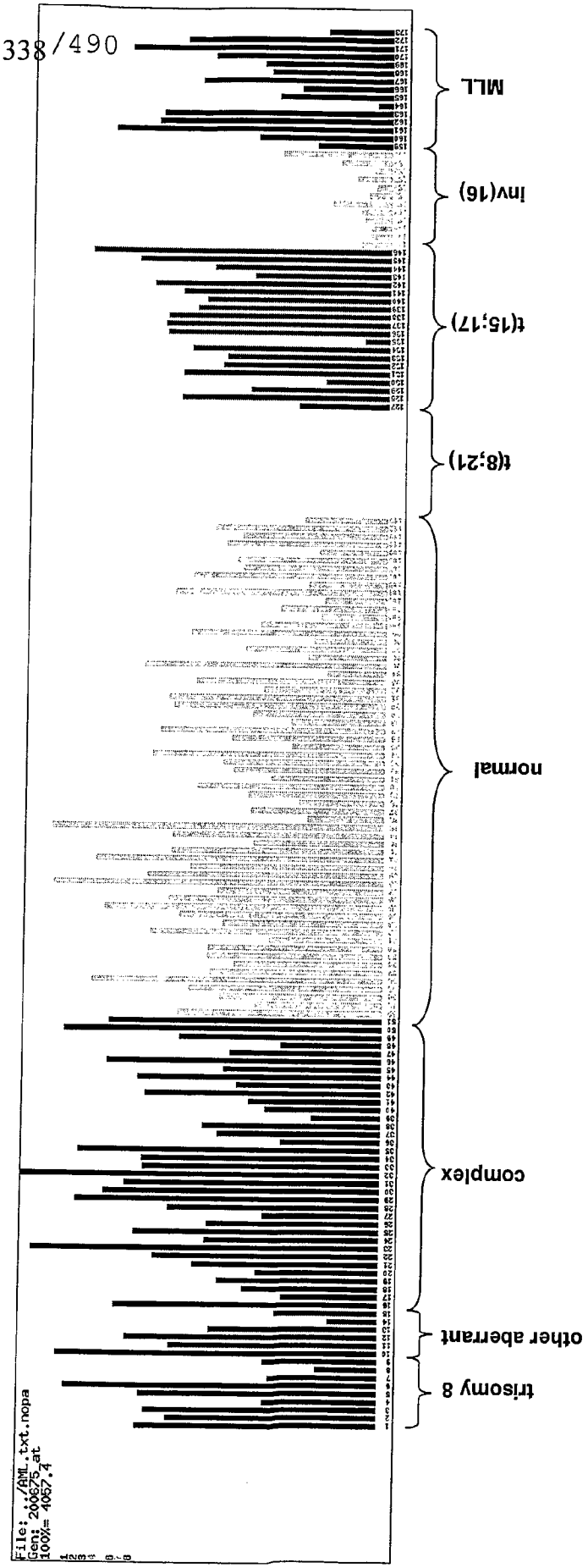

201497_x_at, MYH11, complex vs. inv(16)
File: /AML.txt,nopa
Gen: 201497_x_at
100%= 749.7
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8

Figure 311

200675_at, CD81, complex vs. inv(16)

Figure 312



202746_at, complex vs. MLL

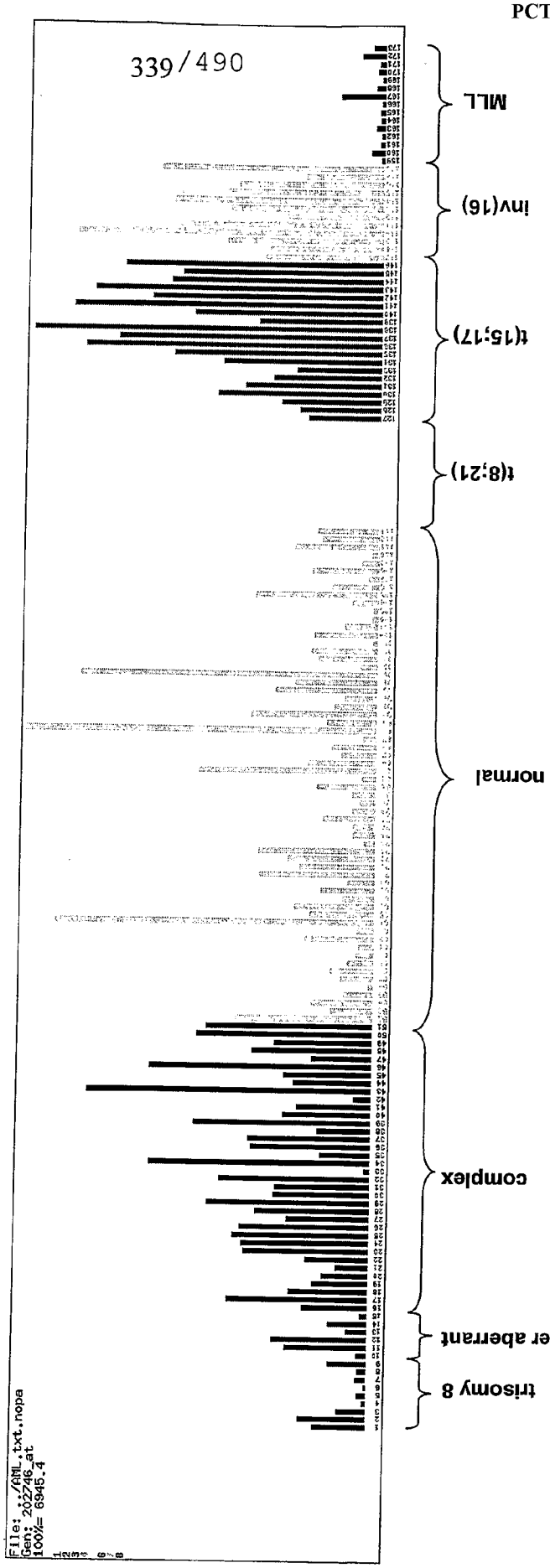


Figure 313

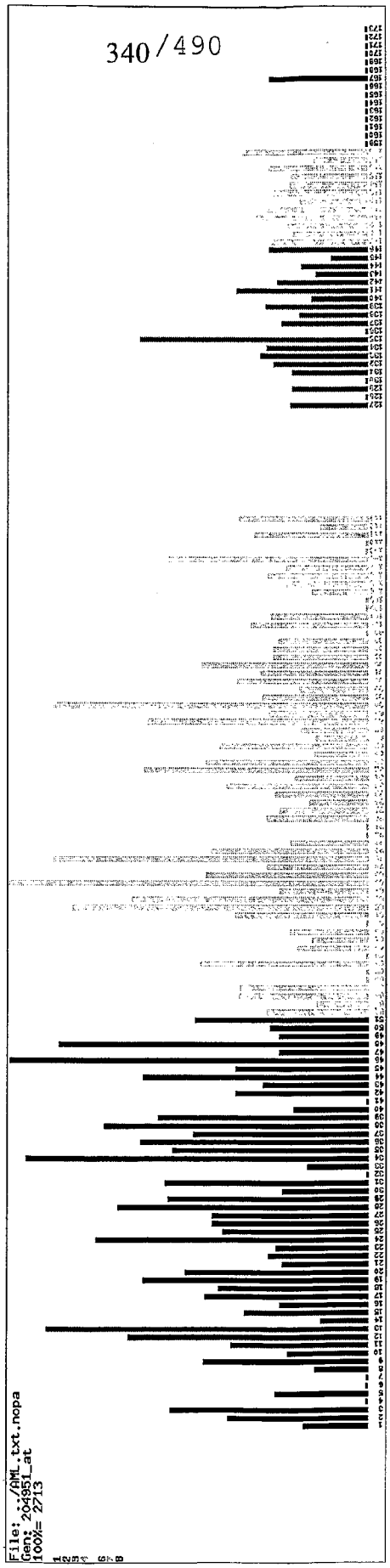

204951_at, ARHH, complex vs. MLL
File: ../AML_txt.nopa
Gen: 204951_at
100%= 2713
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 314

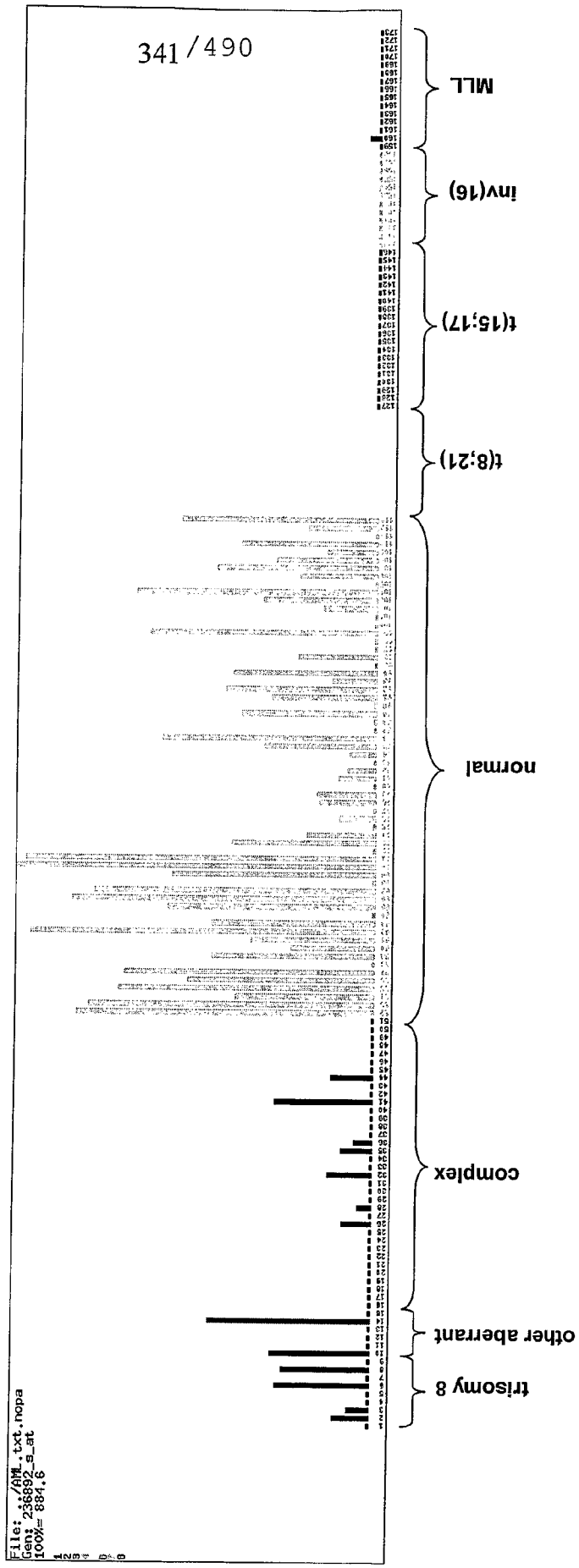

236892_s_at, HOXB6, normal vs. all other AML
File: ../AML.txt.nopa
Gen: 236892_s_at
100%= 884.6
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 315

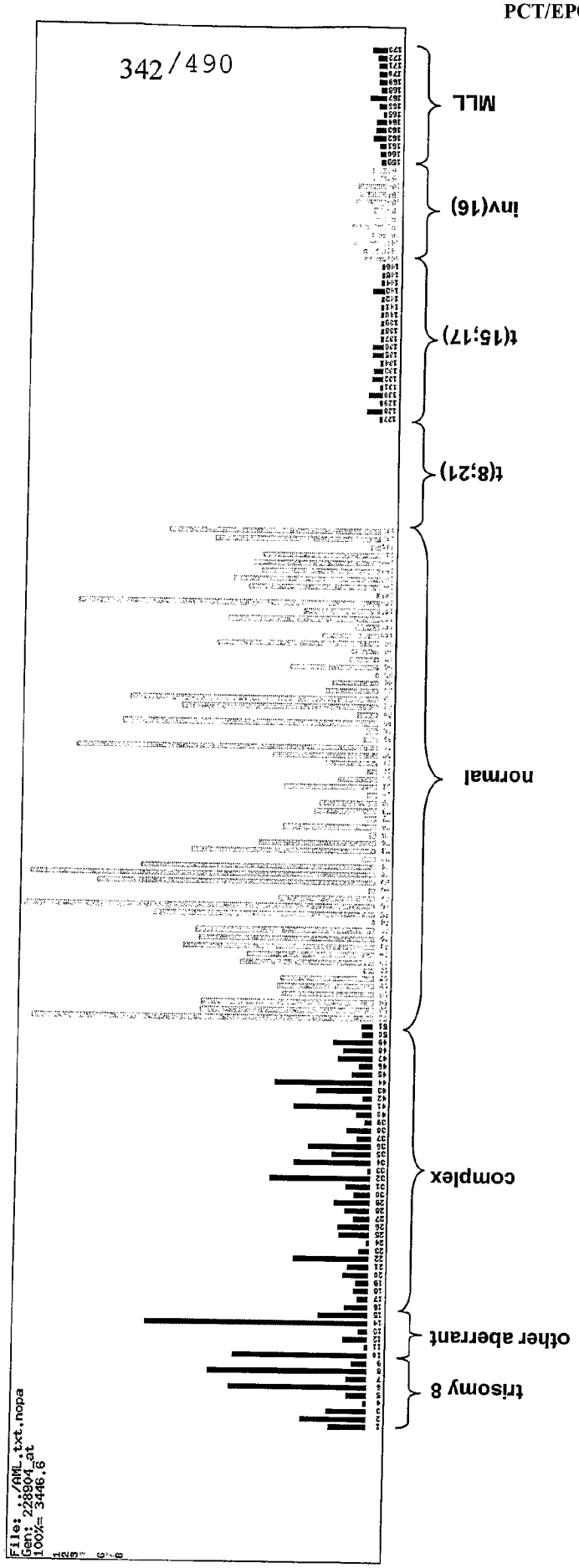

228904_at, normal vs. all other AML
File: ../AML_txt.nopa
Gen: 228904_at
100%= 3446.8
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 316

200679_x_at, HMG1, normal vs. all other AML

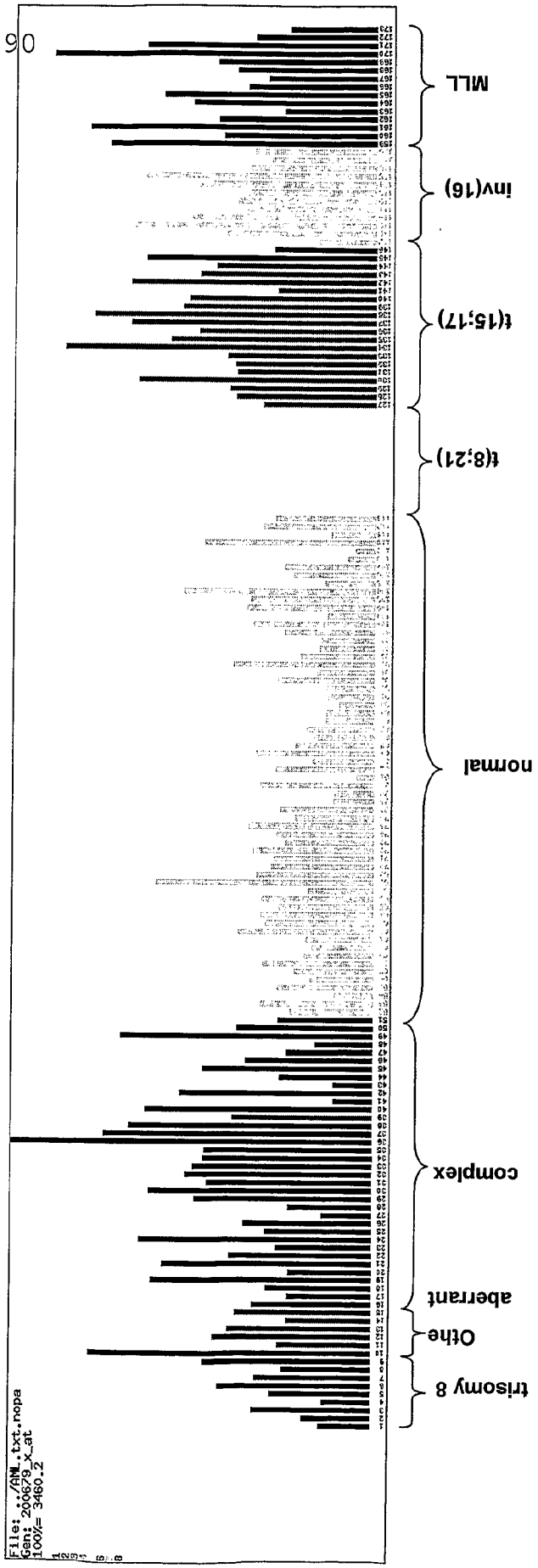


Figure 317

225326_at, KIAA1311, normal vs. all other AML

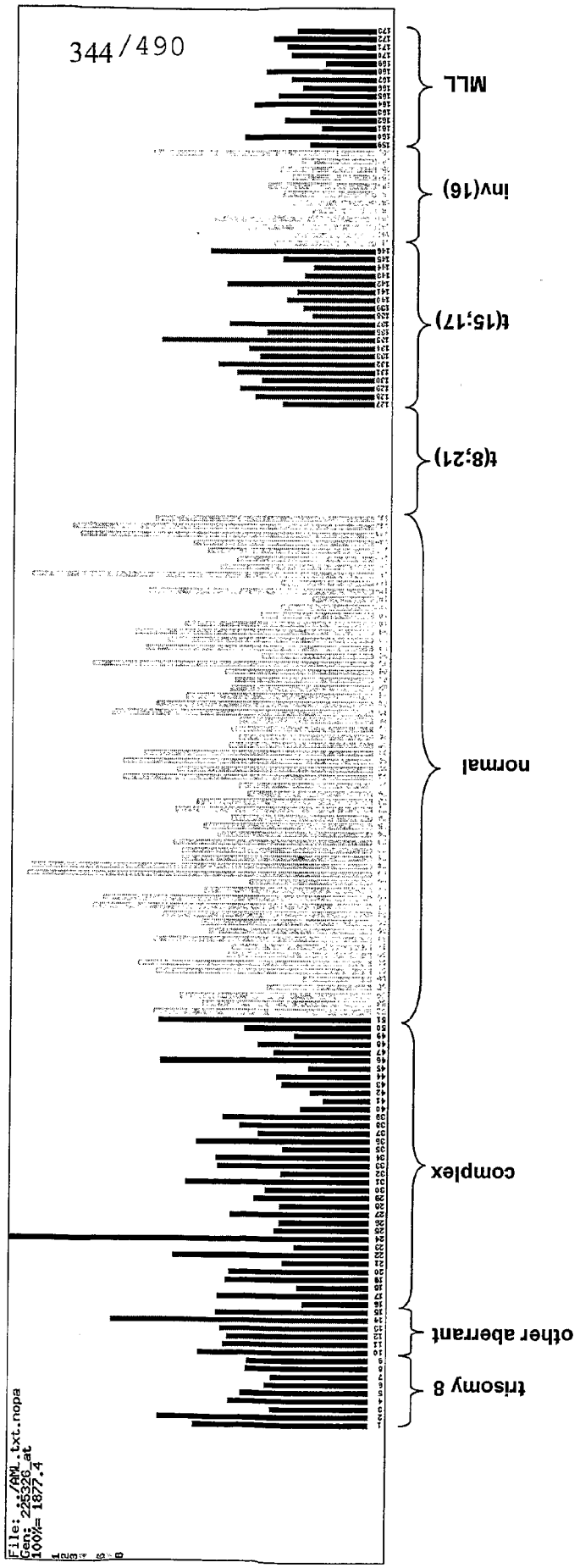


Figure 318

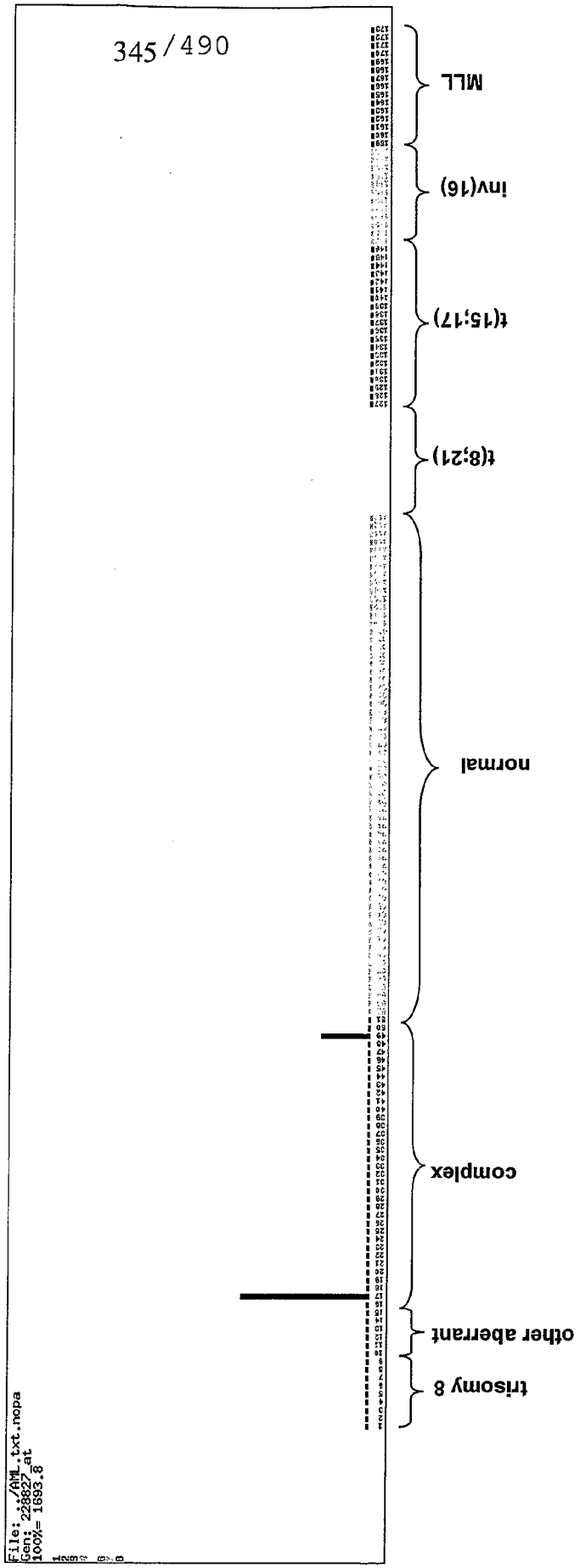

228827_at, normal vs. t(8;21)
File: .../AML.txt.nopa
Gen: 228827_at
100%= 1693.8
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8

Figure 319

212953_x_at, CALR, normal vs. t(15;17)

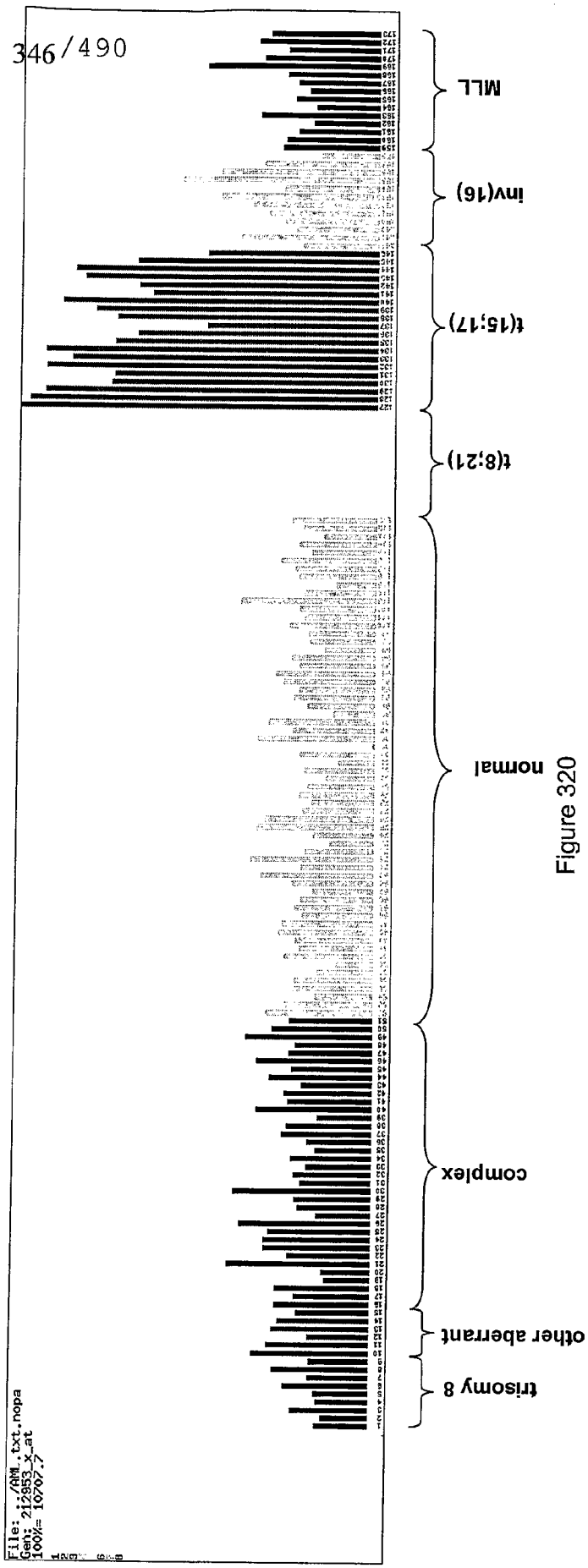


Figure 320

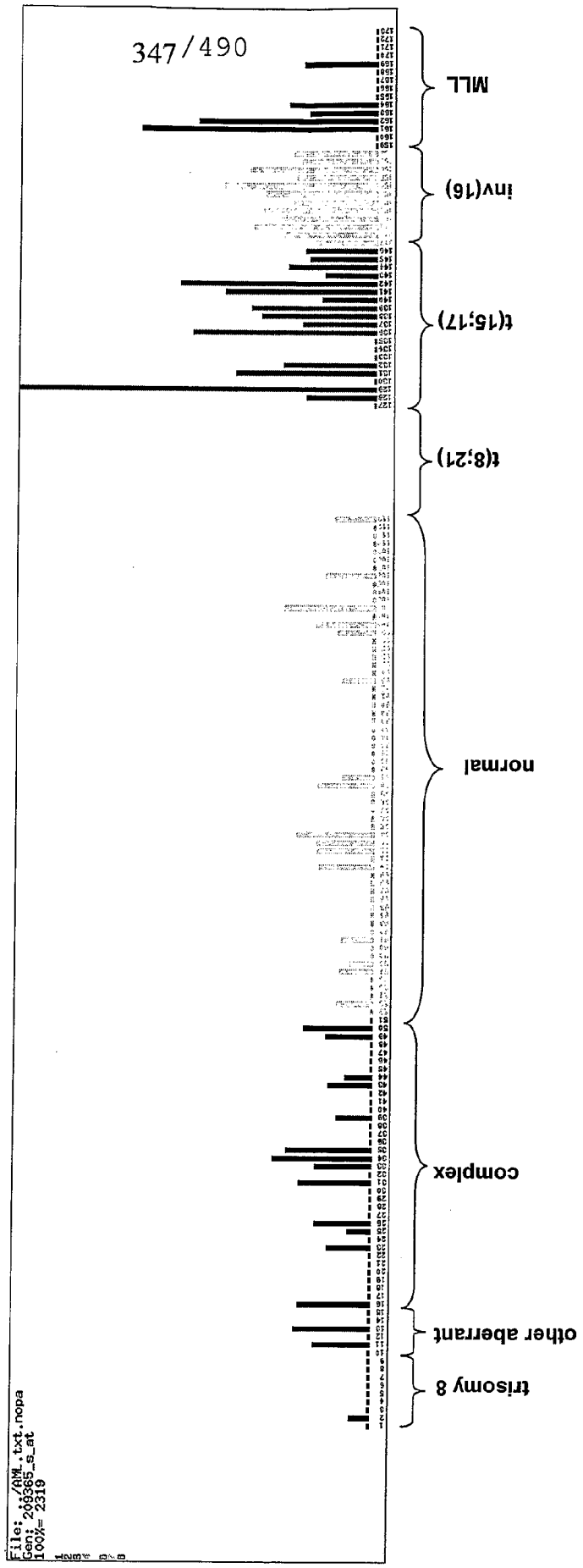

209365_s_at, ECM1, normal vs. inv(16)
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML.txt.nopa
Col: 209365_s_at
100%= 2319

Figure 321

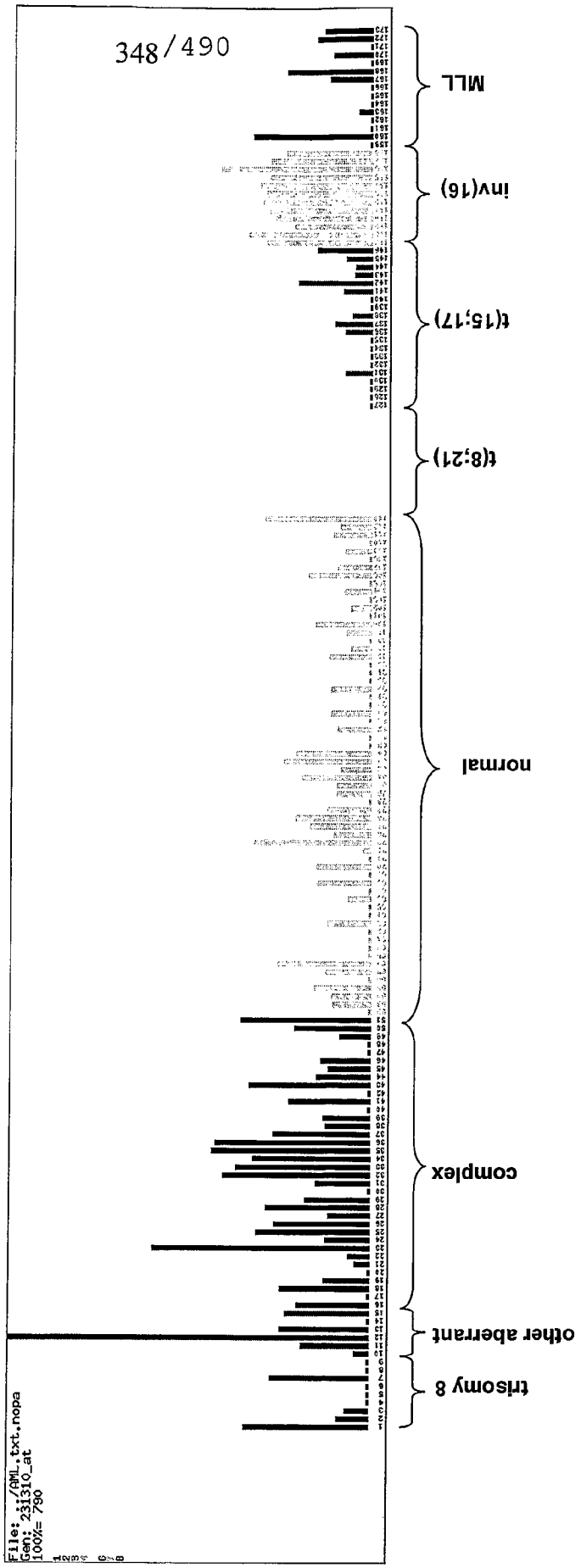

231310_at, normal vs. inv(16)
File: ../AML.txt.nopa
Gen: 231310_at
100%= 790
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 322

202370_s_at, CBFB, normal vs. inv(16)

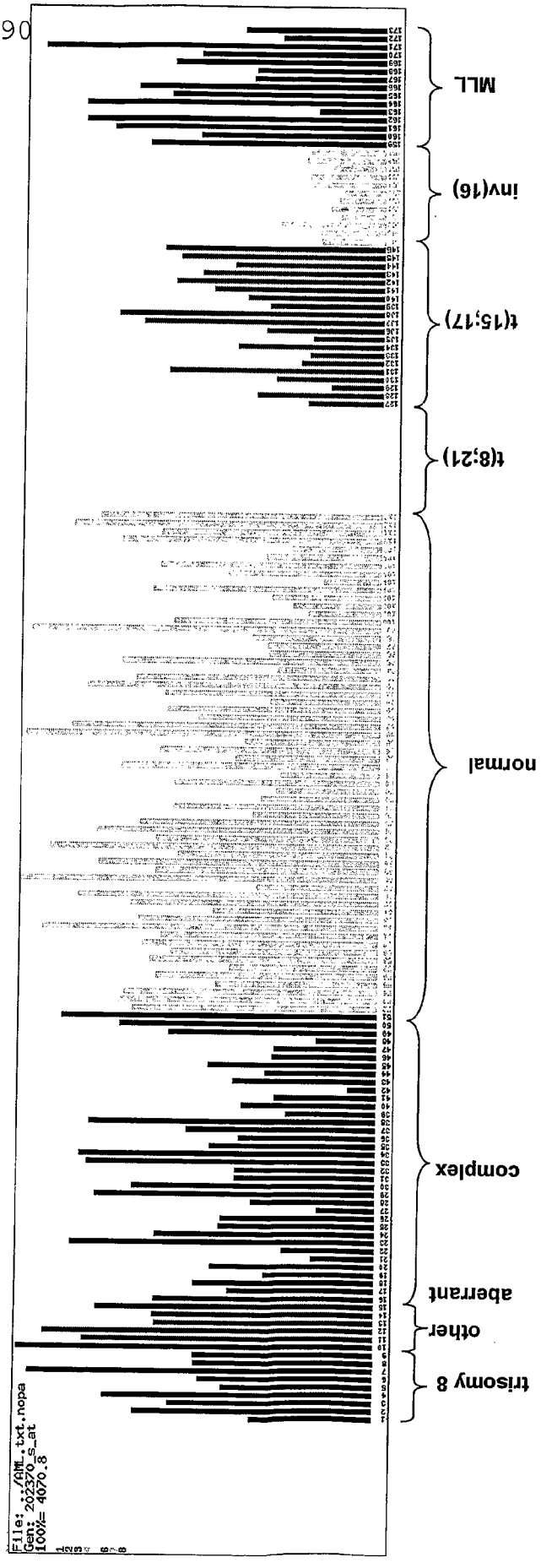


Figure 323

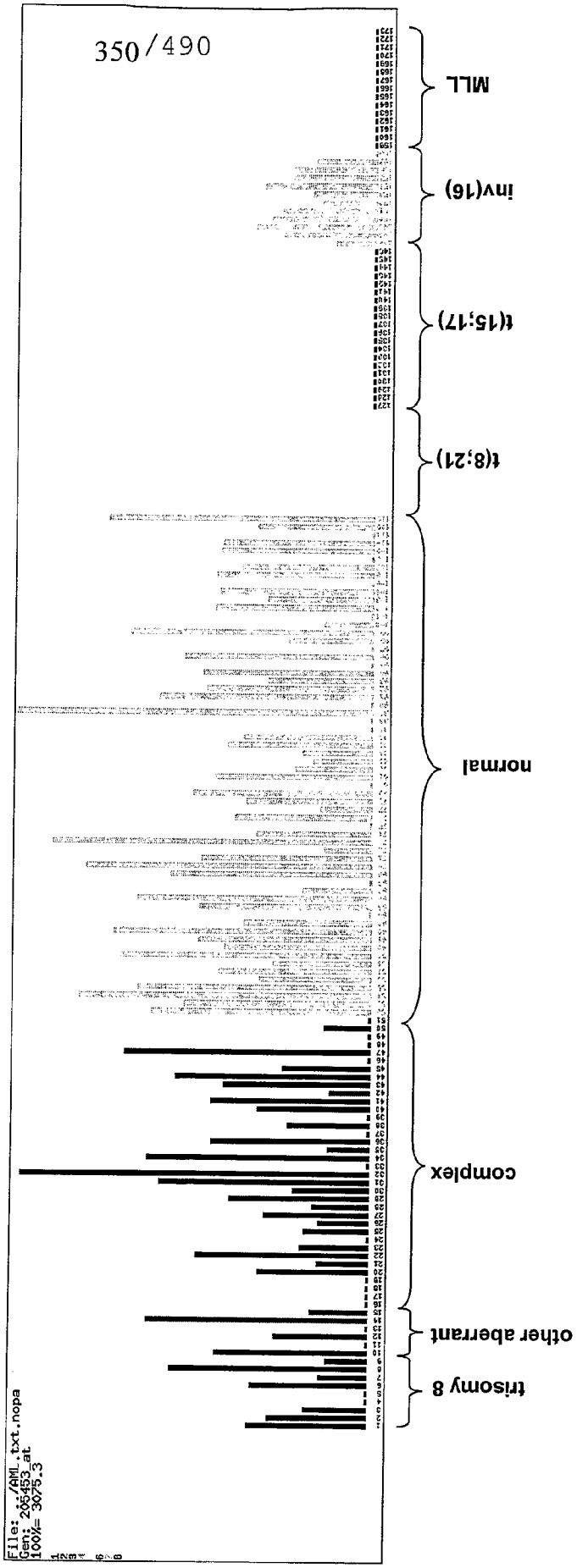

205453_at, HOXB2, normal vs. MLL
File: ../AML.txt.nopa
Gen: 205453_at
100%= 3075.3
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 324

225406_at, TSG, normal vs. MLL

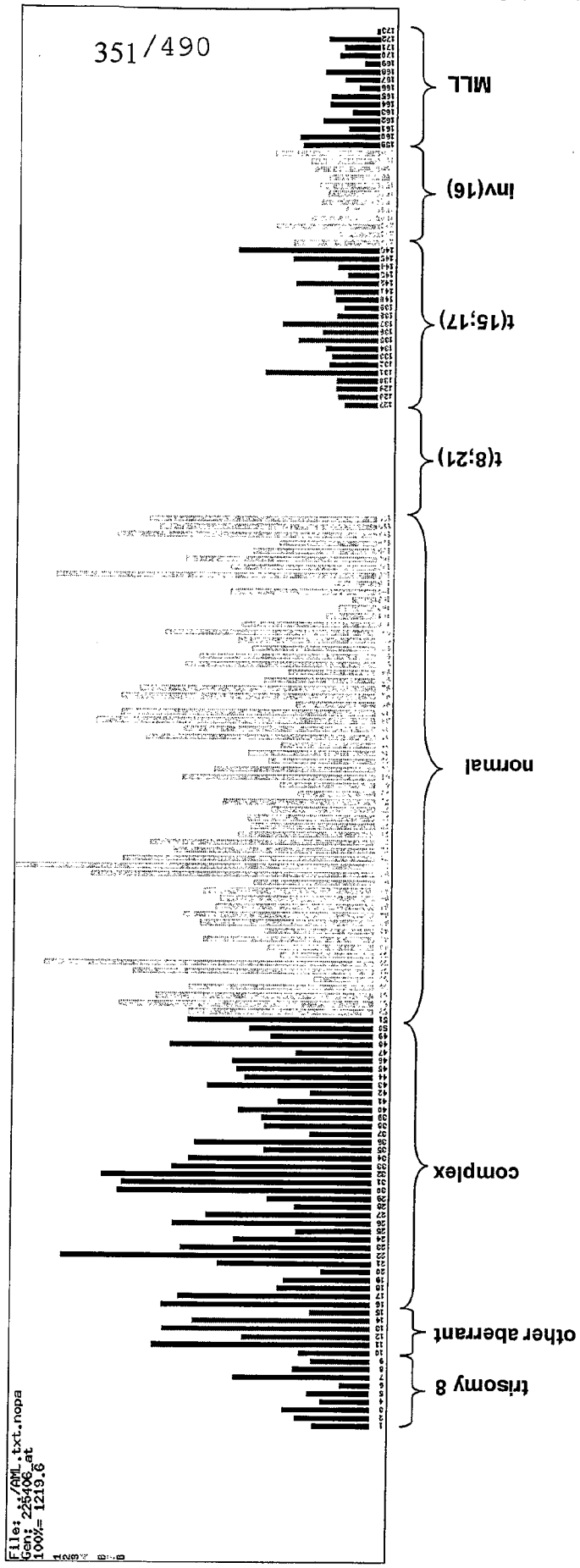


Figure 325

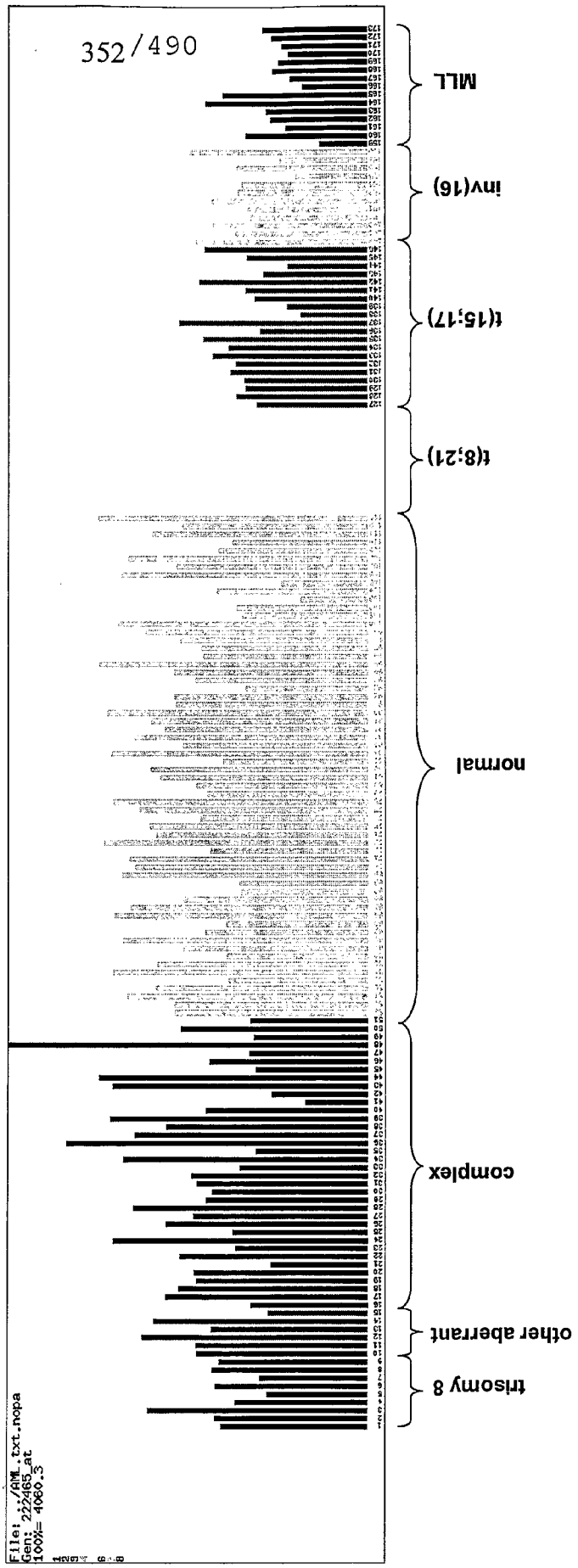

222464_at, C15orf15, normal vs. MLL
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AM_.txt.nopa
Gen: 222464_at
100%= 4060.3

Figure 326

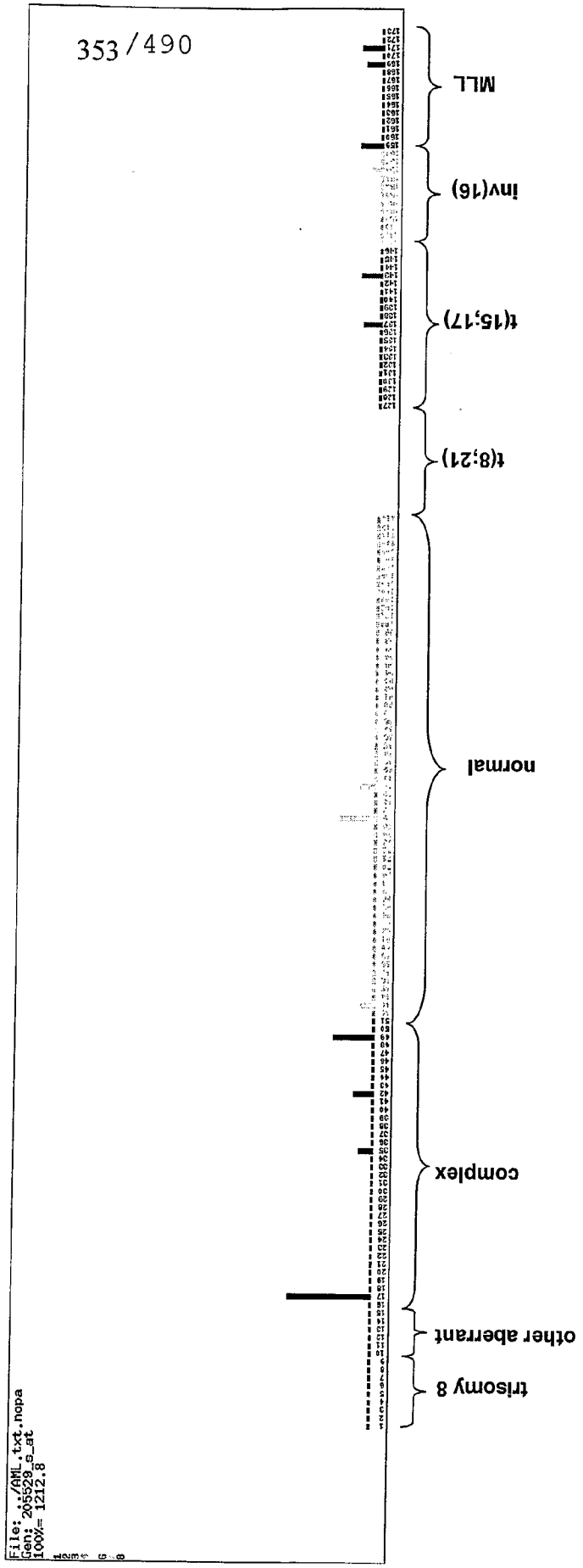

205529_s_at, CBFA2T1, t(8;21) vs. all other AML
File: ../AML.txt.napa
Gen: 205529_s_at
100%= 1212.8
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8

Figure 327

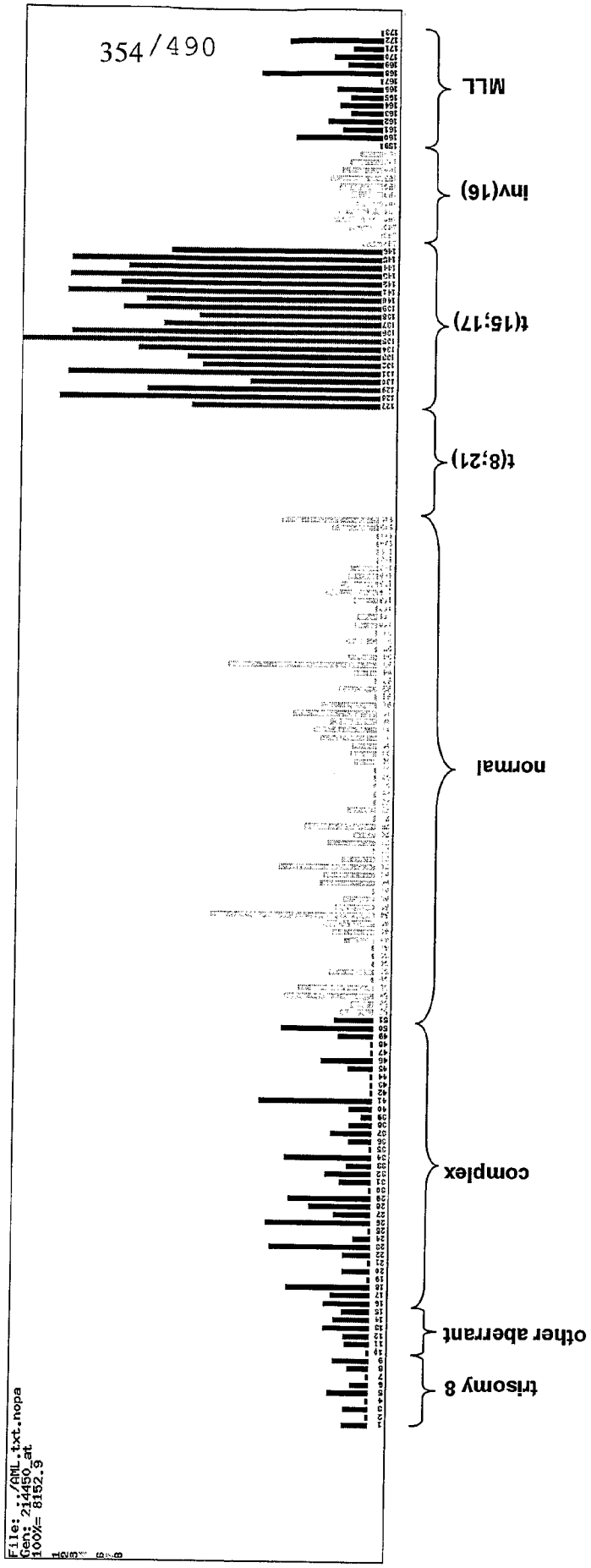

214450_at, CTSW, t(8;21) vs. t(15;17)
File: ../AML.txt.nopa
Gen: 214450_at
100%= 8152.9
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8

Figure 328

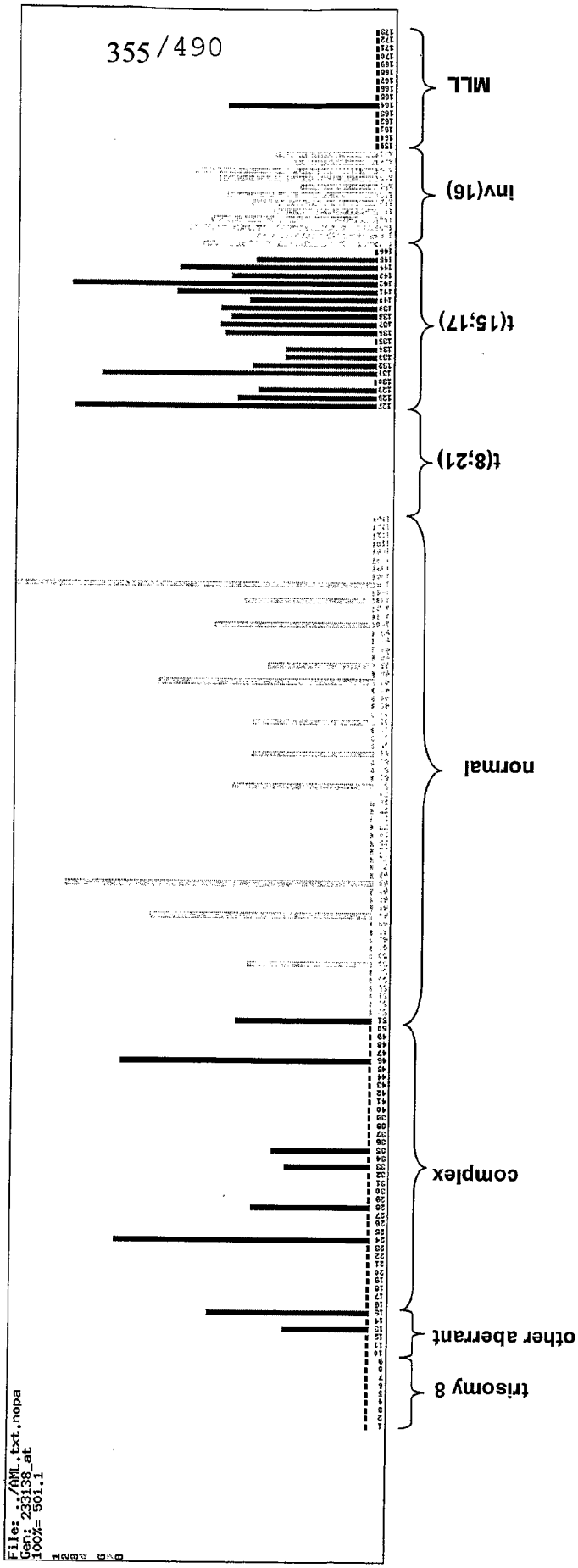
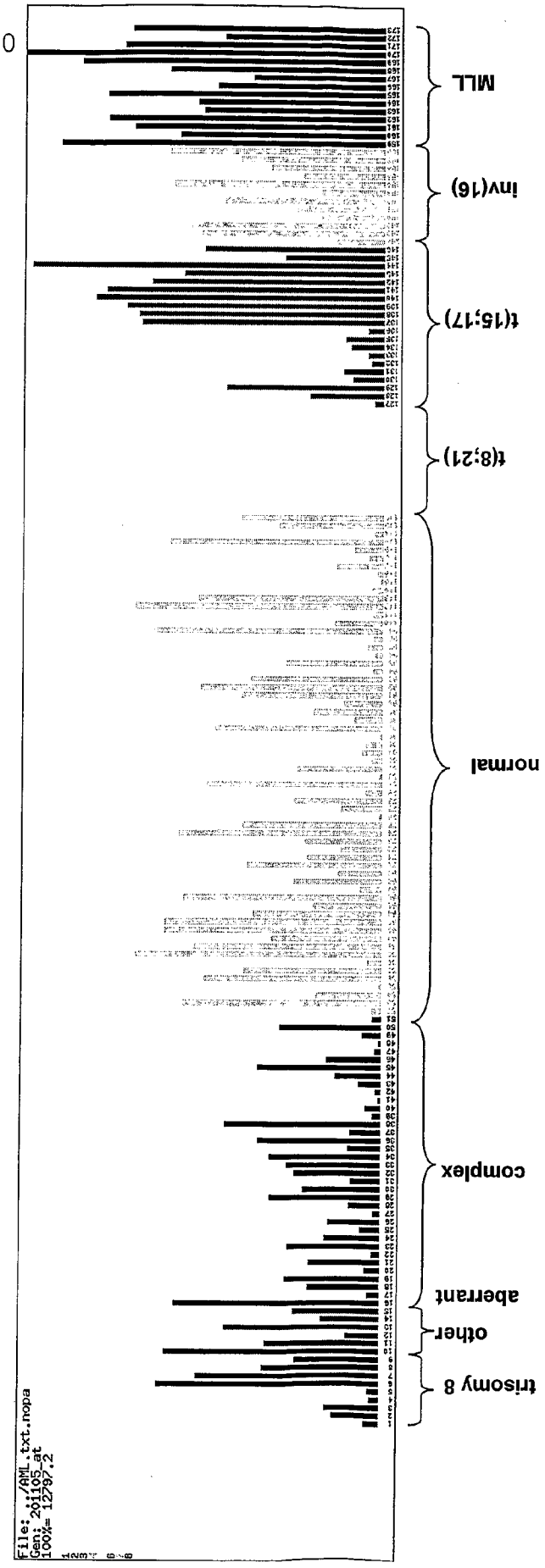

233138_at, t(8;21) vs. inv(16)
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML.txt.nopa
Gene: 233138_at
100%= 501.1

Figure 329

201105_at, LGALS1, t(8;21) vs. MLL

Figure 330



203948_s_at, MPO, t(15;17) vs. all other AML

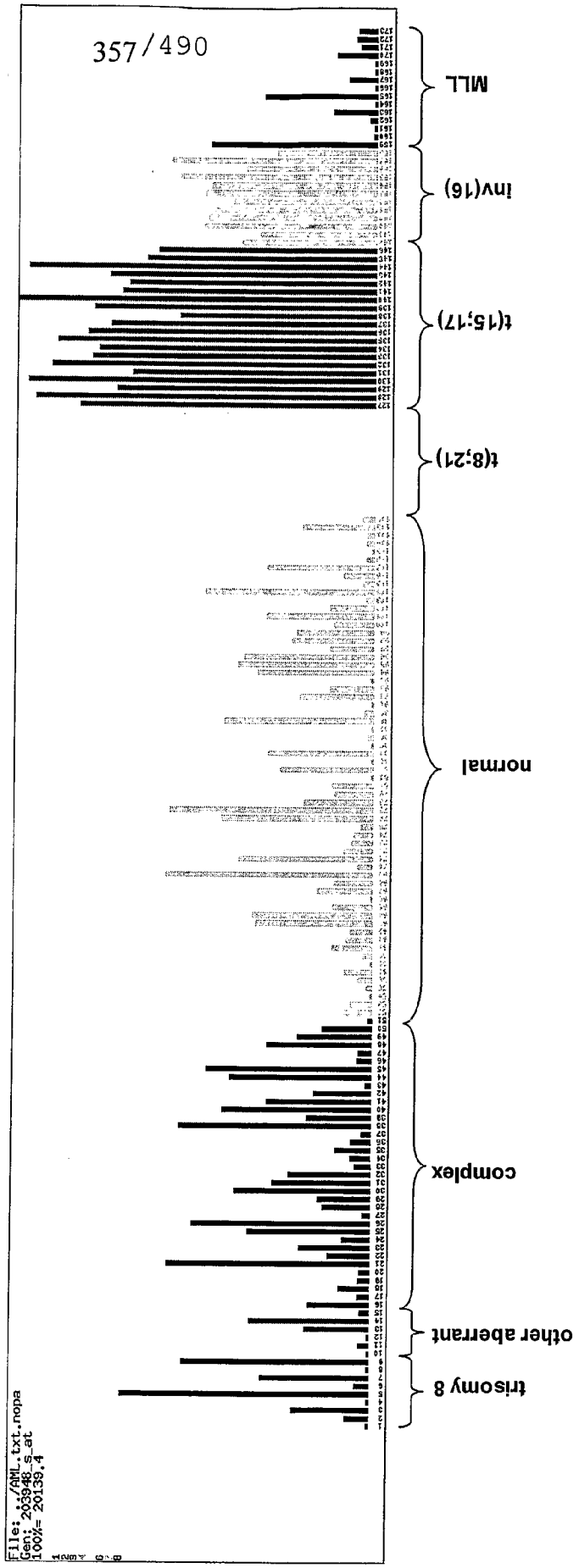
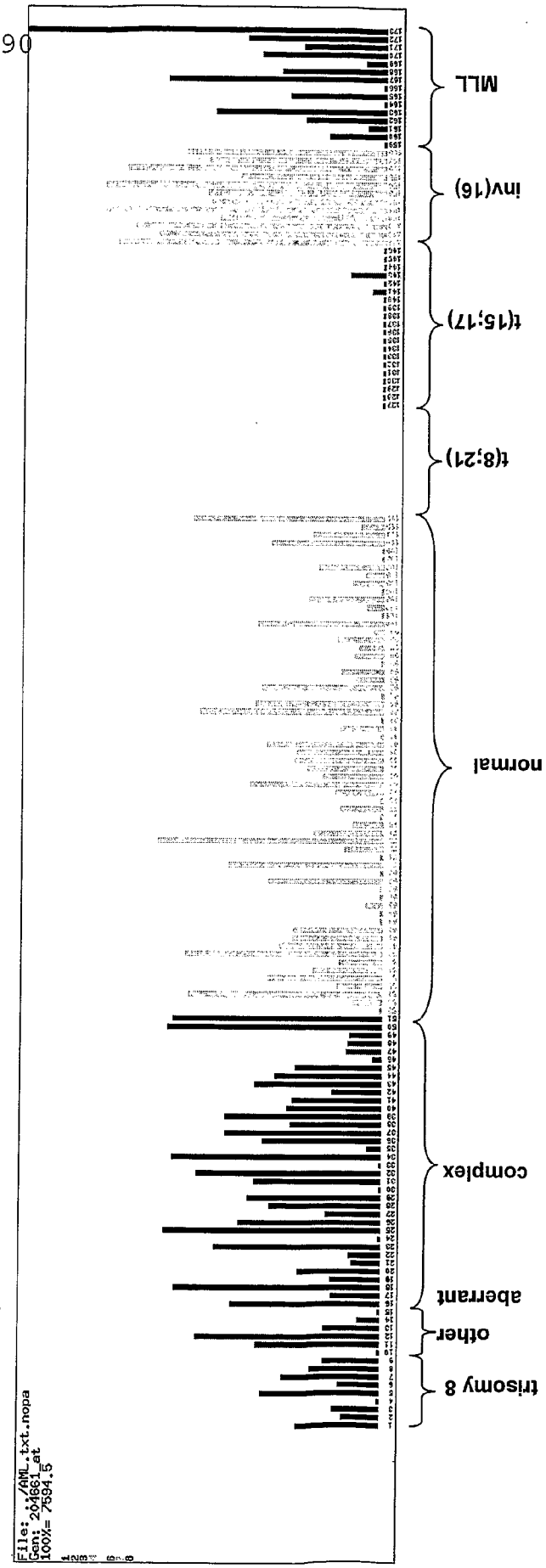


Figure 331

204661_at, CDW52, t(15;17) vs. inv(16)

Figure 332



205624_at, CPA3, t(15;17) vs. MLL

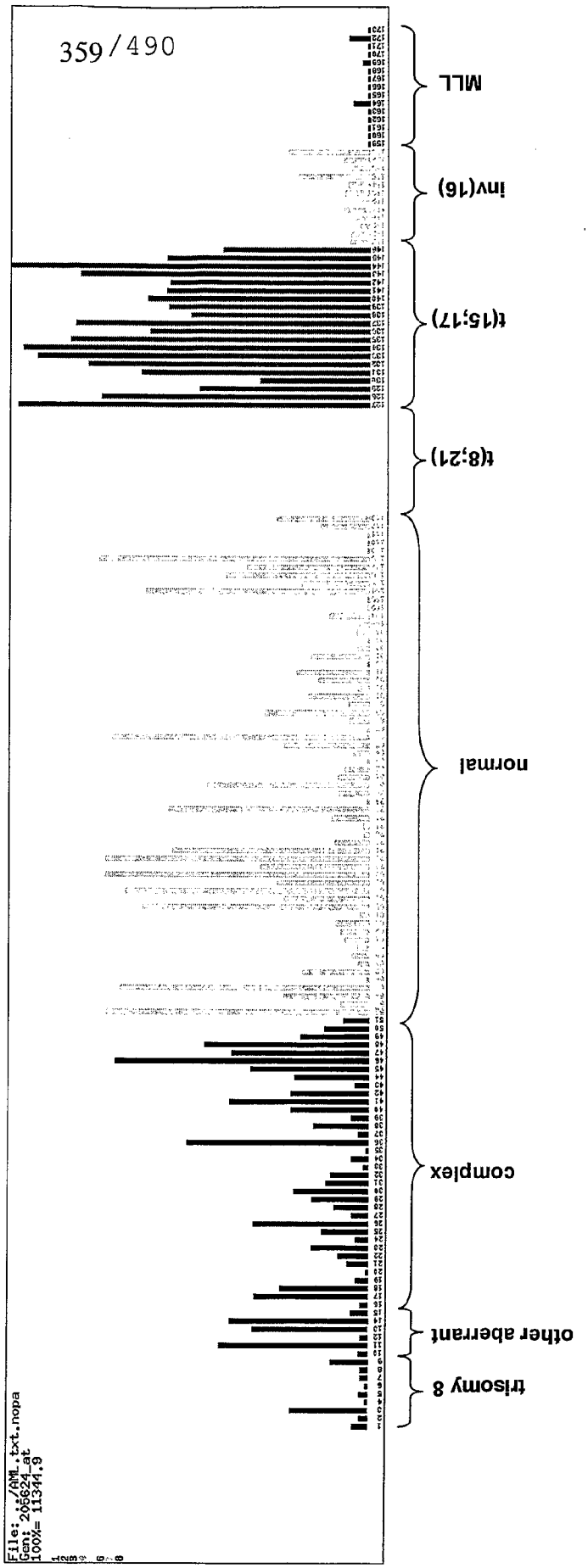


Figure 333

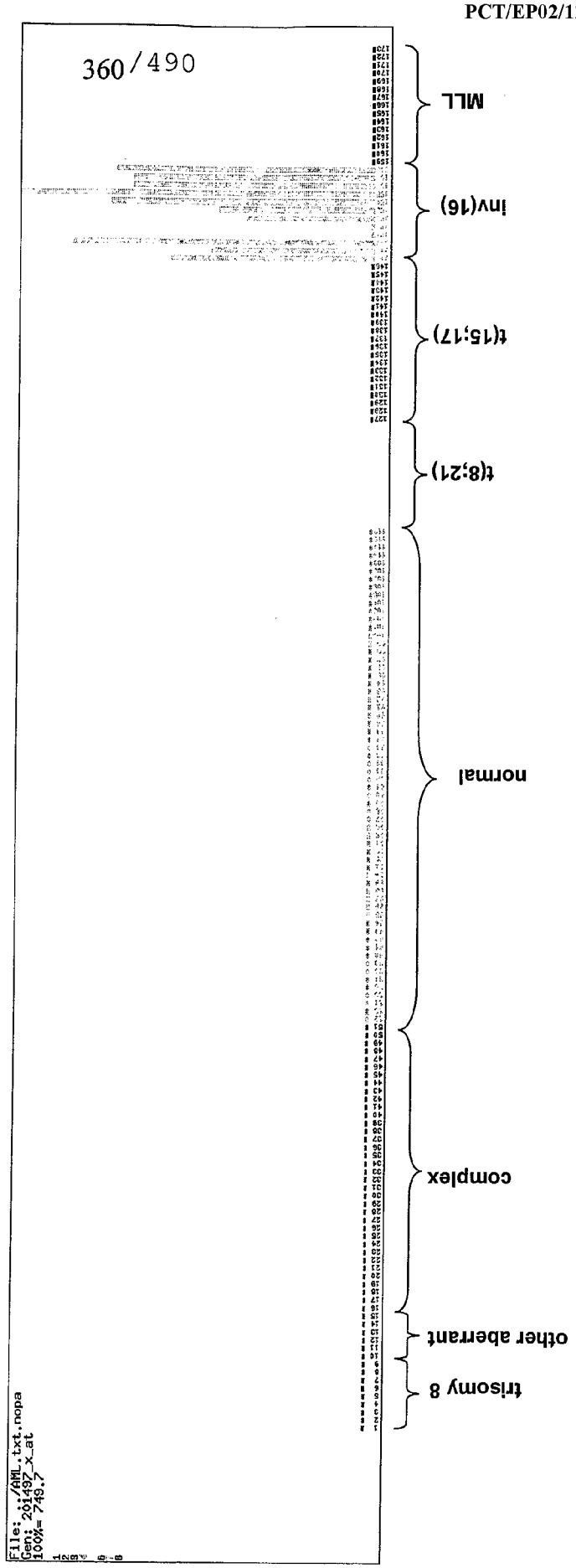

201497_x_at, MYH11, inv(16) vs. all other AML
File: /AML.txt.nopa
Gen: 201497_x_at
100%= 749.7
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8

Figure 334

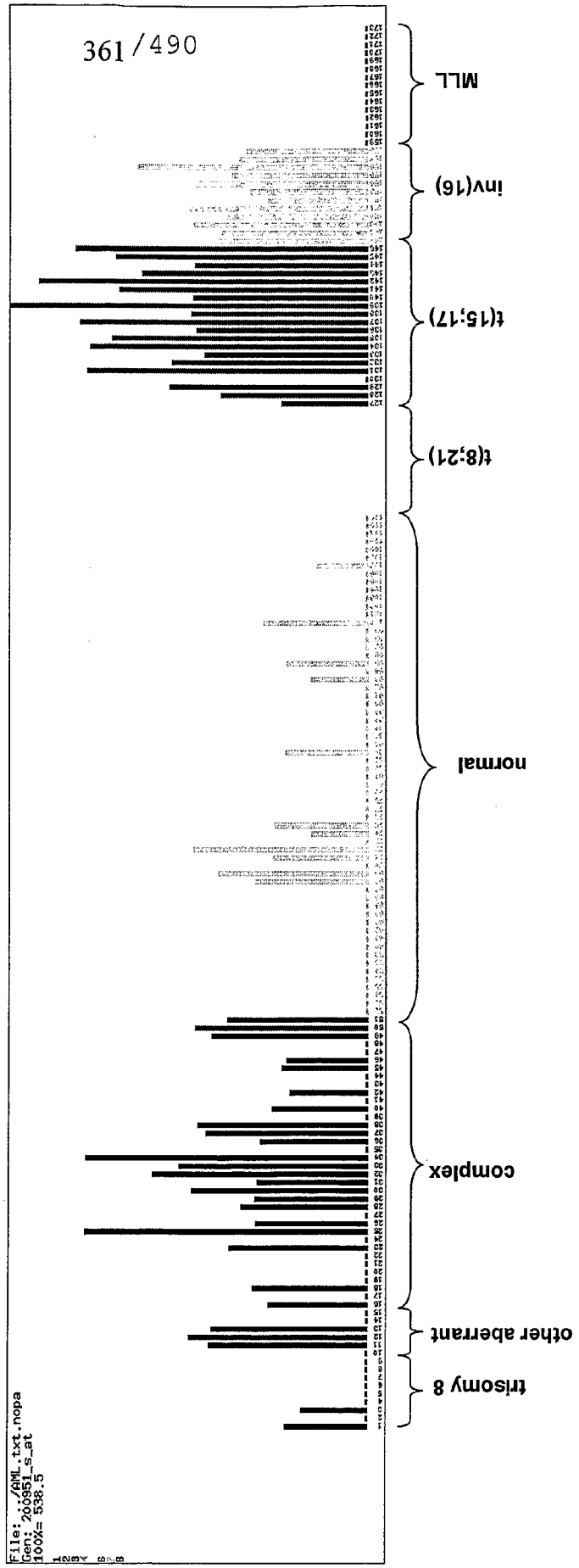
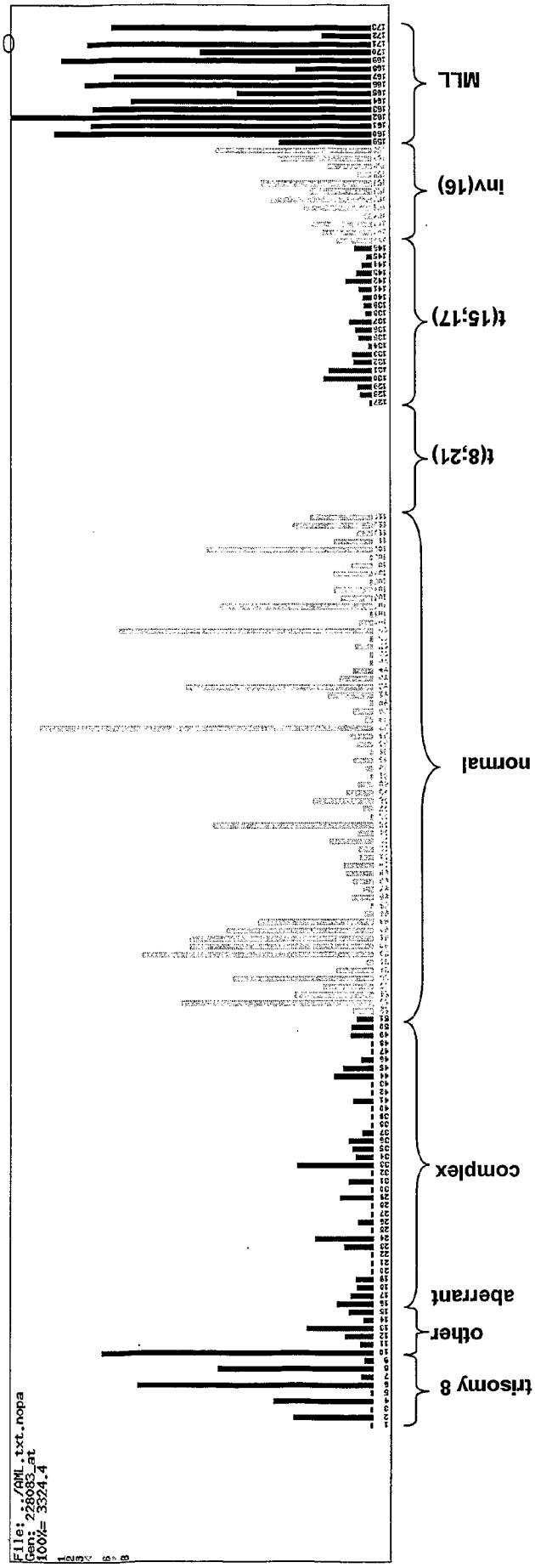

200951_s_at, CCND2, inv(16) vs. MLL
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML_txt.nopa
Gen: 200951_s_at
100%= 538.5

Figure 335

228083_at, MLL vs. all other AML

Figure 336



635_s_at, PPP2R5B, other low

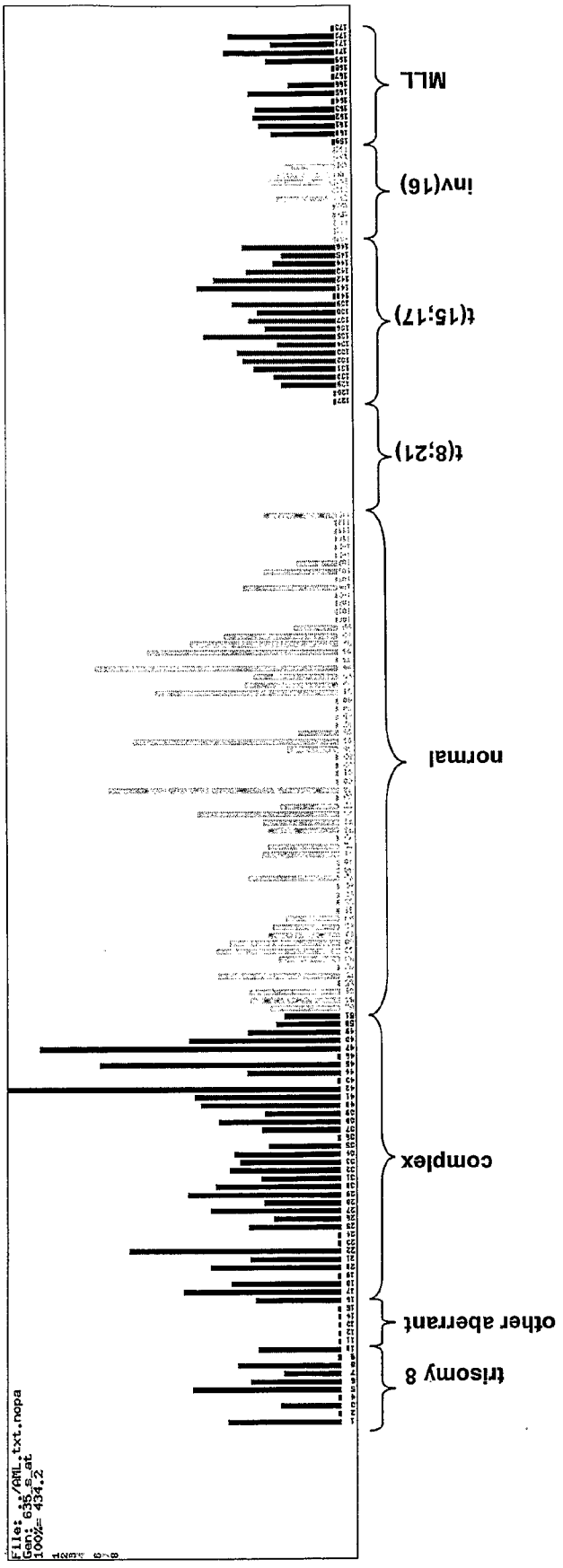


Figure 337

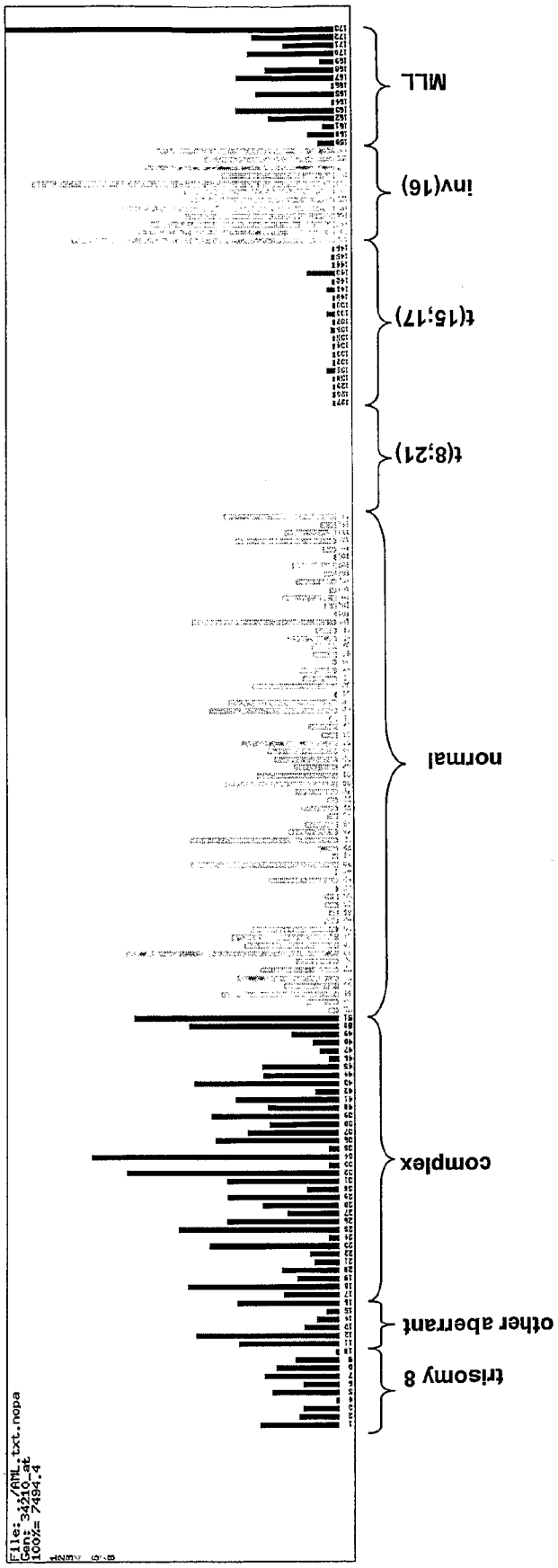

34210_at, CDW52, AML t(15;17) low
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8
File: ../AML_txt.nopa
Gene: 34210_at
100%= 7494.4

Figure 338

38487_at, FLJ12442, AML t(15;17) high

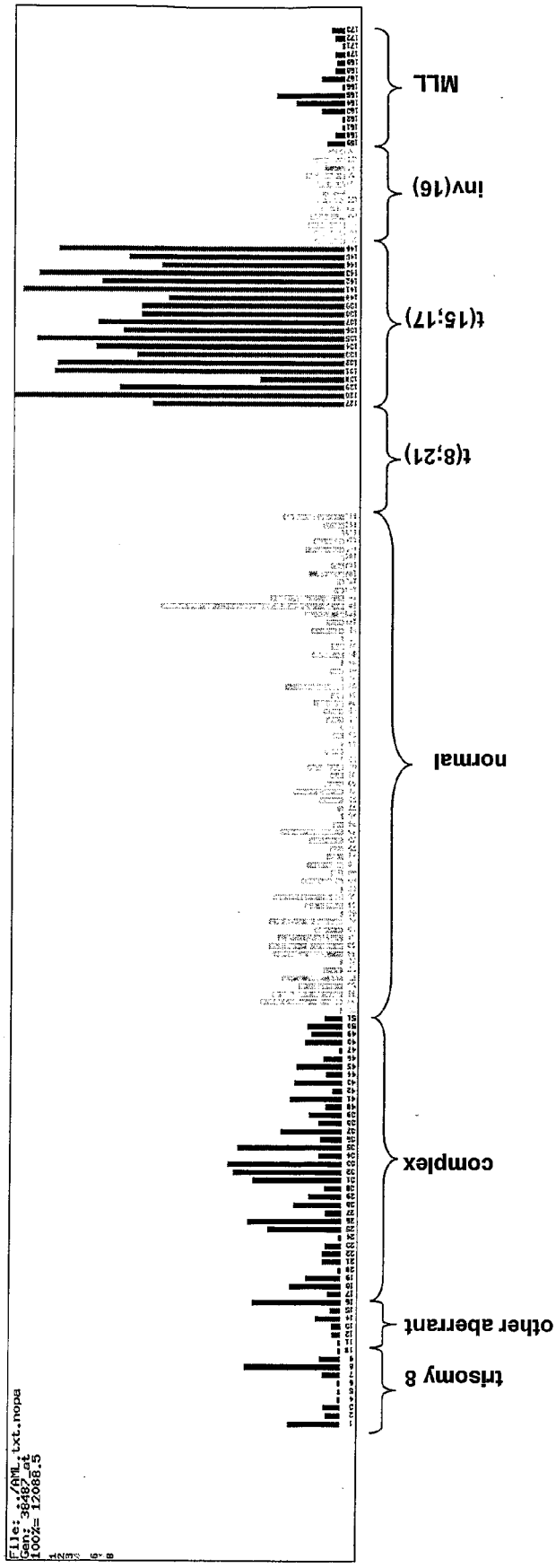


Figure 339

200675_at, CD81, AML inv(16) low

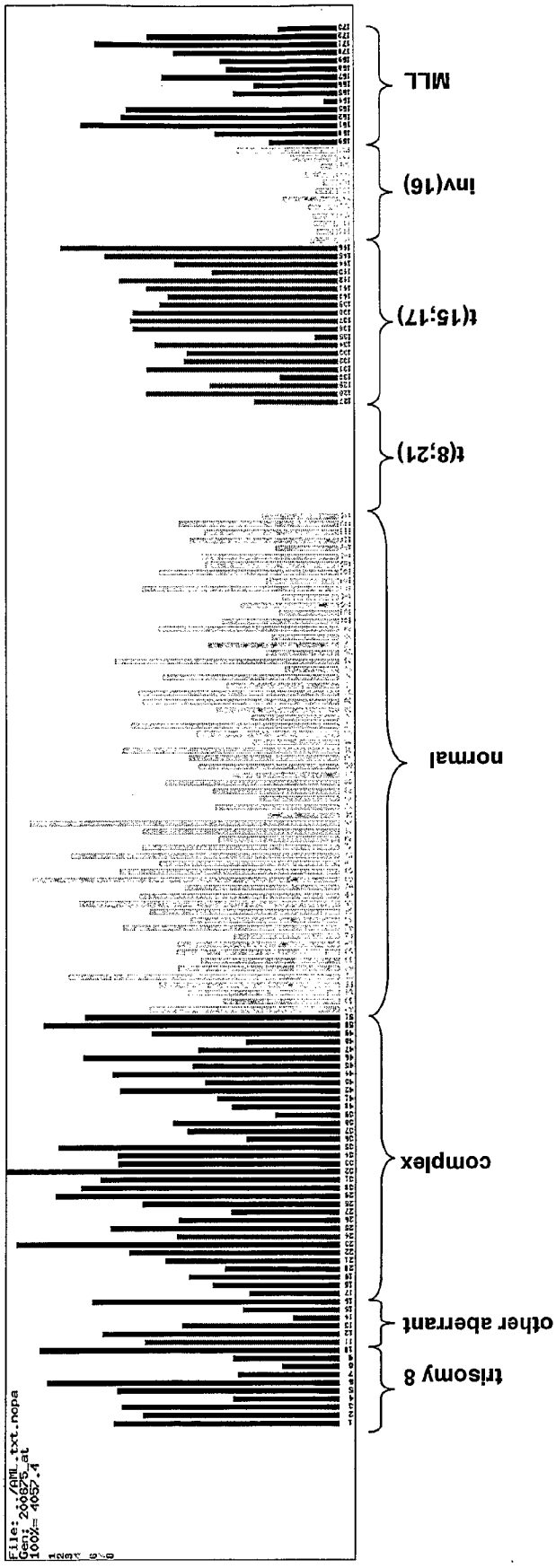


Figure 340

201137_s_at, HLA-DPB1, AML t(15;17) low

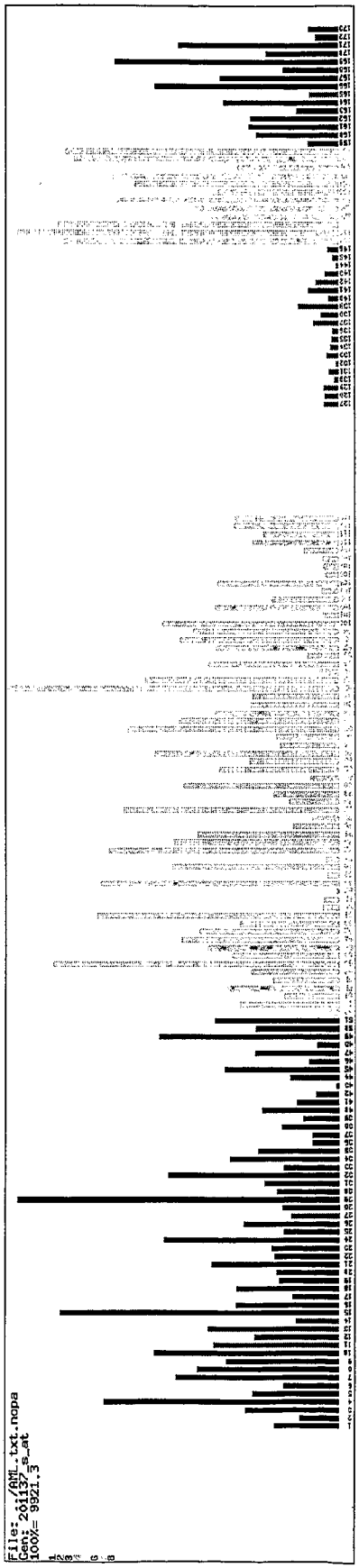


Figure 341

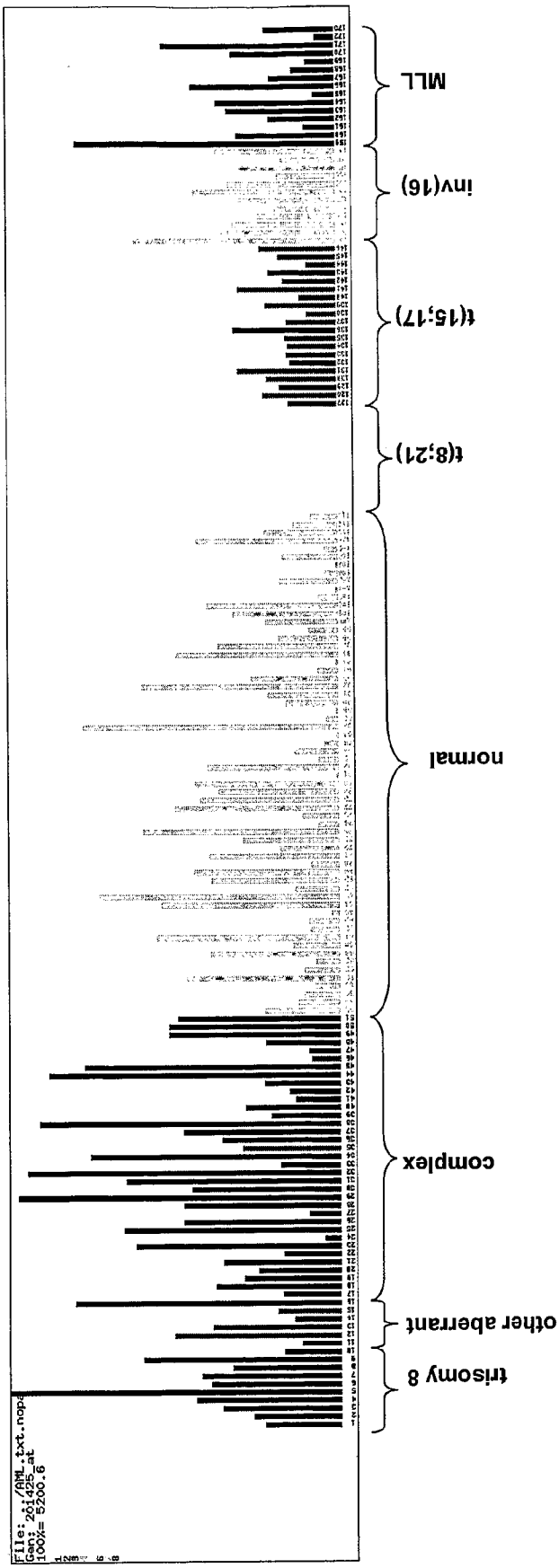

201425_at, ALDH2, AML t(8;21) low
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 342

201496_x_at, MYH11, AML inv(16) high

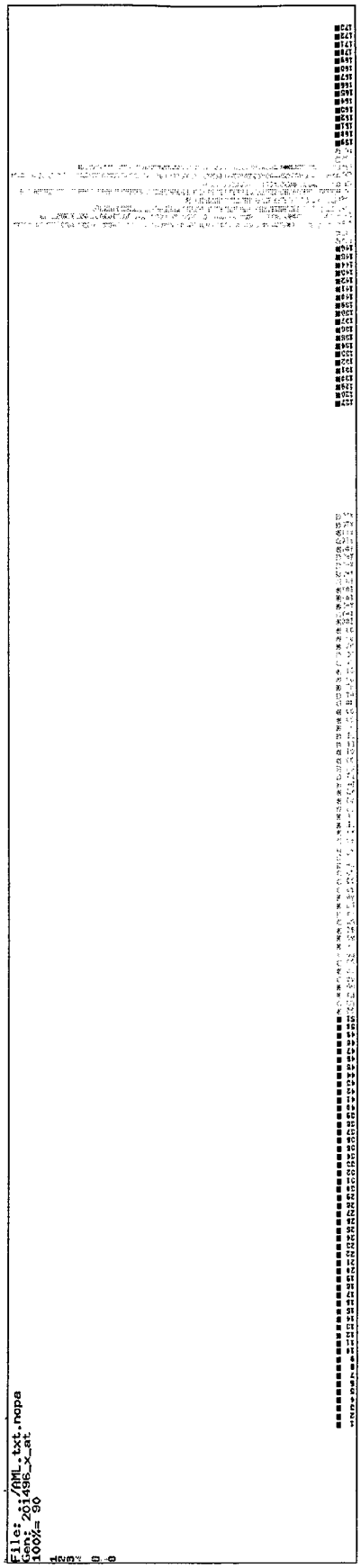


Figure 343

201497_x_at, MYH11, AML inv(16) high

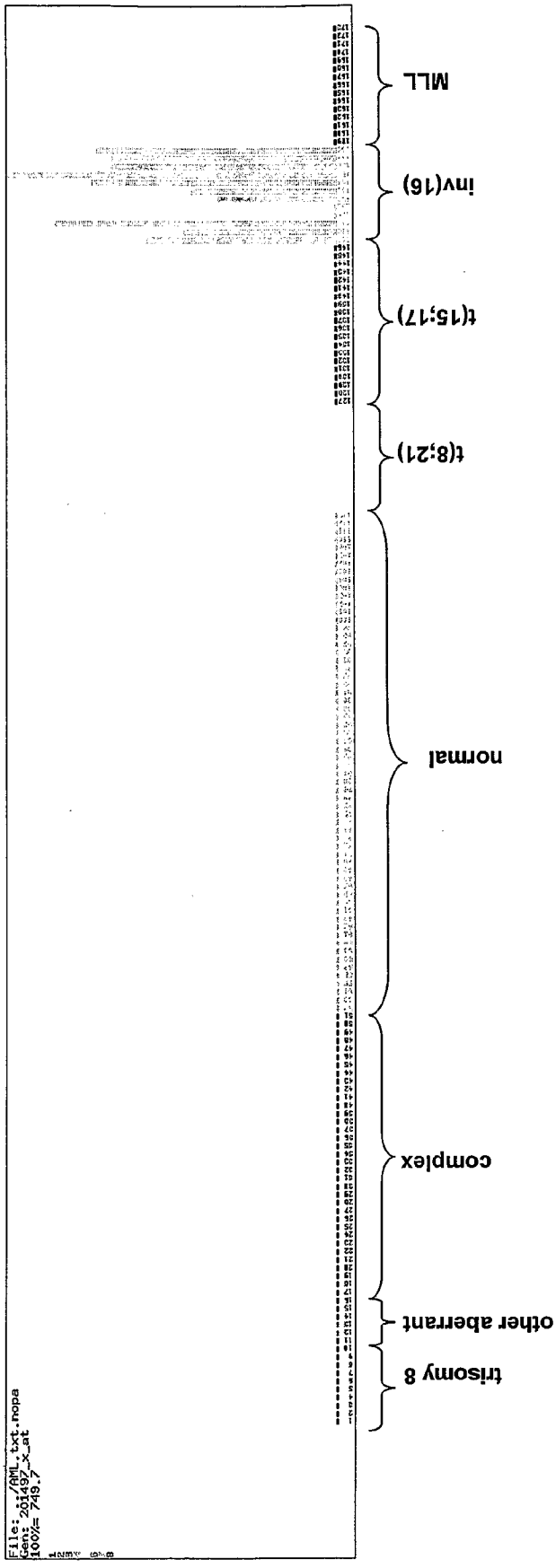


Figure 344

201596_x_at, KRT18, AML t(8;21) low

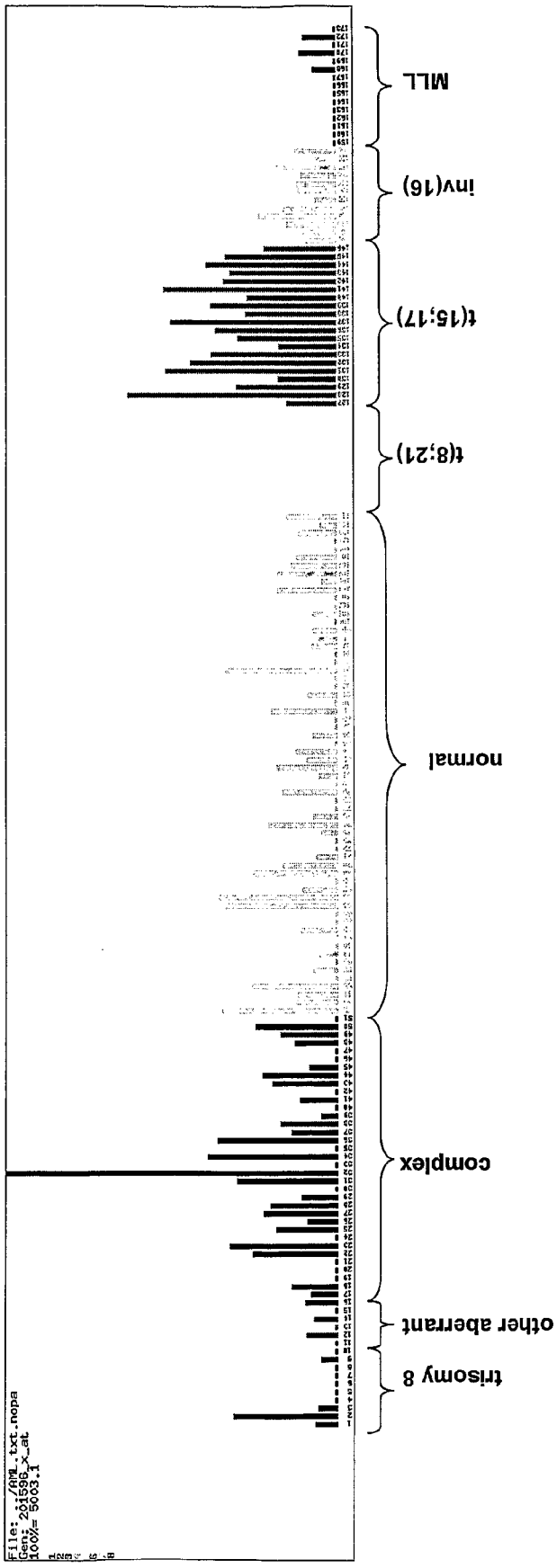


Figure 345

202085_at, TJP2, AML inv(16) low

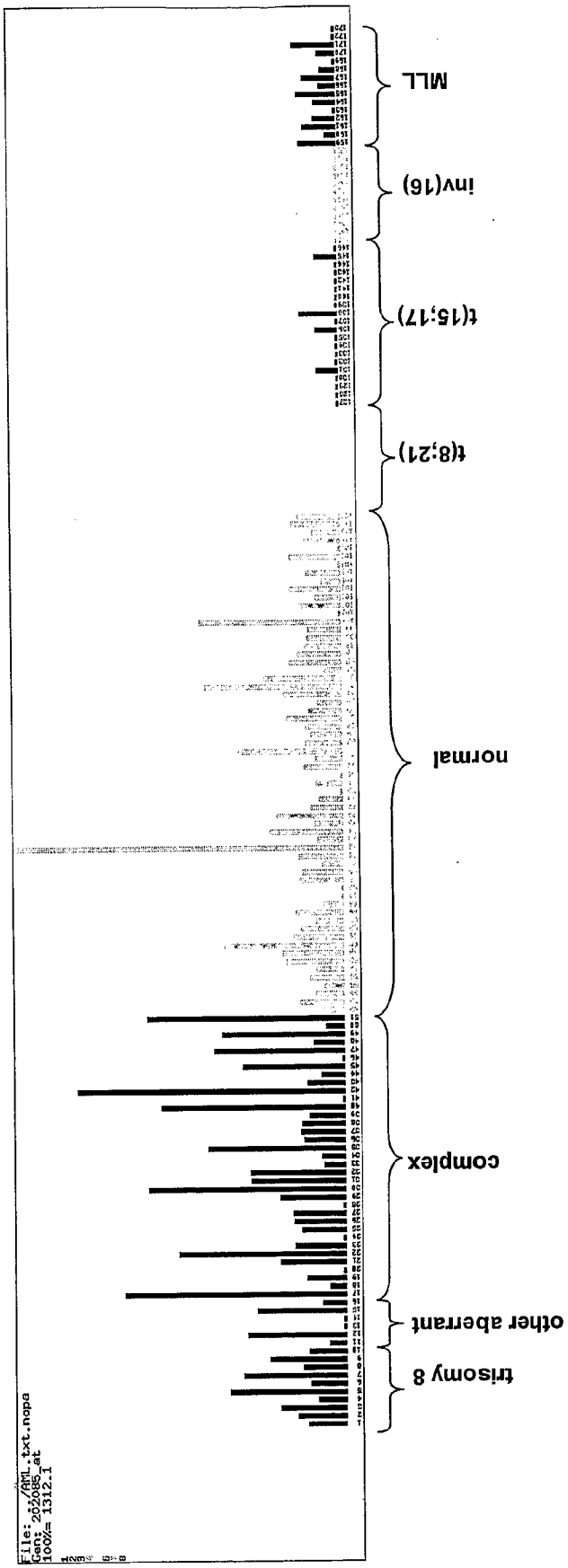


Figure 346

202619_s_at, PLOD2, AML MLL low

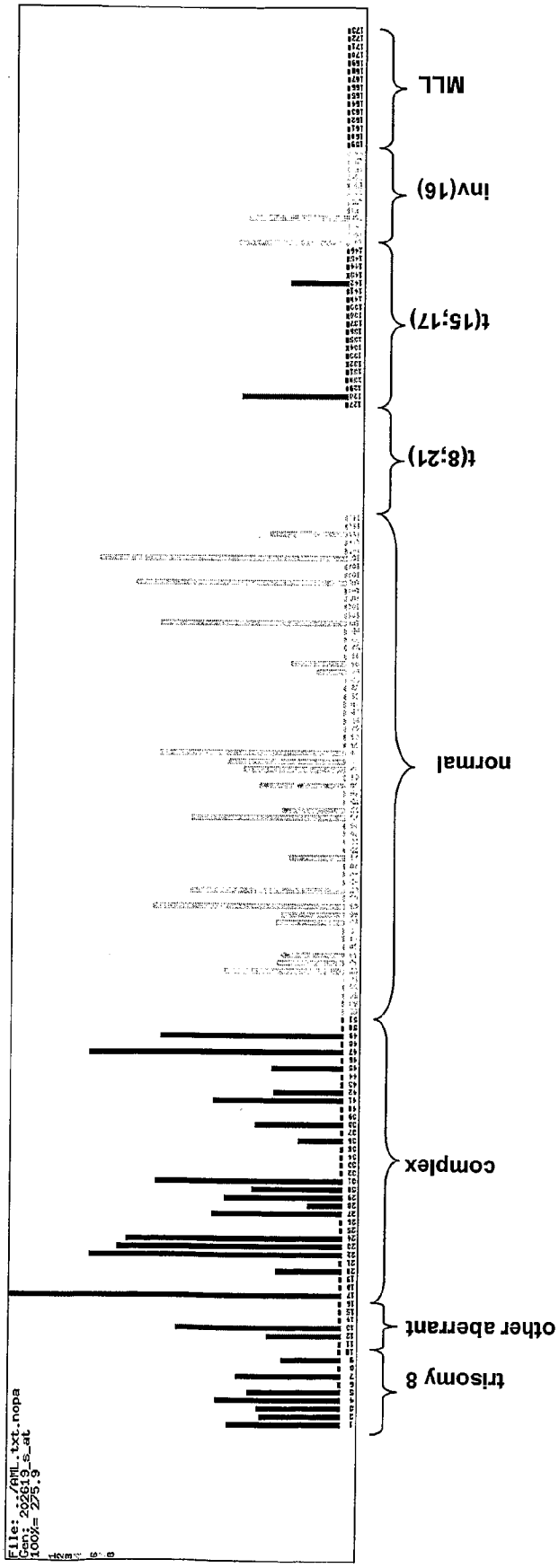


Figure 347

202718_at, IGFBP2, AML t(15;17) high

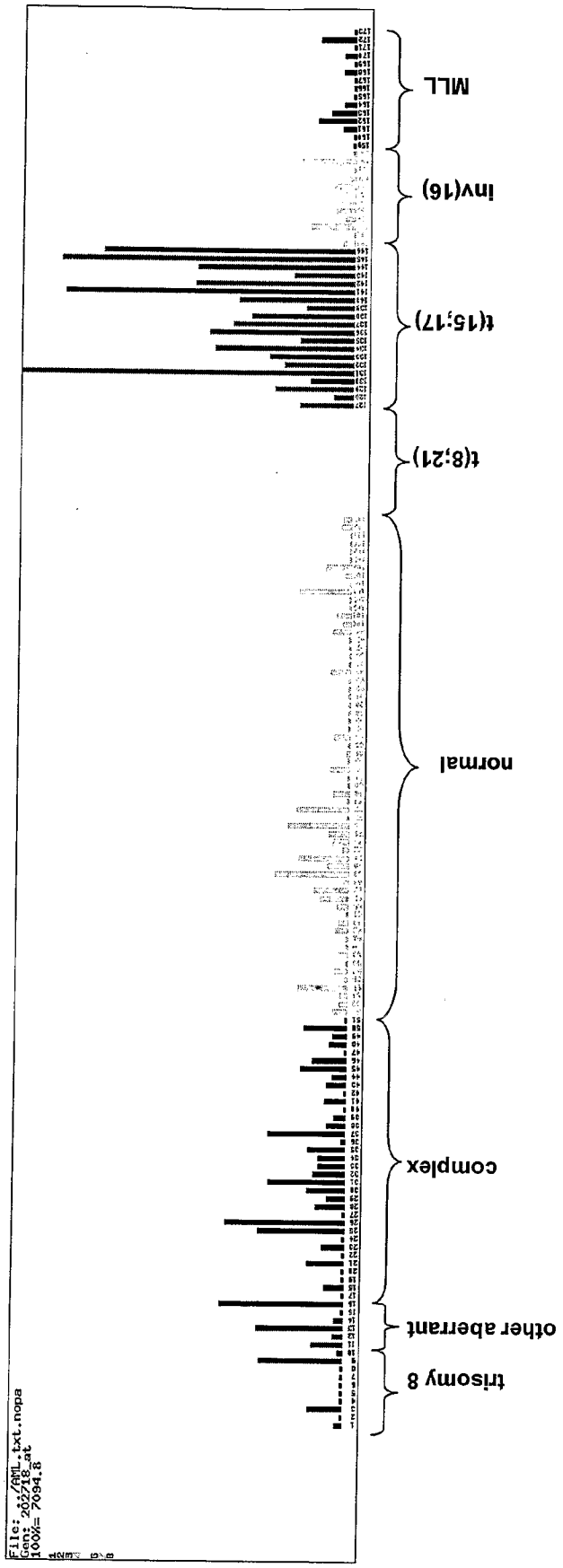


Figure 348

202746_at, AML MLL low

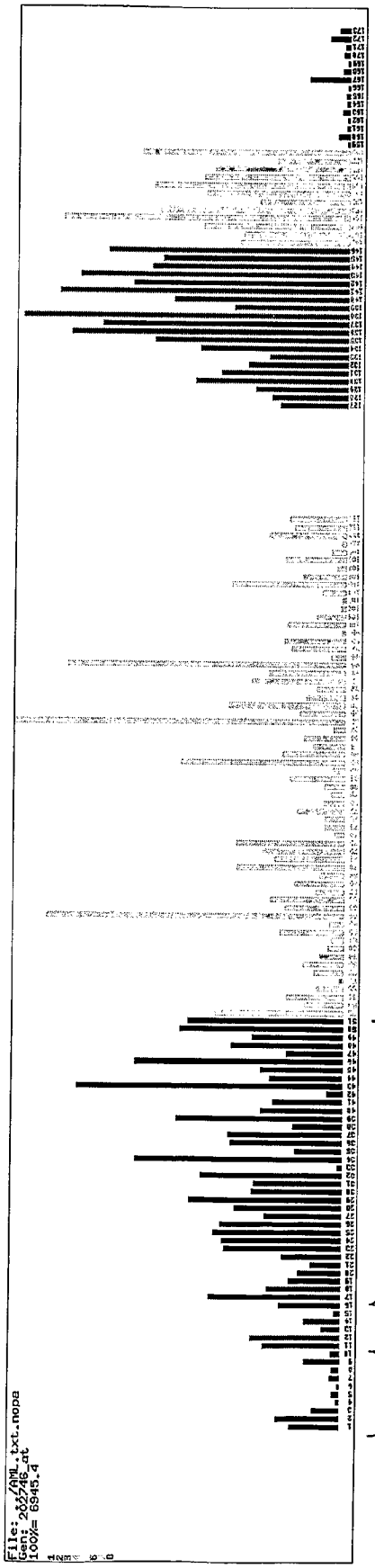


Figure 349

203074_at, ANXA8, AML t(15;17) high

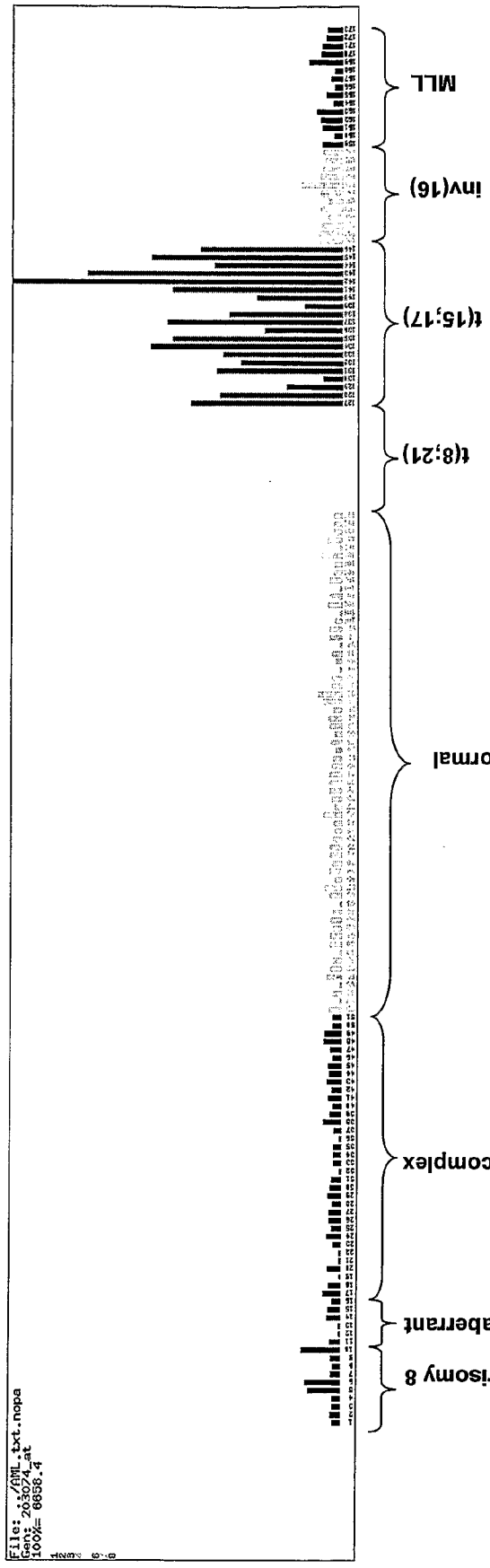


Figure 350

203092_at, TIMM44, AML inv(16) low

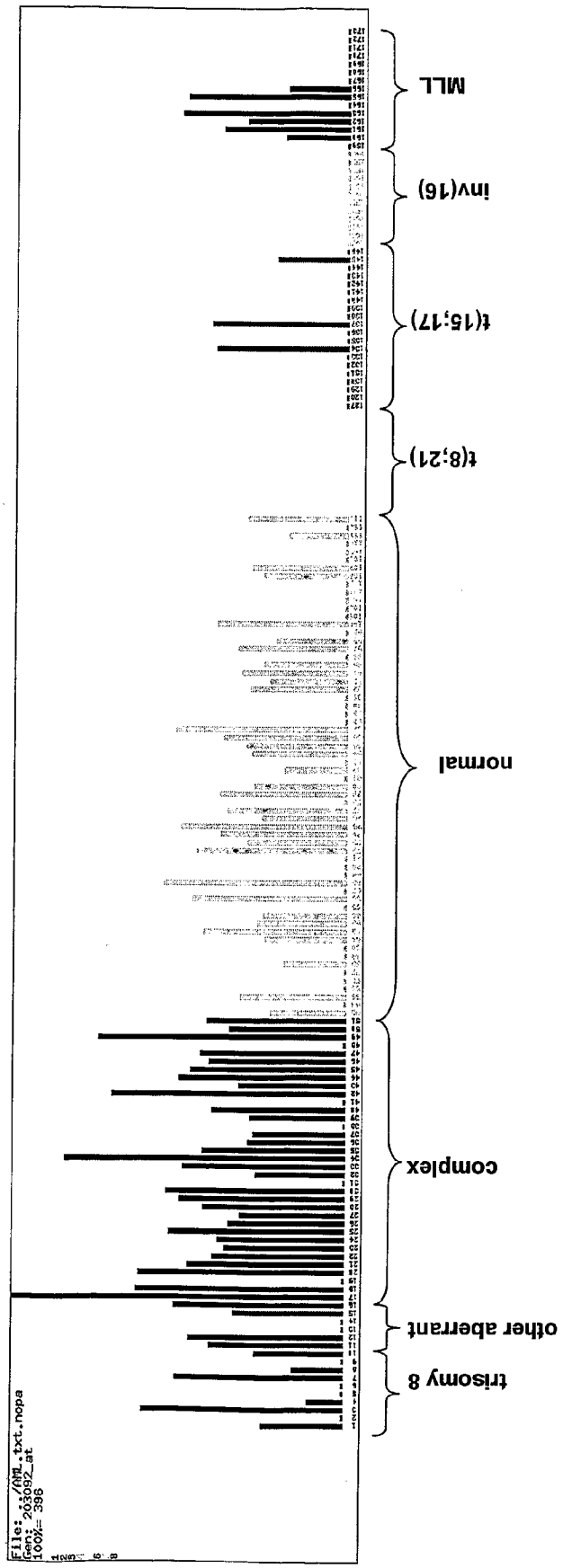


Figure 351

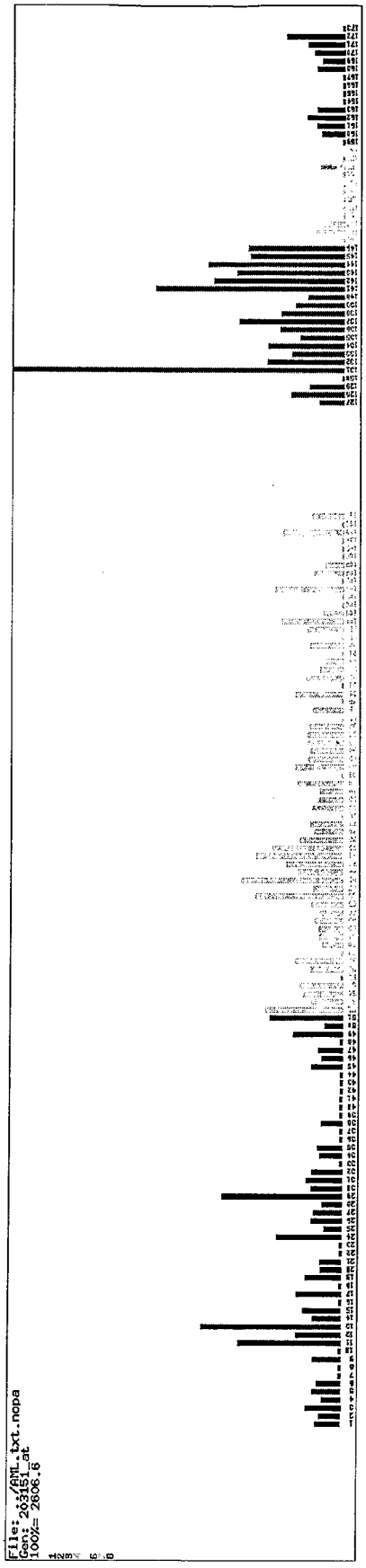

203151_at, MAP1A, AML t(8;21) low
File: /AML.txt.nopa
Cent: 203151_at
100%= 2606.8
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 352

205528_s_at, CBFA2T1, AML t(8;21) high

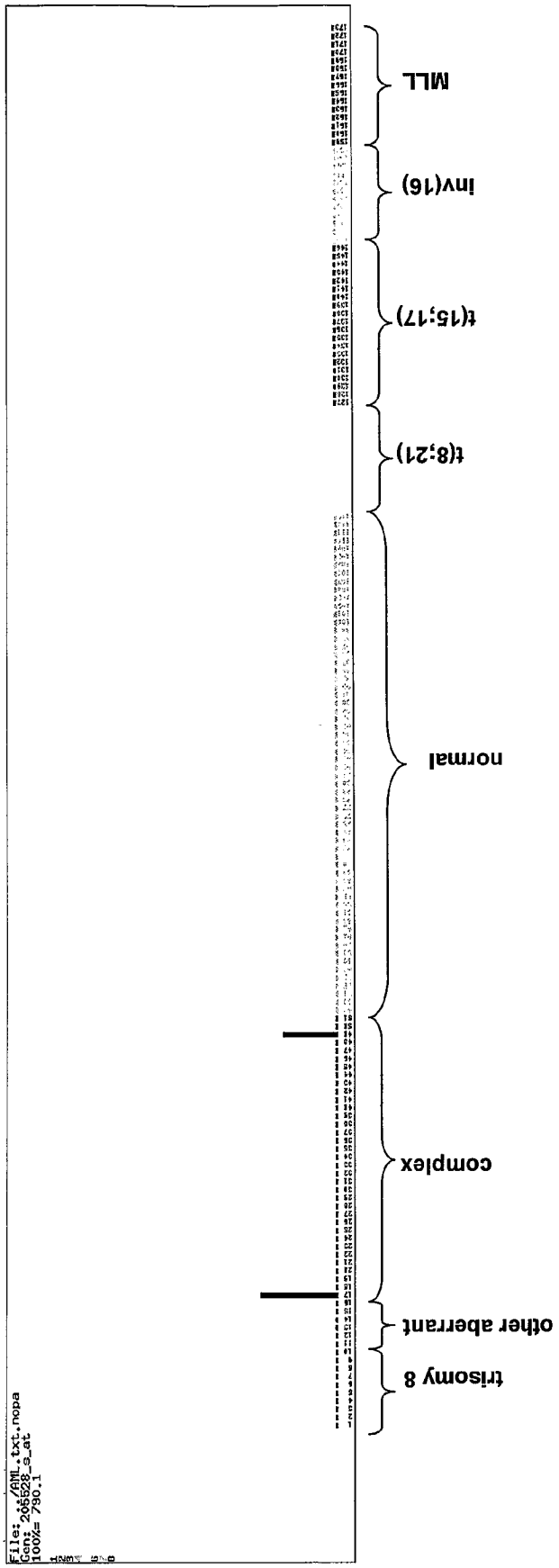


Figure 353

205529_s_at, CBFA2T1, AML t(8;21) high

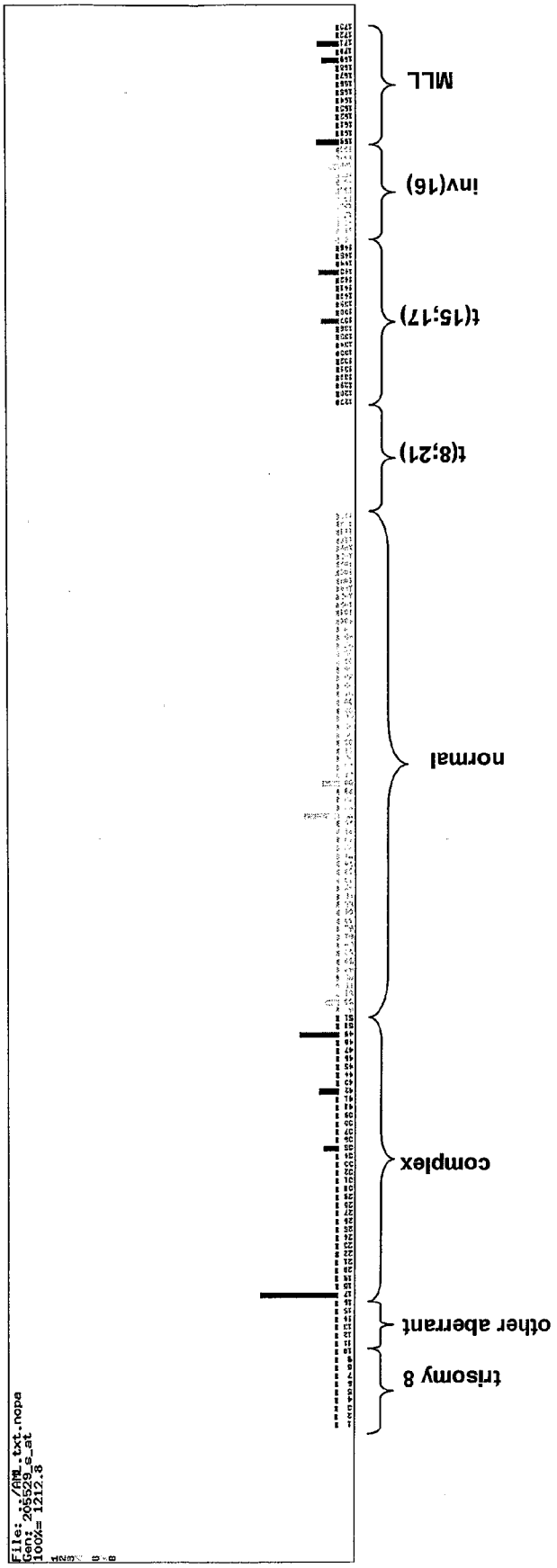


Figure 354

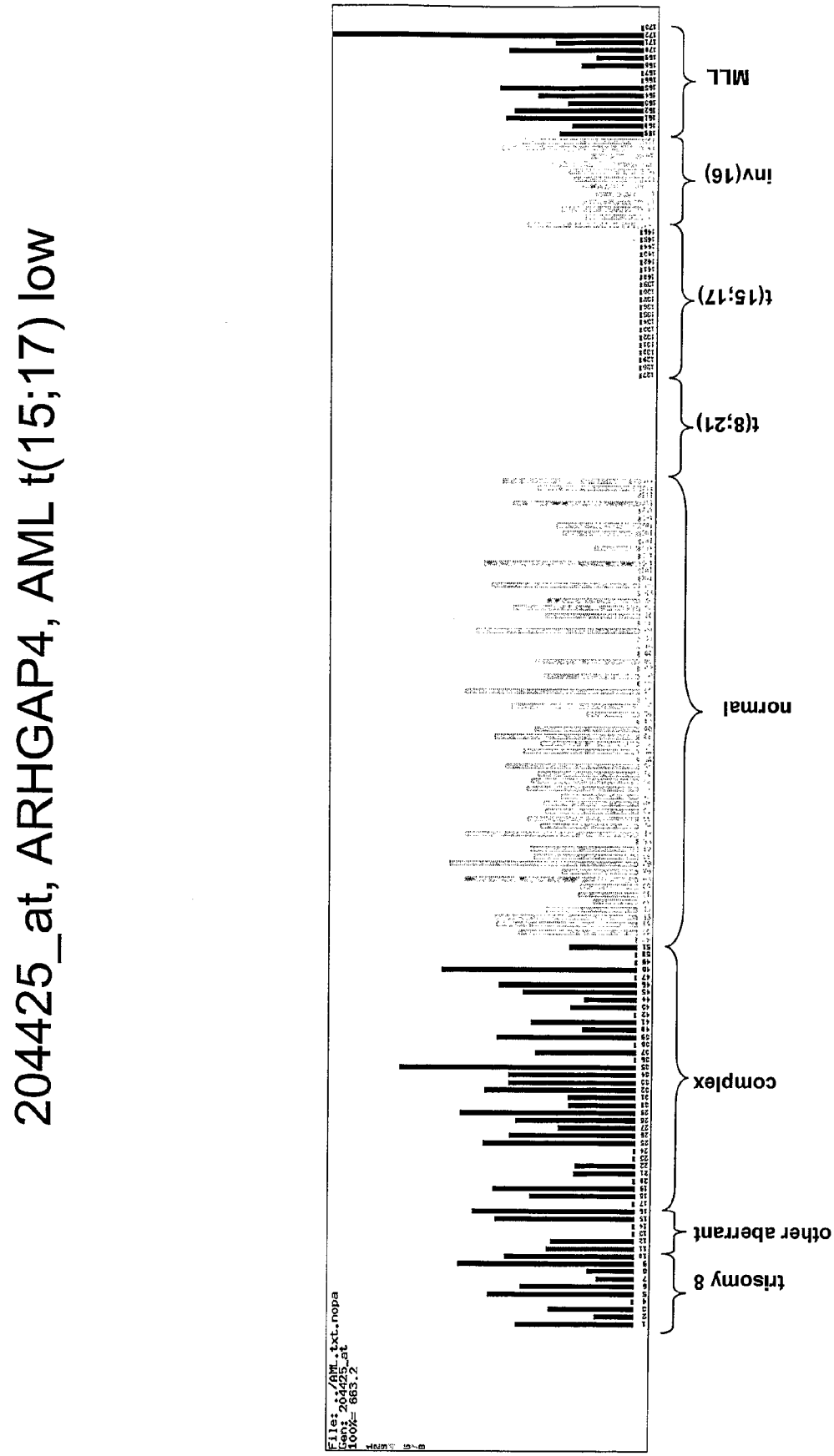

204425_at, ARHGAP4, AML t(15;17) low
File: /AML.txt.nopa
Gene: 204425_at
100%= 863.2
trisomy 8
other aberrant
complex
normal
t(8;21)
t(15;17)
inv(16)
MLL

Figure 355

205366_s_at, HOXB6, AML t(8;21) low, AML t(15;17) low, AML inv(16) low, AML MLL low

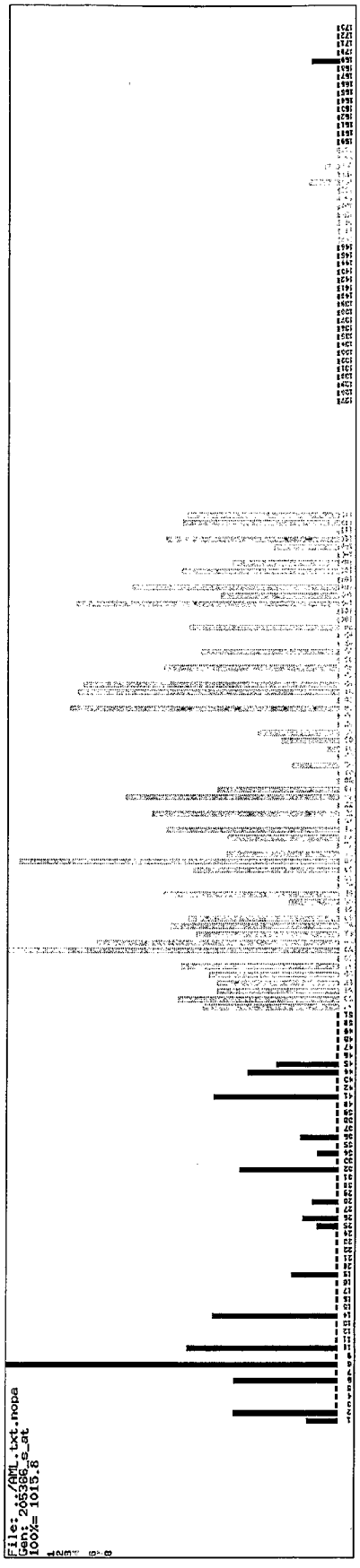


Figure 356

205380_at, PDZK1, other high

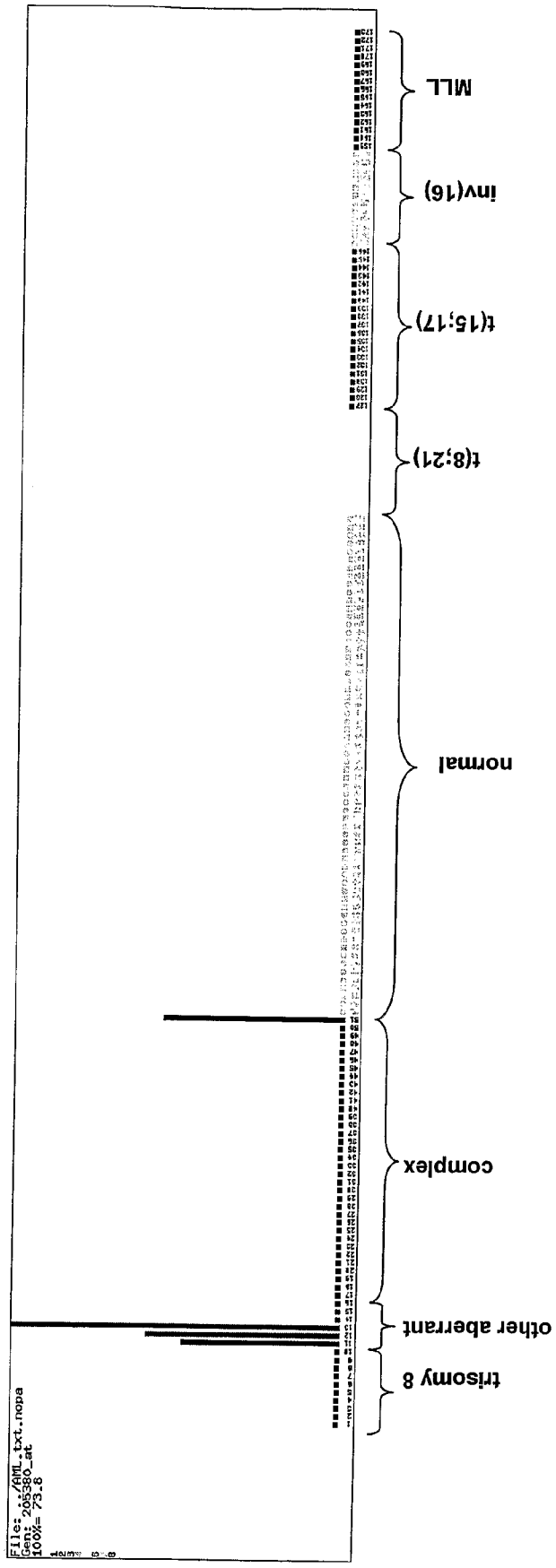


Figure 357

205472_s_at, DACH, AML MLL high

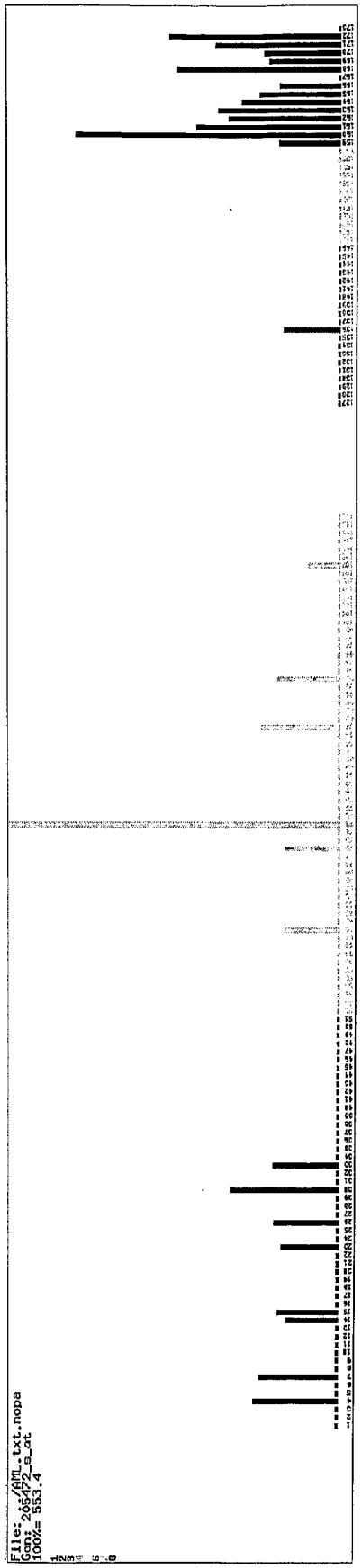


Figure 358

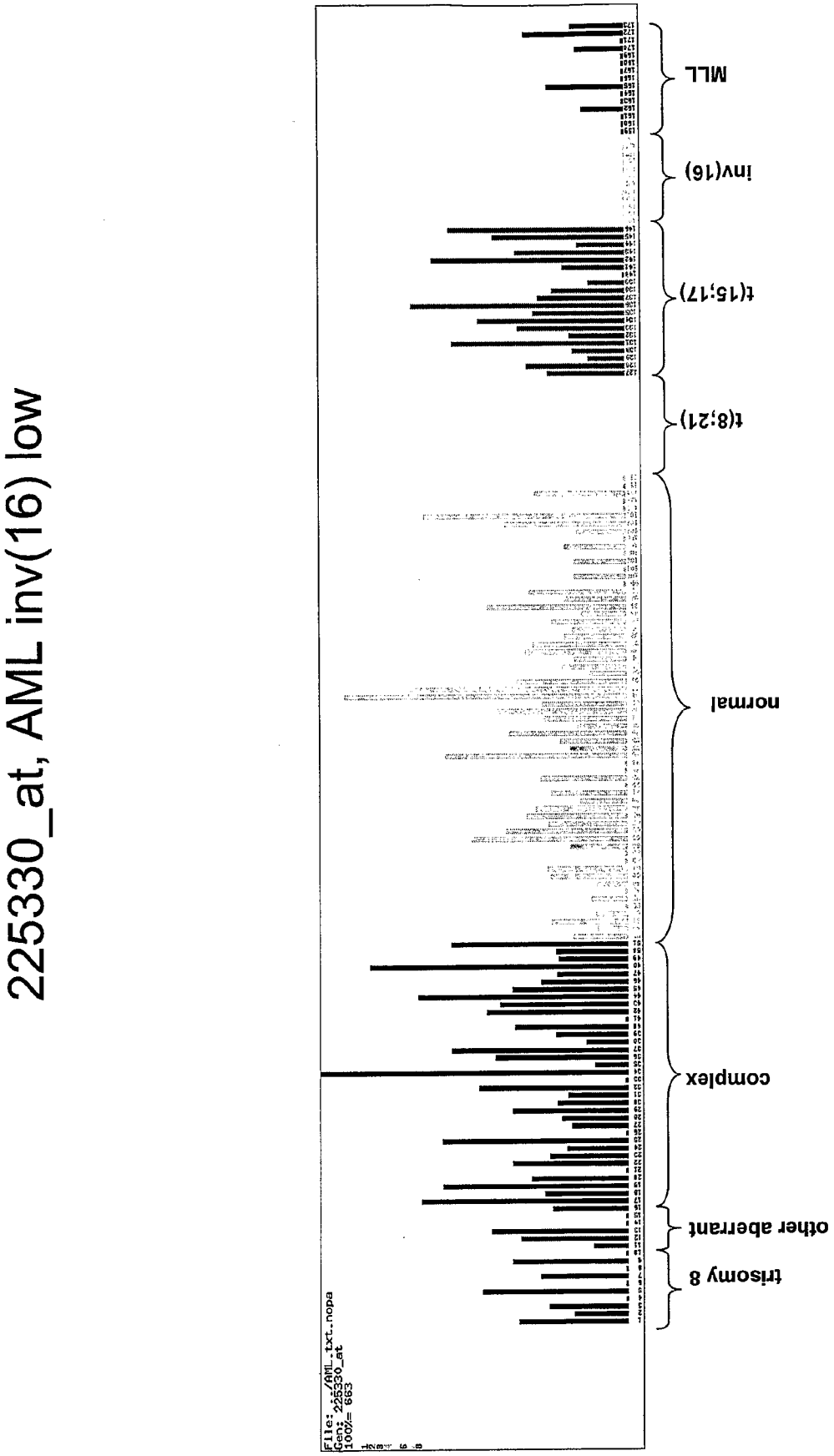

225330_at, AML inv(16) low
MLL
inv(16)
t(15;17)
t(8;21)
normal
complex
other aberrant
trisomy 8

Figure 359

228660_x_at, SEMA4F, other high

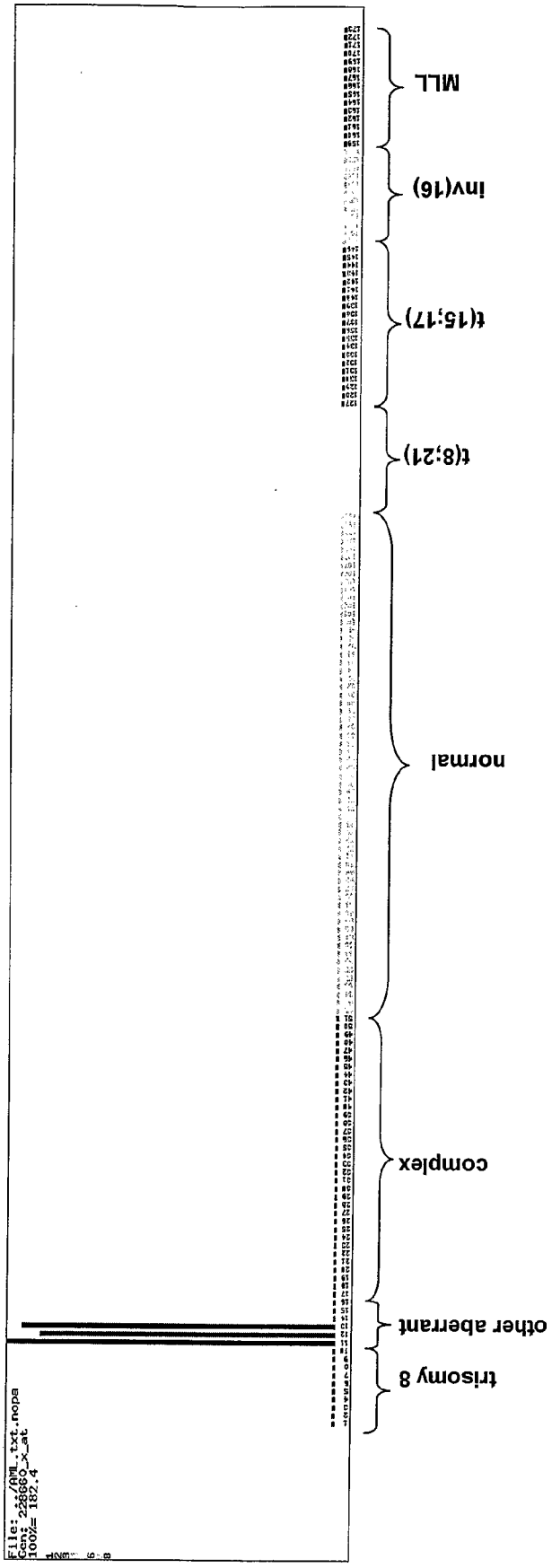


Figure 360

206761_at, TACTILE, AML MLL low

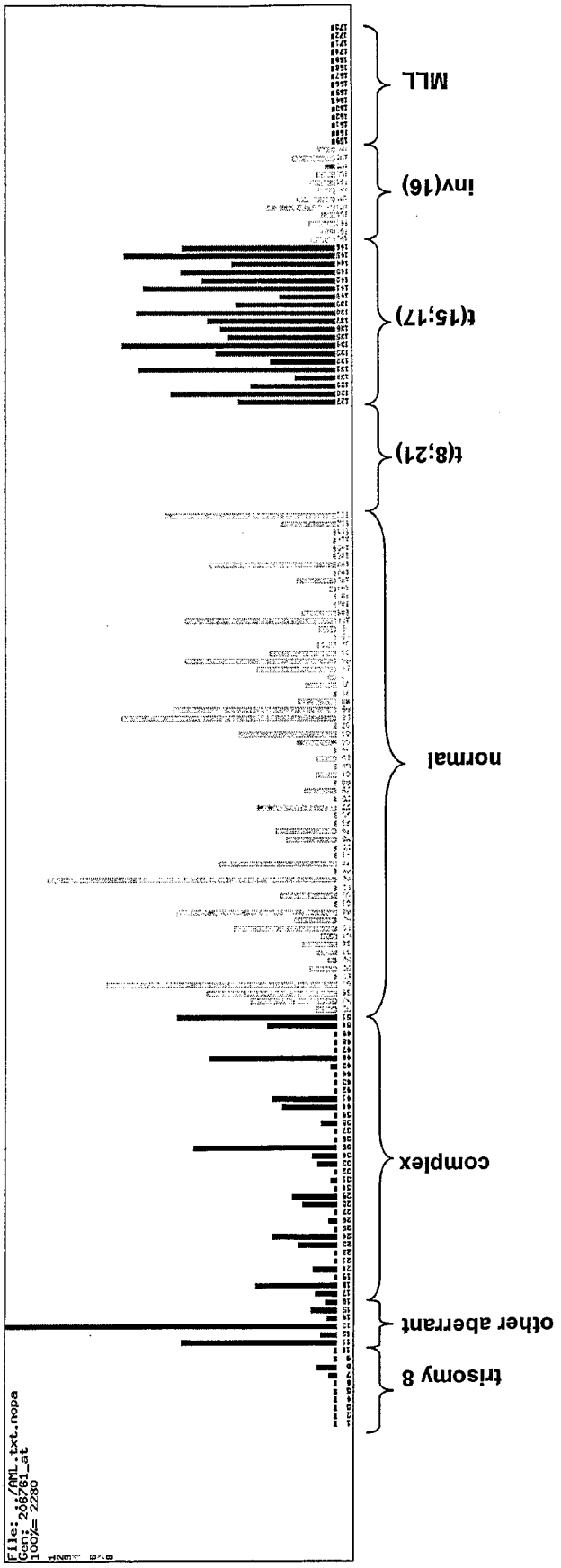


Figure 361

206940_s_at, POU4F1, AML t(8;21) high

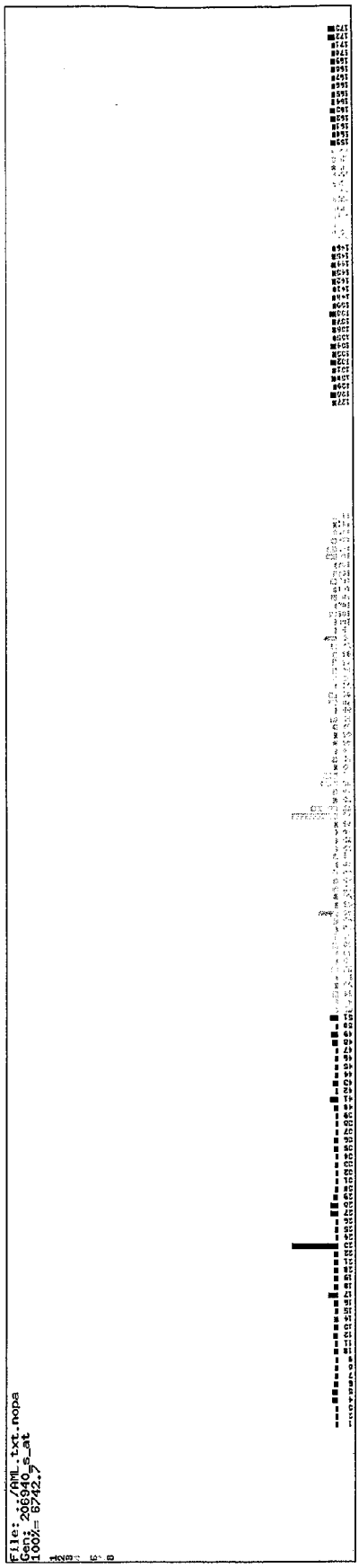


Figure 362

211341_at, POU4F1, AML t(8;21) high

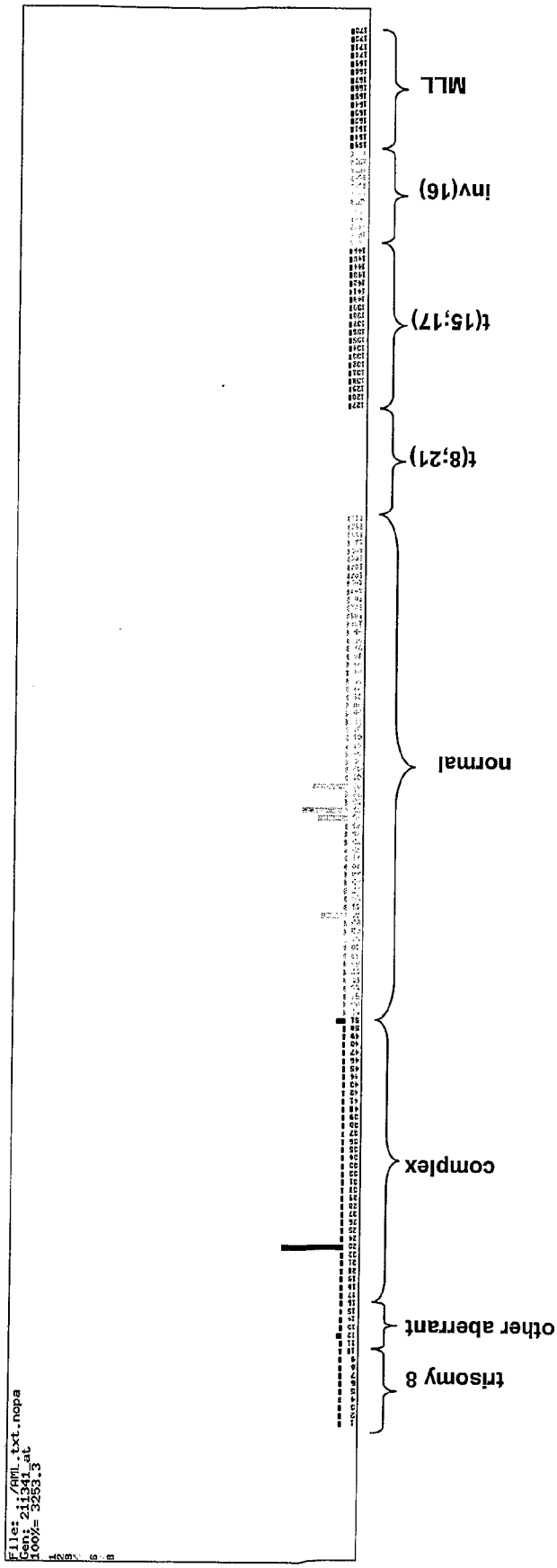


Figure 363

212850_s_at, LRP4, AML inv(16) high

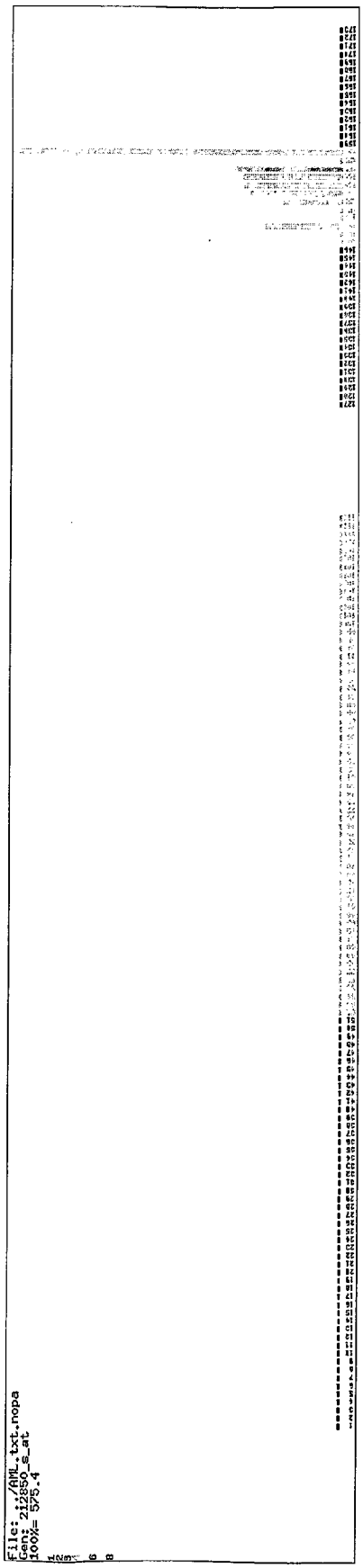


Figure 364

222166_at, AML +8 low

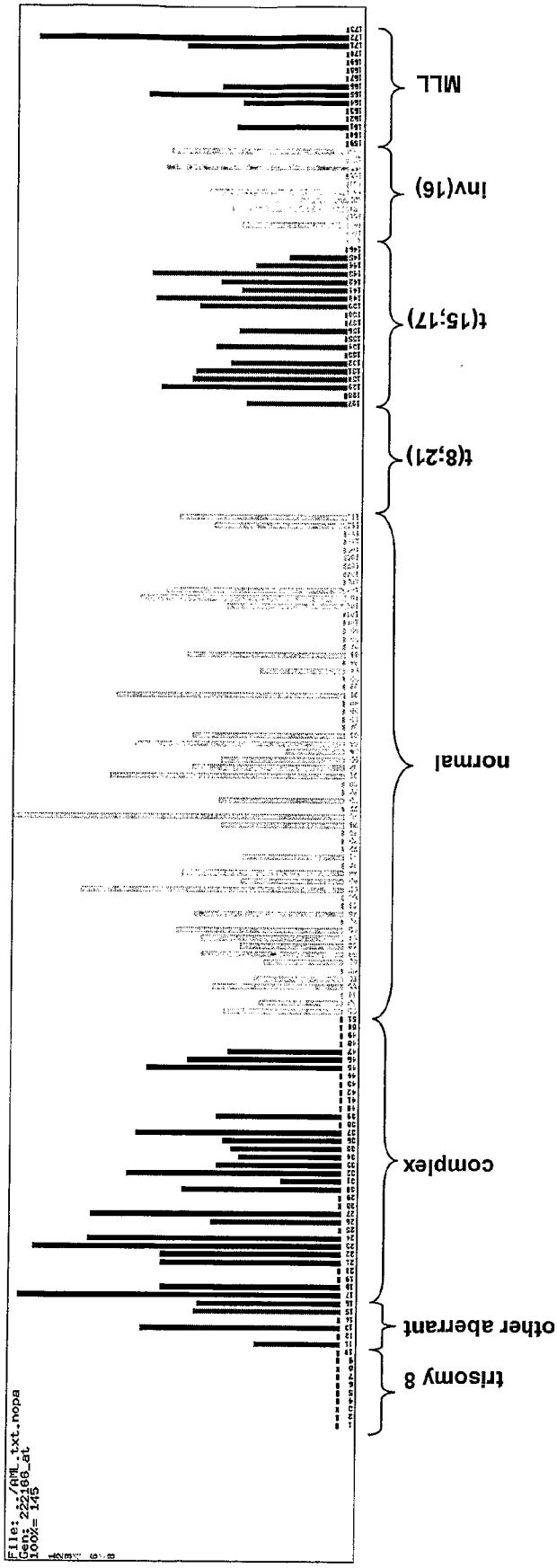


Figure 365

222335_at, AML MLL low

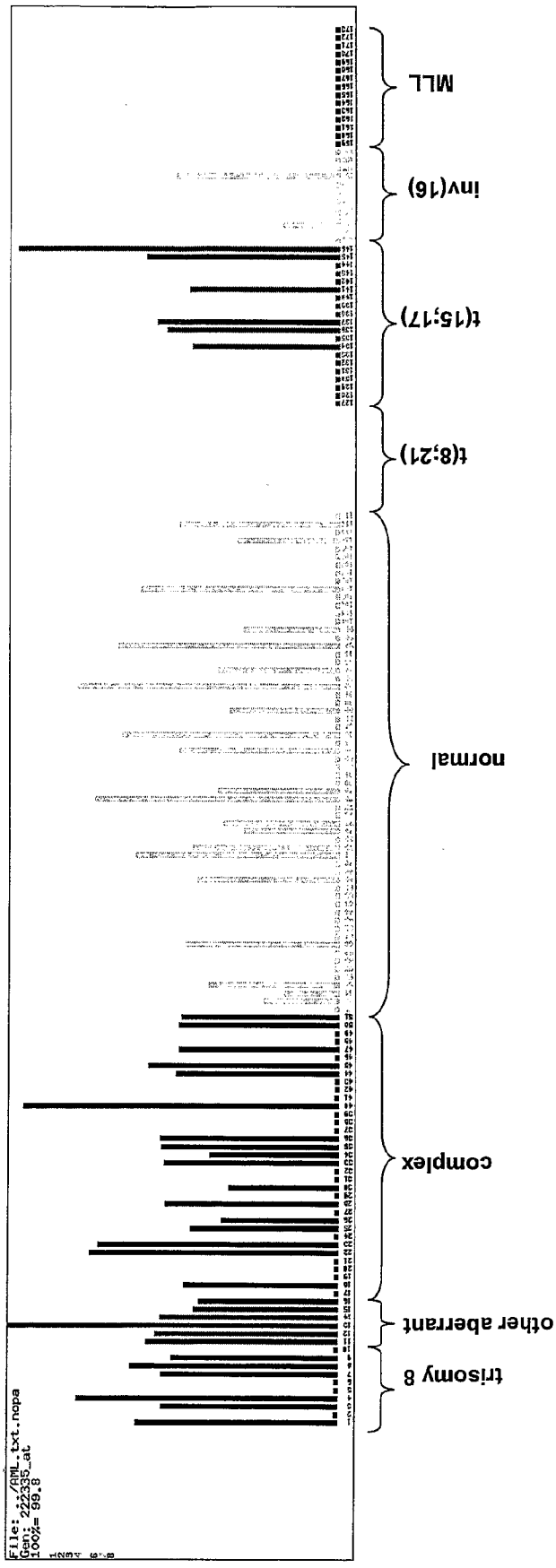


Figure 366

223318_s_at, MGC10974, AML complex low

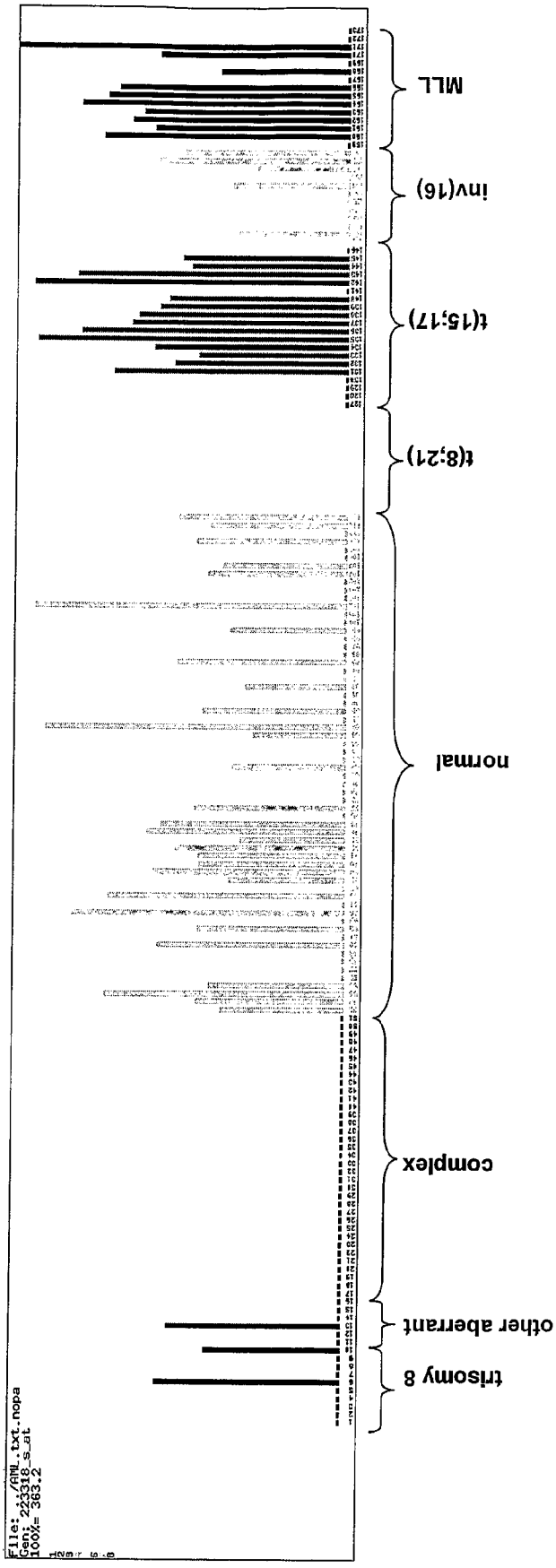


Figure 367

228827_at, AML t(8;21) high

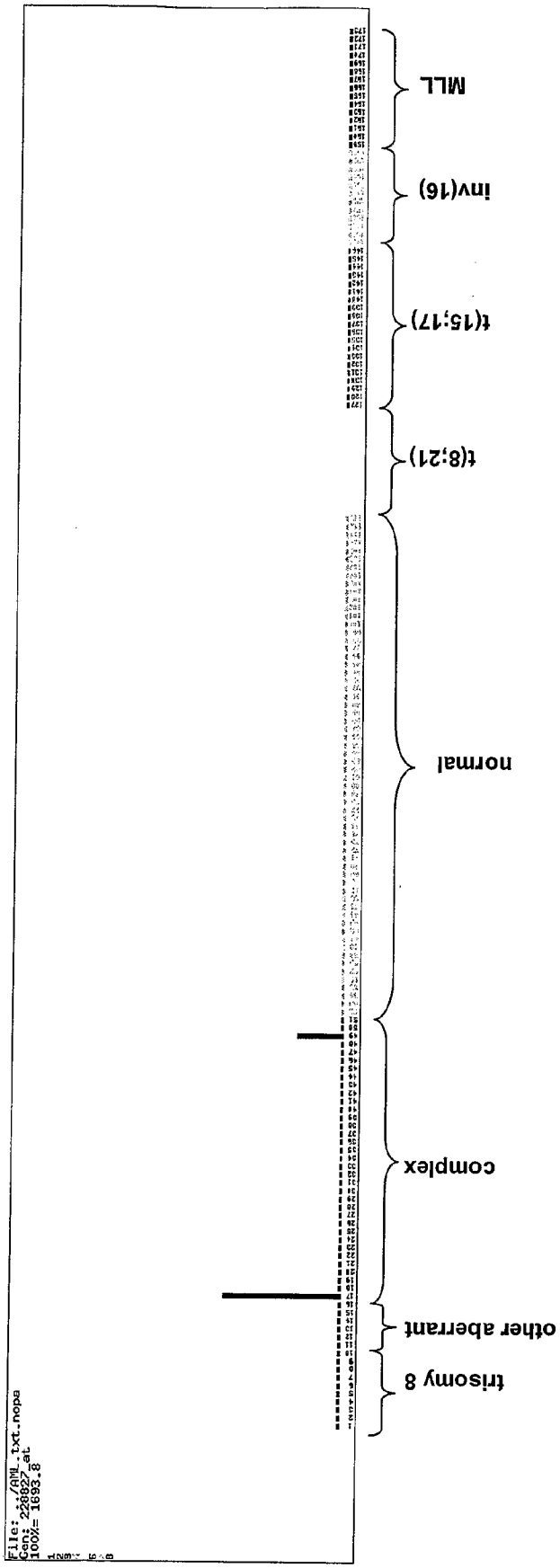


Figure 368

228904_at, AML t(8;21) low, AML t(15;17) low,
AML inv(16) low, AML MLL low

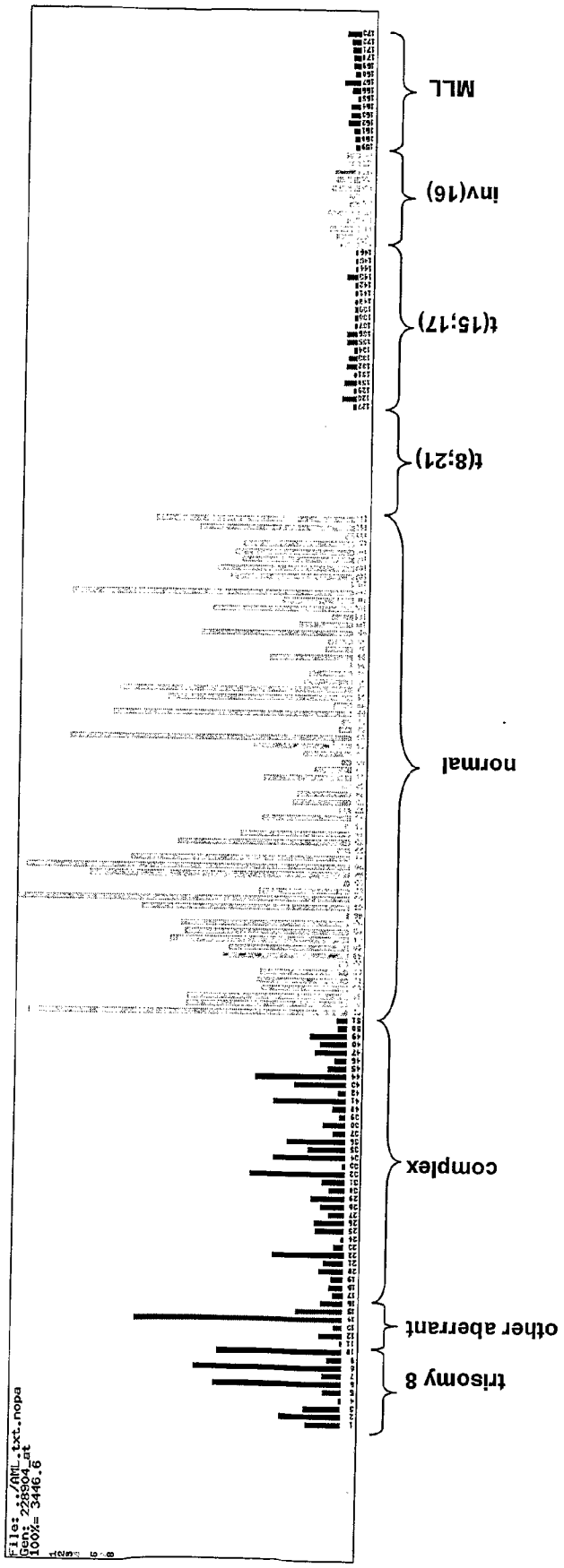


Figure 369

231277_x_at, AML complex low

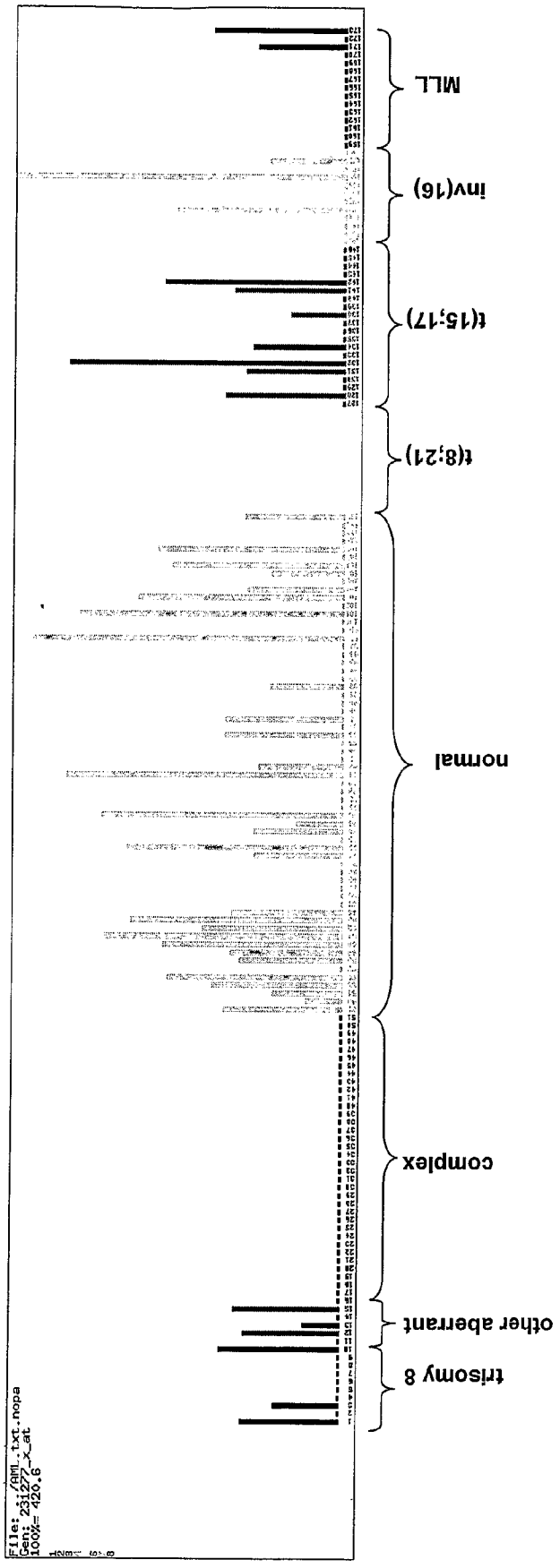


Figure 370

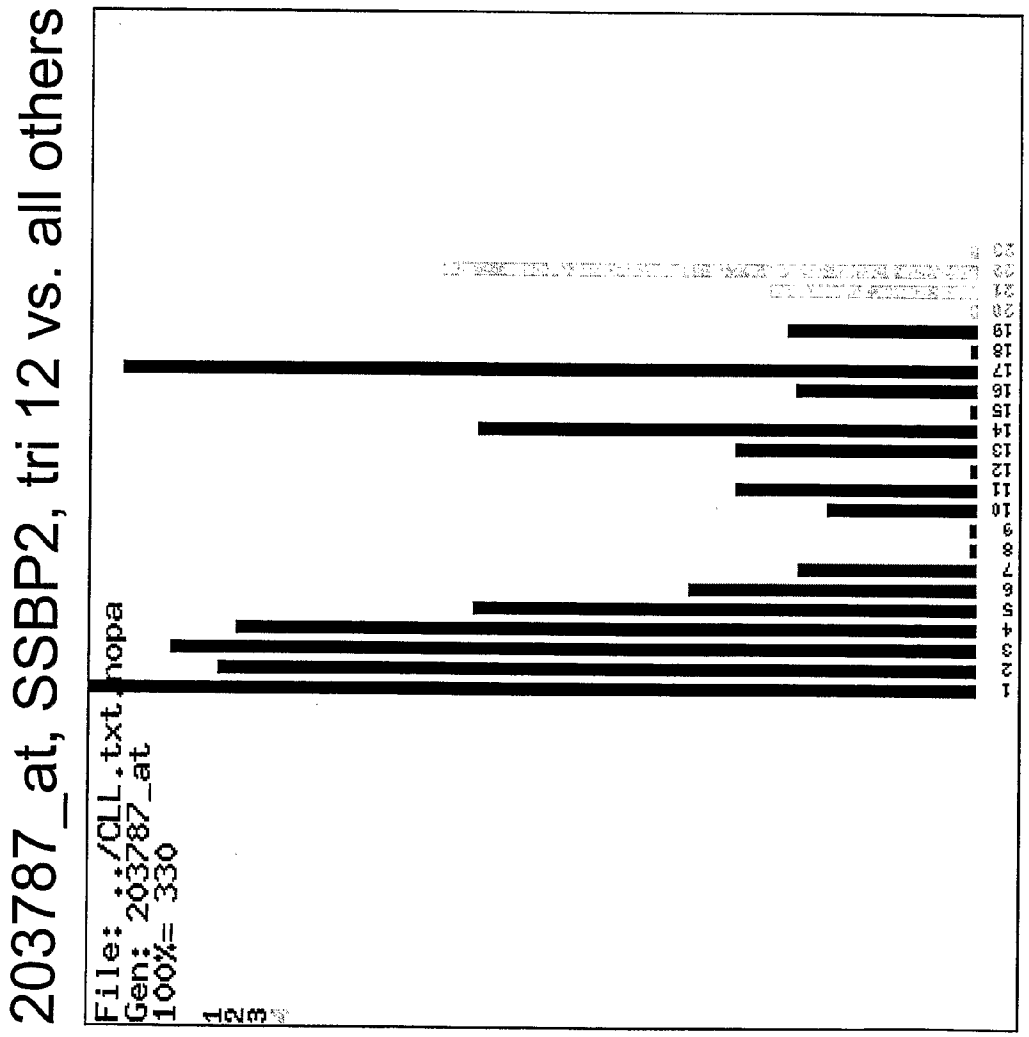

203787_at, SSBP2, tri 12 vs. all others
File: ../CLL.txt
Gen: 203787_at
100%= 330
+12
11q-
13q-
17p-
normal

Figure 371

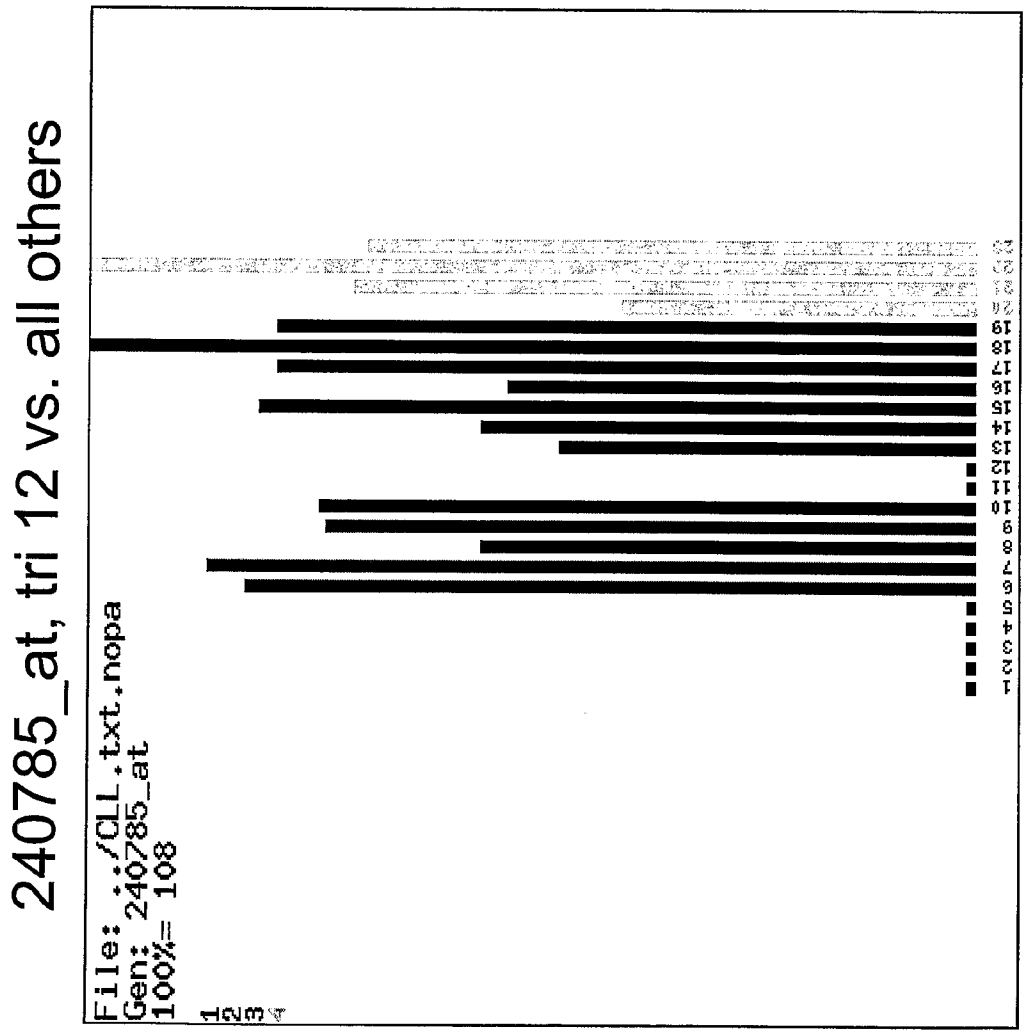

240785_at, tri 12 vs. all others
File: ../CLL.txt.nopa
Gen: 240785_at
100%= 108
1 2 3
+12
11q-
13q-
17p-
normal

Figure 372

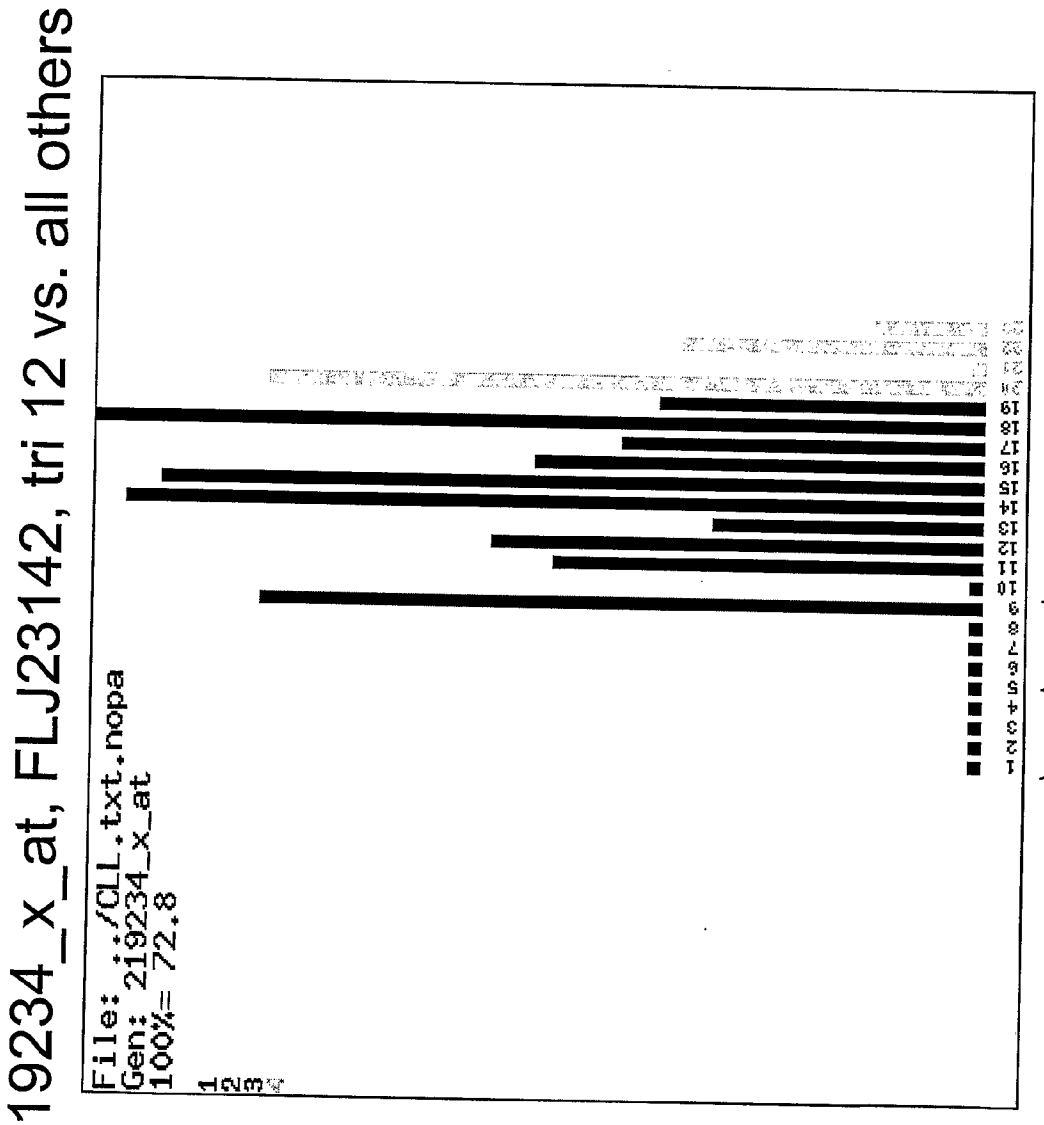

219234_x_at, FLJ23142, tri 12 vs. all others
File: ../CLL.txt.nopa
Gen: 219234_x_at
100%= 72.8
1 2 3
+12
11q-
13q-
17p-
normal

Figure 373

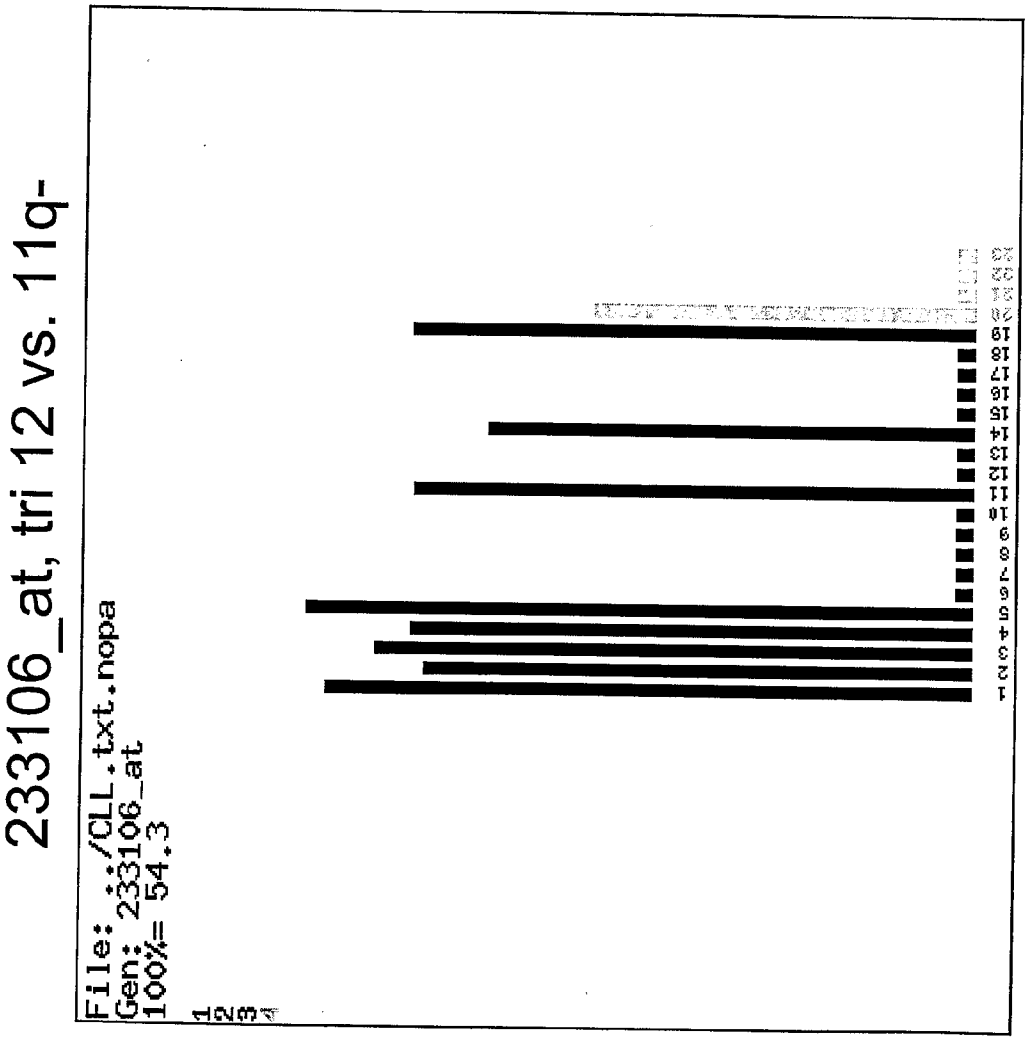

233106_at, tri 12 vs. 11q-
File: ../CLL.txt.nopa
Gen: 233106_at
100%= 54.3
1 2 3 4
+12
11q-
13q-
17p-
normal

Figure 374

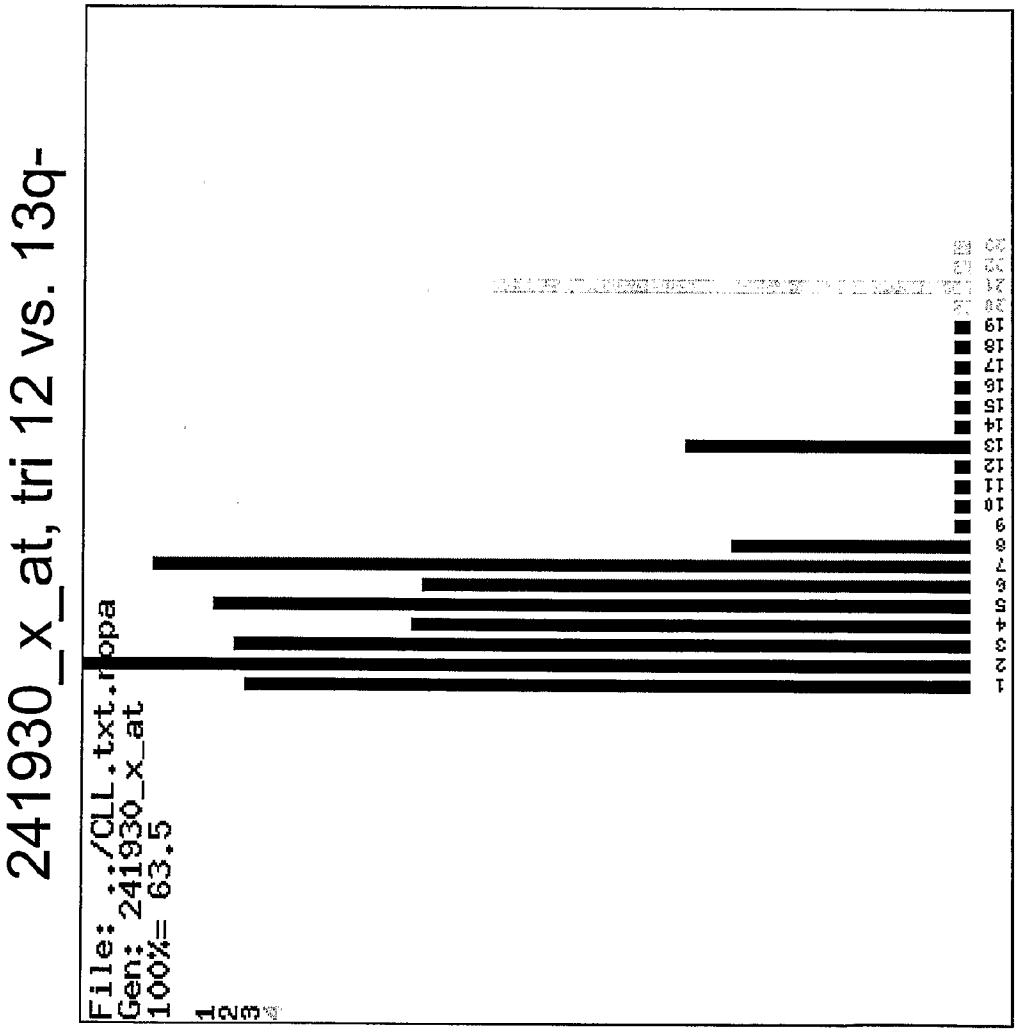

241930_x_at, tri 12 vs. 13q-
File: ../CLL.txt.noppa
Gen: 241930_x_at
100%= 63.5
1 2 3
+12
11q-
13q-
17p-
normal

Figure 375

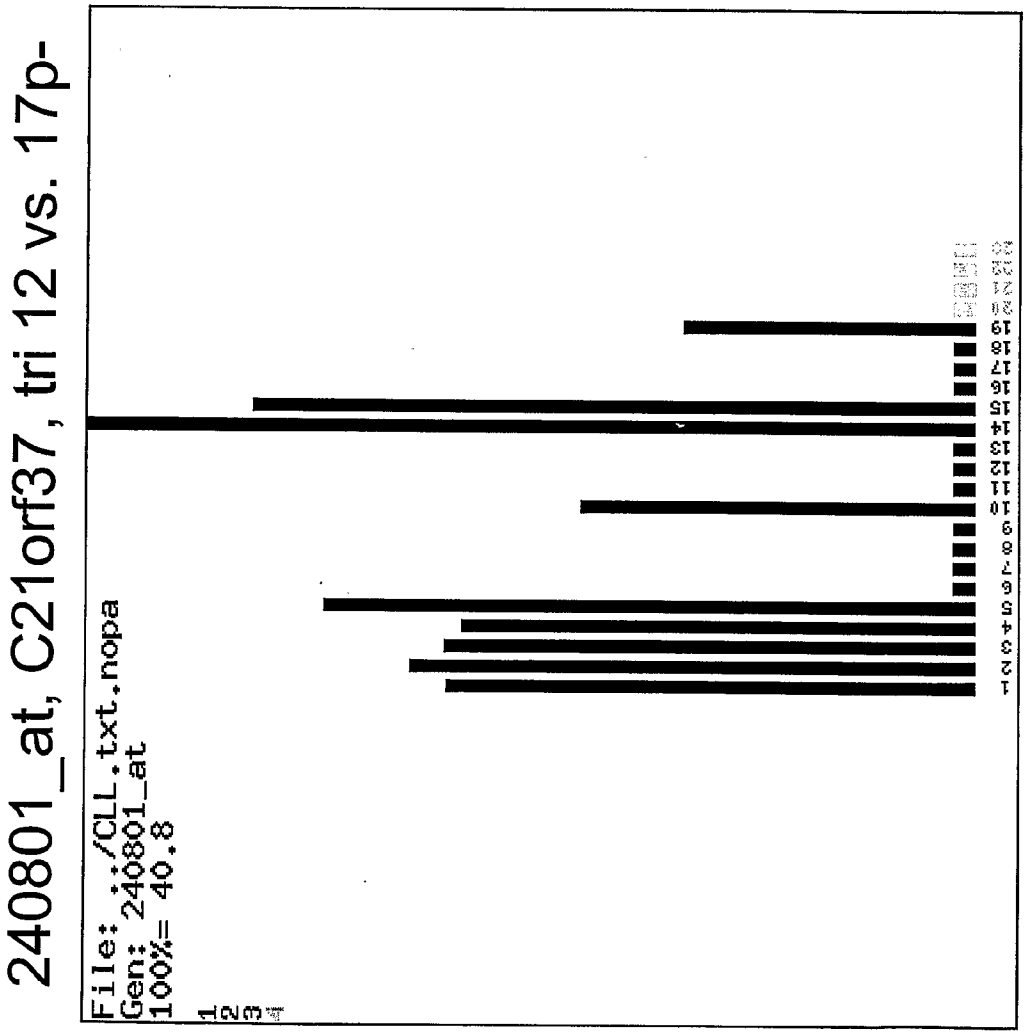

240801_at, C21orf37, tri 12 vs. 17p-
File: ../CLL.txt.nopa
Gen: 240801_at
100%= 40.8
1
2
3
+12
11q-
13q-
17p-
normal

Figure 376

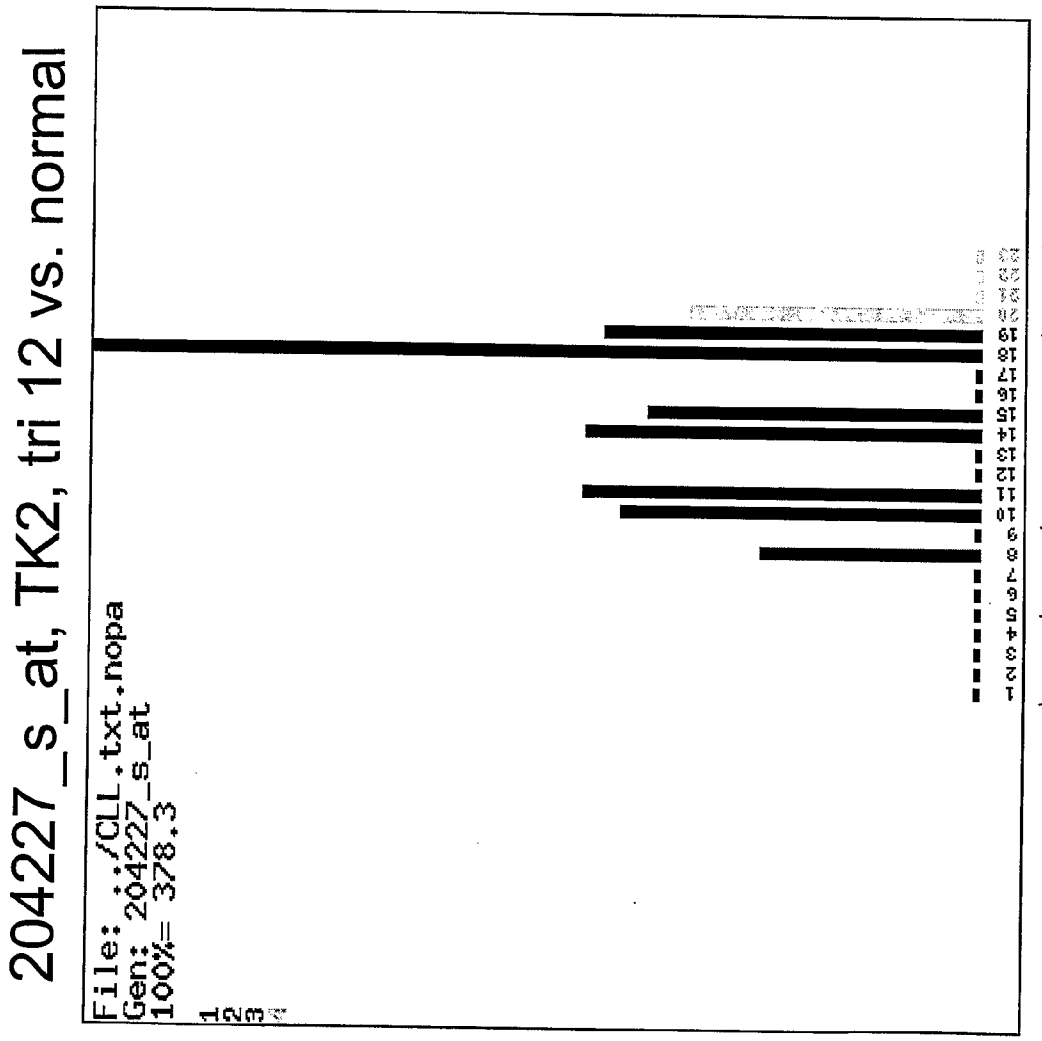

204227_s_at, TK2, tri 12 vs. normal
File: ../CLL.txt.nopa
Gen: 204227_s_at
100%= 378.3
1 2 3
+12
11q-
13q-
17p-
normal

Figure 377

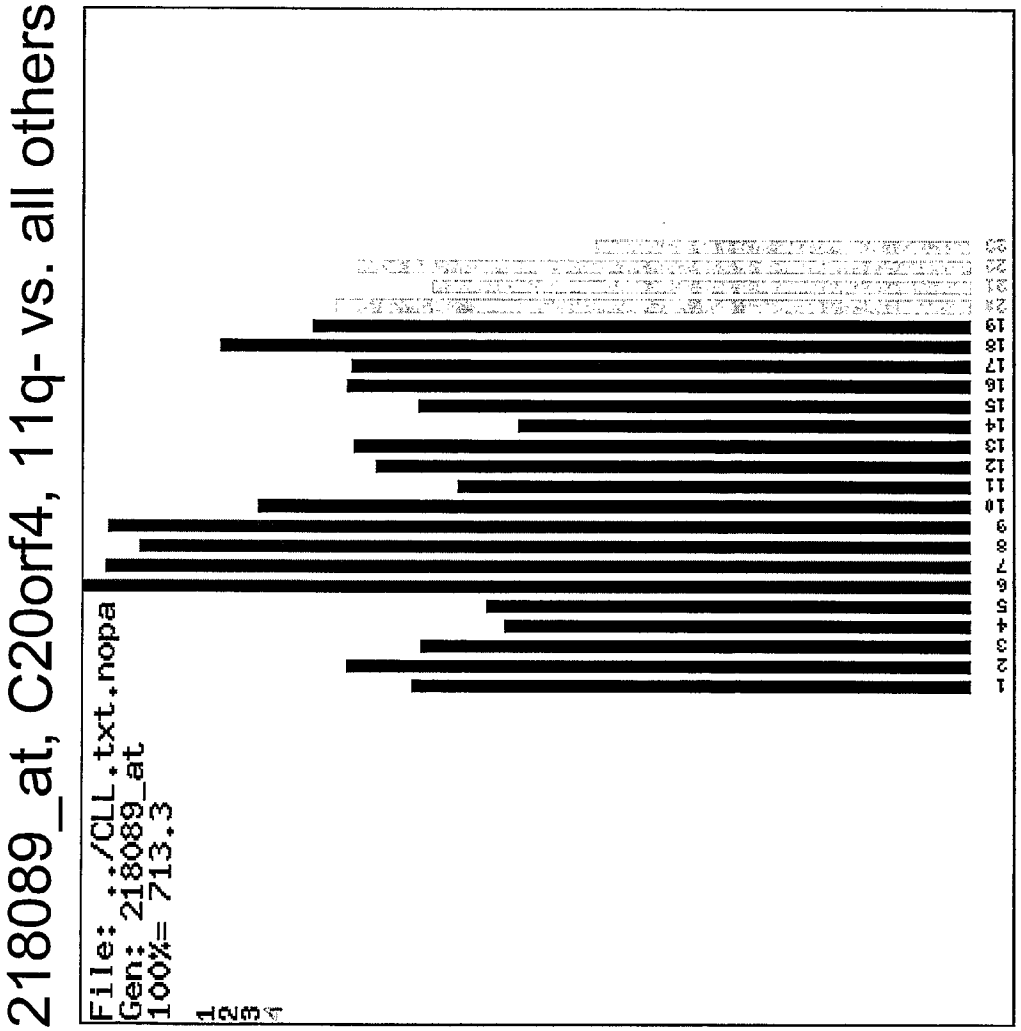

218089_at, C20orf4, 11q- vs. all others
File: ../CLL.txt.nopa
Gen: 218089_at
100%= 713.3
+12
11q-
13q-
17p-
normal

Figure 378

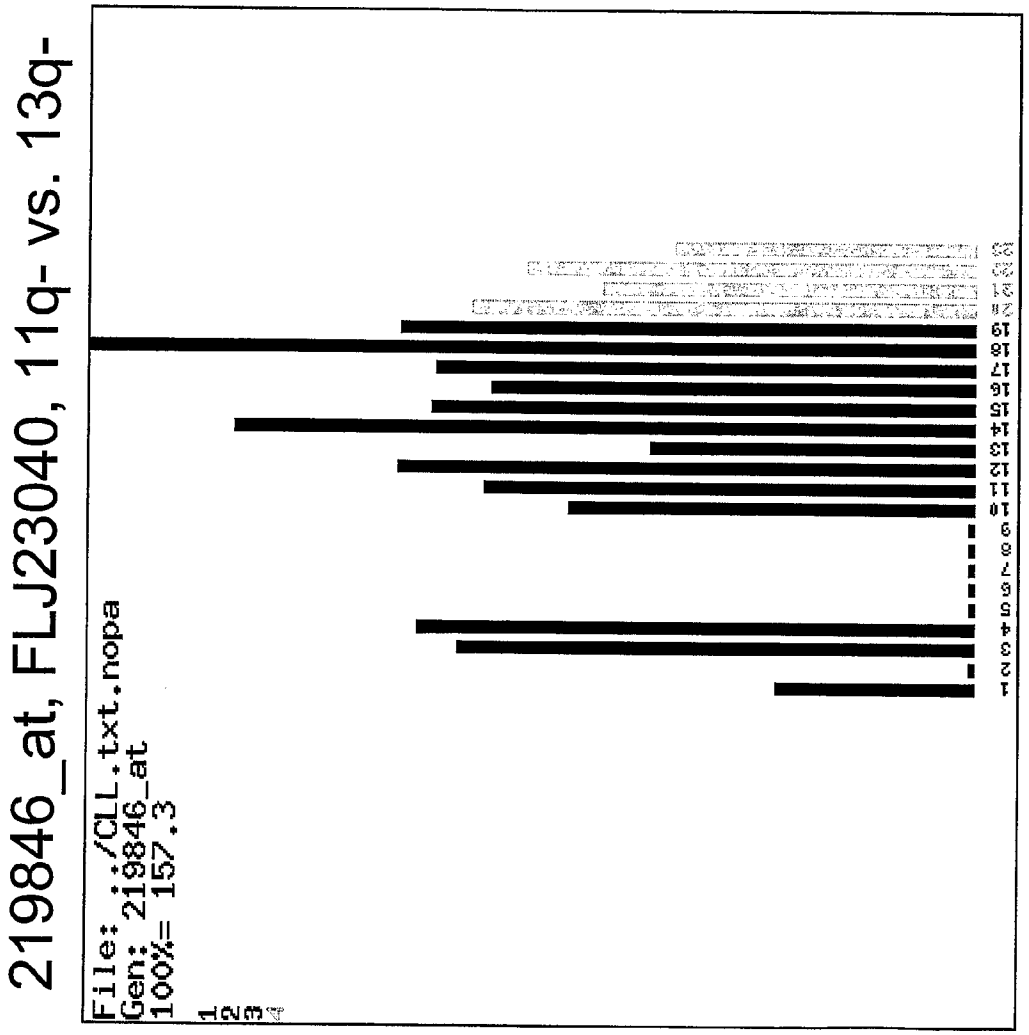

219846_at, FLJ23040, 11q- vs. 13q-
File: ../CLL.txt.nopa
Gen: 219846_at
100%= 157.3
1
2
3
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22

Figure 379

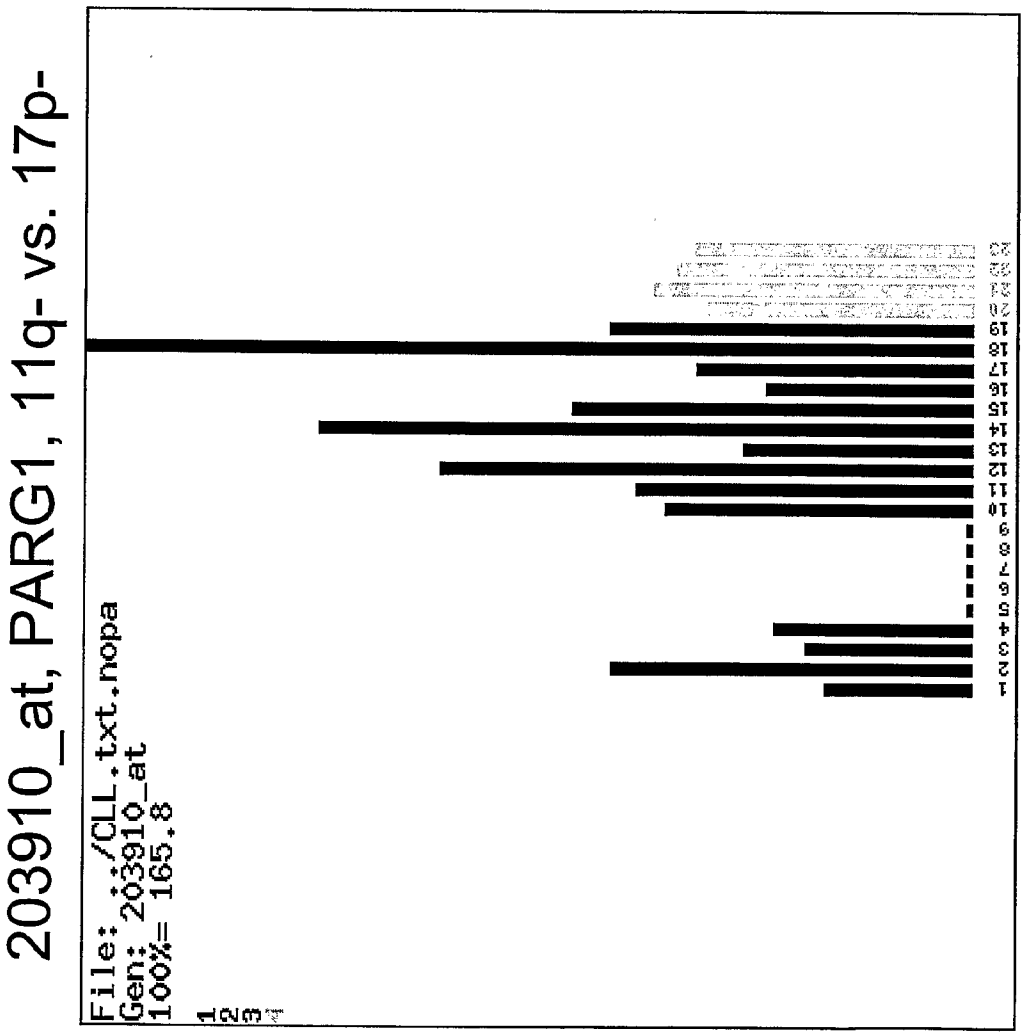

203910_at, PARG1, 11q- vs. 17p-
File: ../CLL.txt.nopa
Gen: 203910_at
100%= 165.8
1
2
3
+12
11q-
13q-
17p-
normal

Figure 380

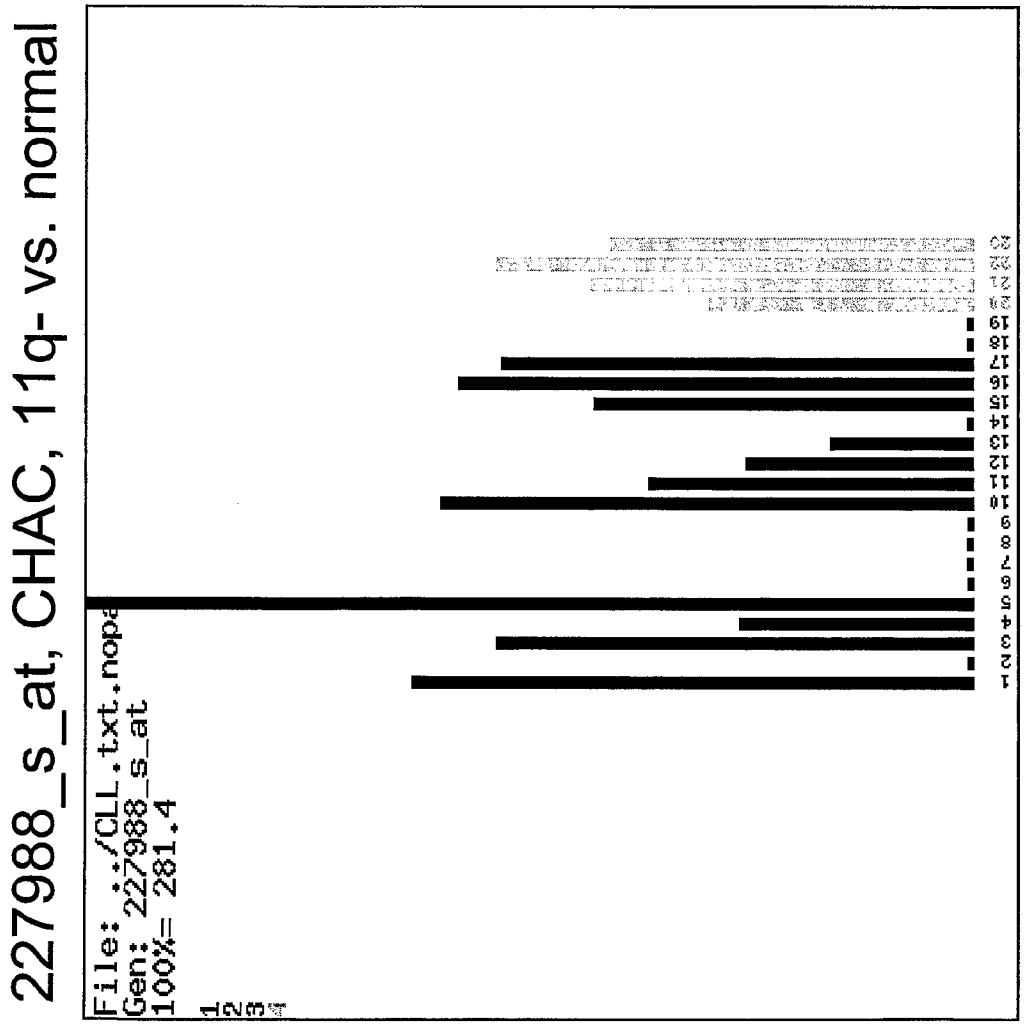

227988_s_at, CHAC, 11q- vs. normal
File: ../CLL.txt.nopa
Gen: 227988_s_at
100%= 281.4
1
2
3
4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
+12
11q-
13q-
17p-
normal

Figure 381

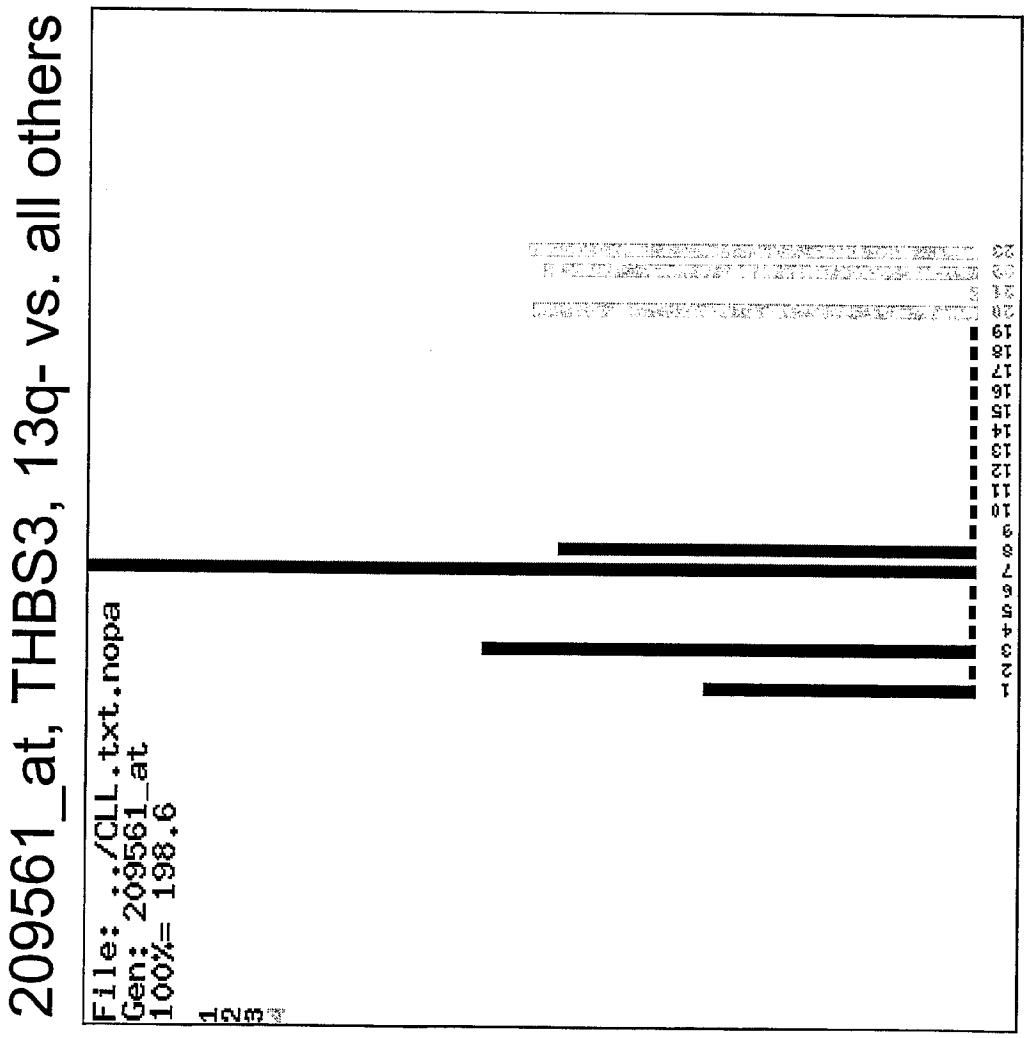

209561_at, THBS3, 13q- vs. all others
File: ../CLL.txt.nopa
Gen: 209561_at
100%= 198.6
+12
11q-
13q-
17p-
normal

Figure 382

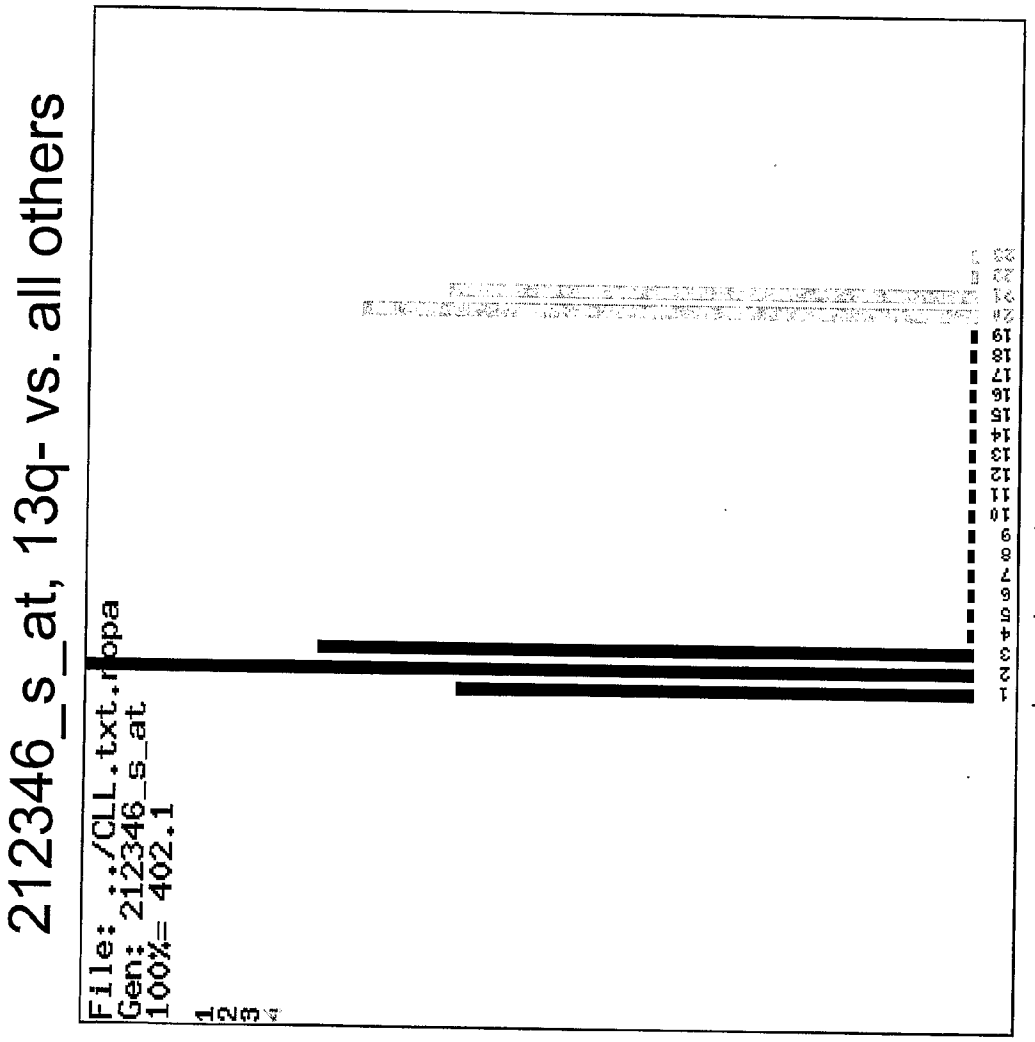

212346_s_at, 13q- vs. all others
File: ../CLL.txt.rdpa
Gen: 212346_s_at
100%= 402.1
1
2
3
4
+12
11q-
13q-
17p-
normal

Figure 383

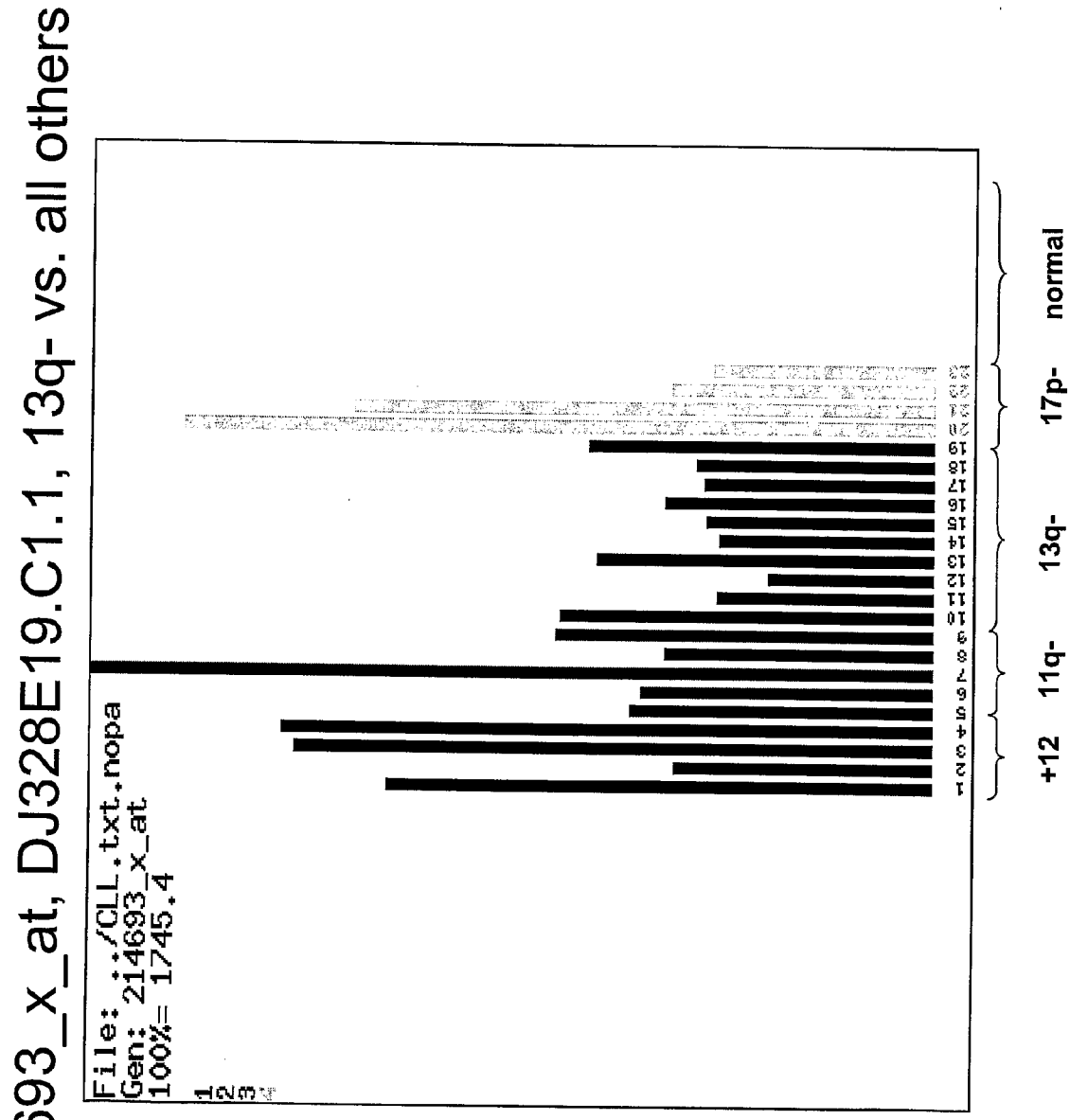

214693_x_at, DJ328E19.C1.1, 13q- vs. all others
File: ../CLL.txt.nopa
Gen: 214693_x_at
100%= 1745.4
1
2
3
4
+12
11q-
13q-
17p-
normal

Figure 384

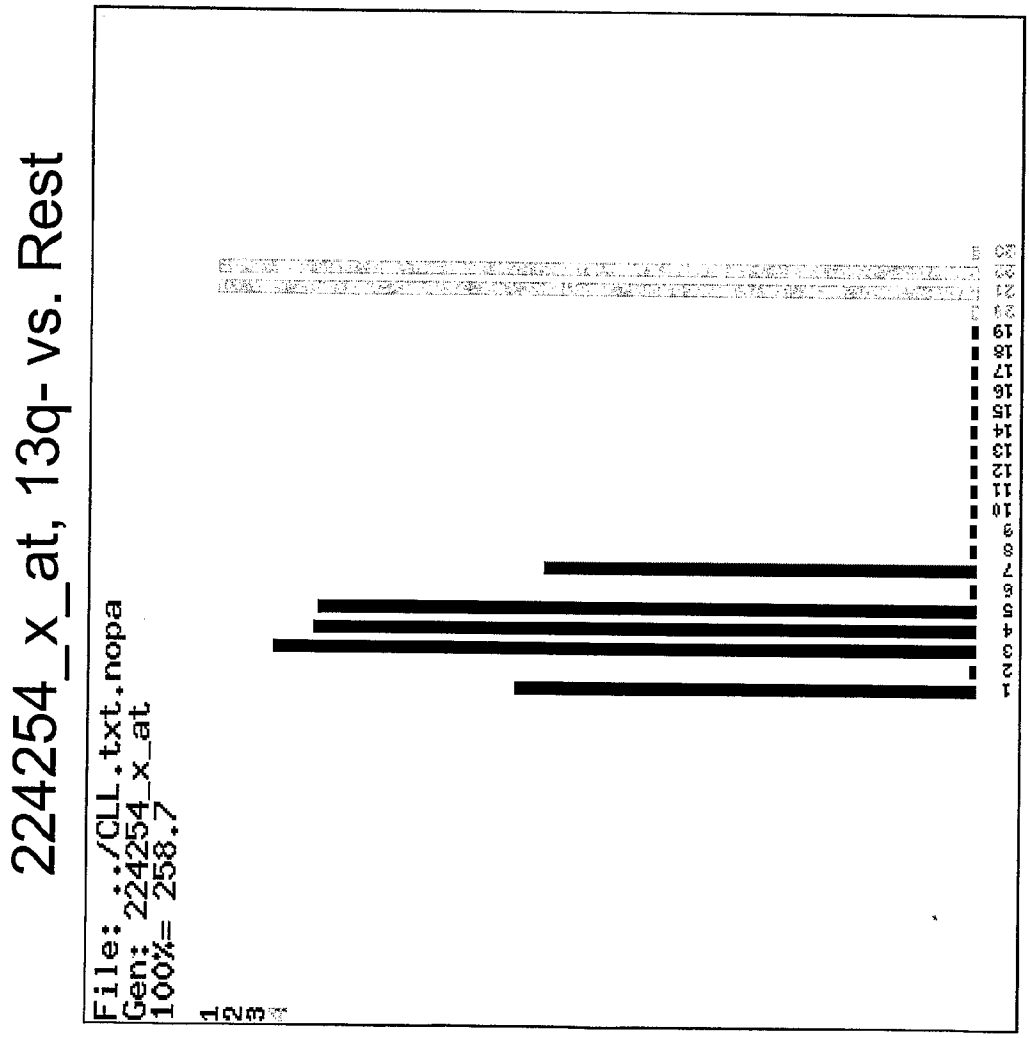

224254_x_at, 13q- vs. Rest
File: ../CLL.txt.nopa
Gen: 224254_x_at
100%= 258.7
+12
11q-
13q-
17p-
normal

Figure 385

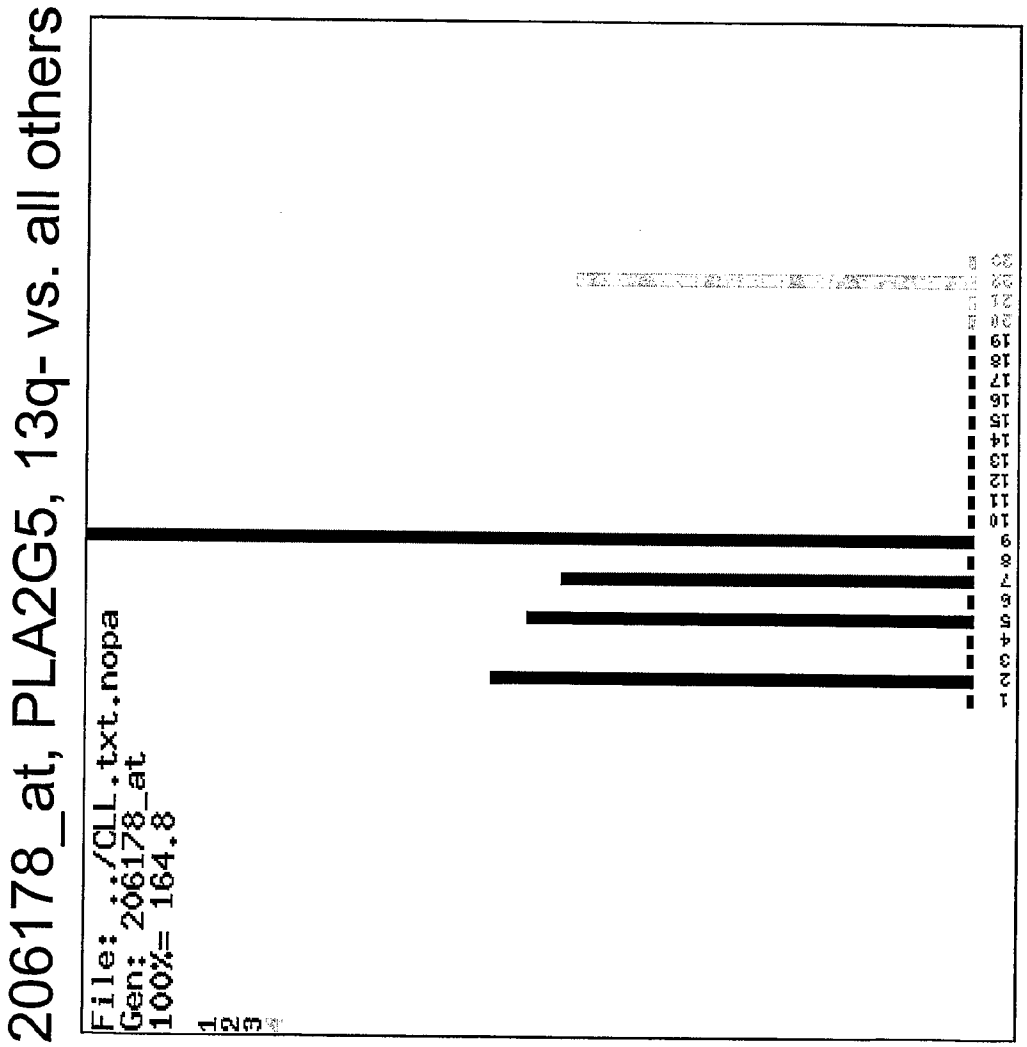

206178_at, PLA2G5, 13q- vs. all others
File: .:./CLL.txt.nopa
Gen: 206178_at
100%= 164.8
1 2 3
+12
11q-
13q-
17p-
normal

Figure 386

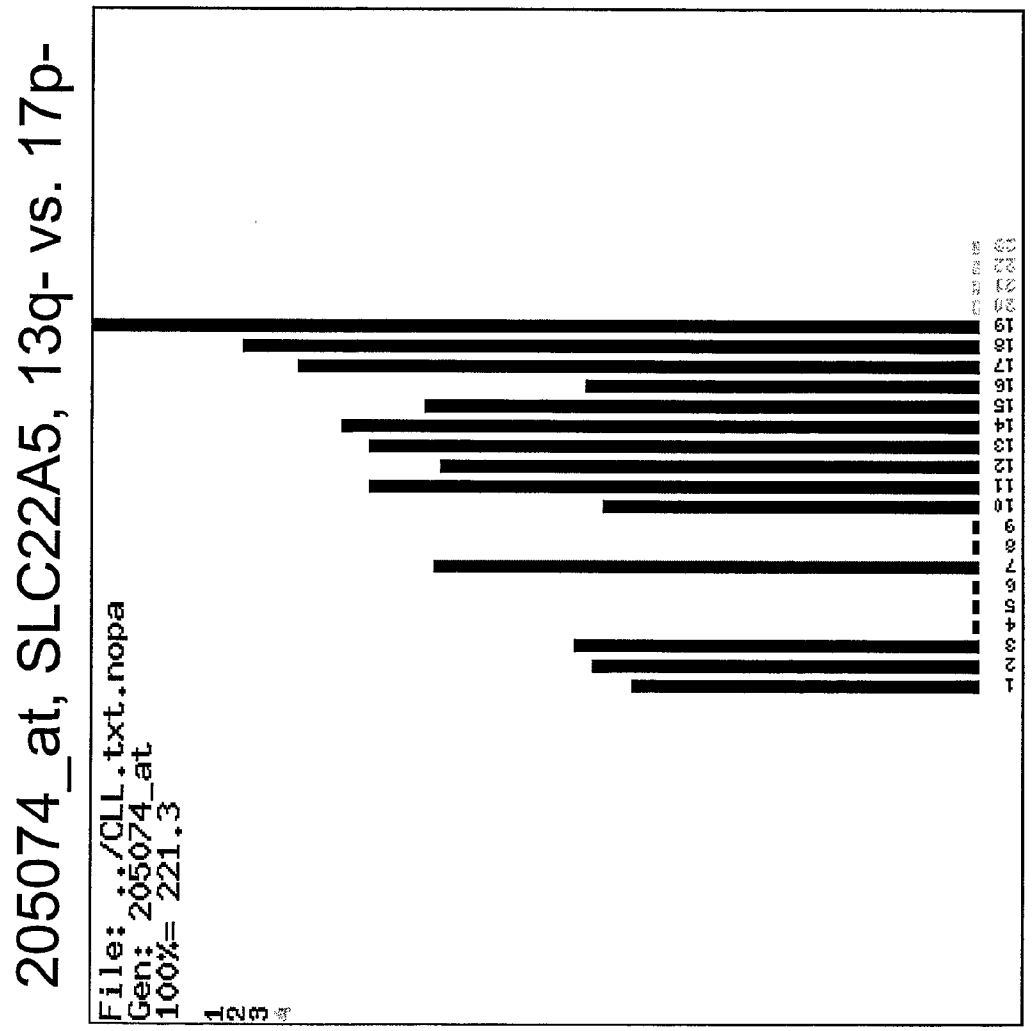

205074_at, SLC22A5, 13q- vs. 17p-
File: ../CLL.txt.nopa
Gen: 205074_at
100%= 221.3
1 2 3
+12
11q-
13q-
17p-
normal

Figure 387

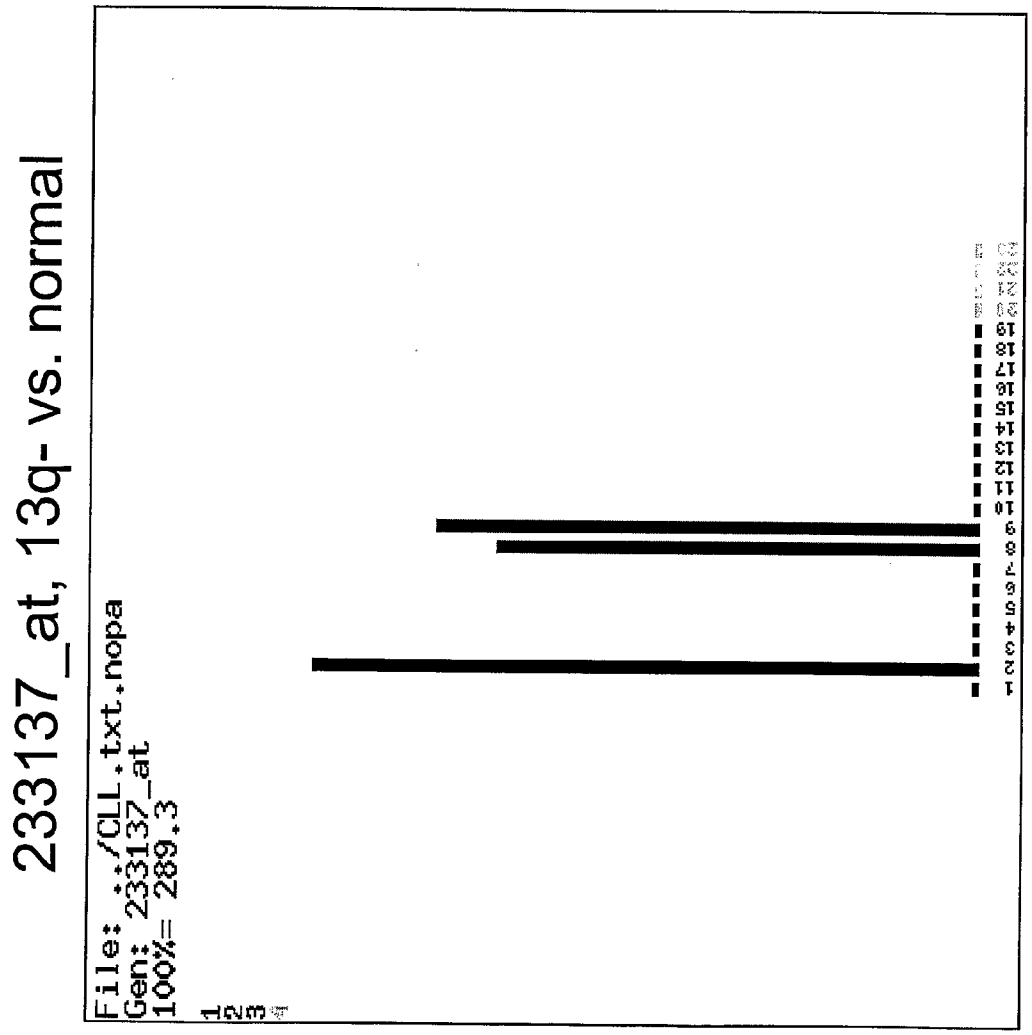

233137_at, 13q- vs. normal
File: ../CLL.txt.nopa
Gen: 233137_at
100%= 289.3
+12
11q-
13q-
17p-
normal

Figure 388

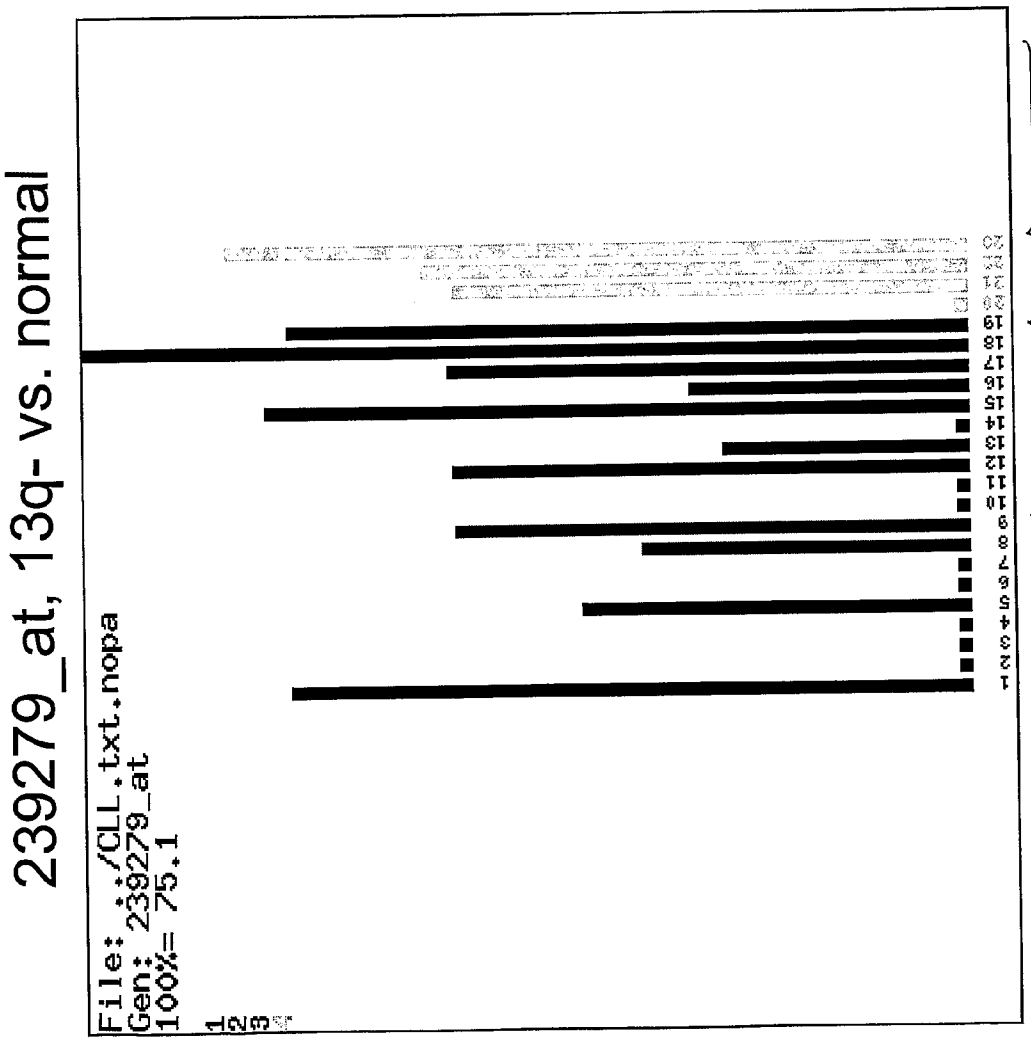

239279_at, 13q- vs. normal
File: ../CLL.txt.nopa
Gen: 239279_at
100%= 75.1
+12
11q-
13q-
17p-
normal

Figure 389

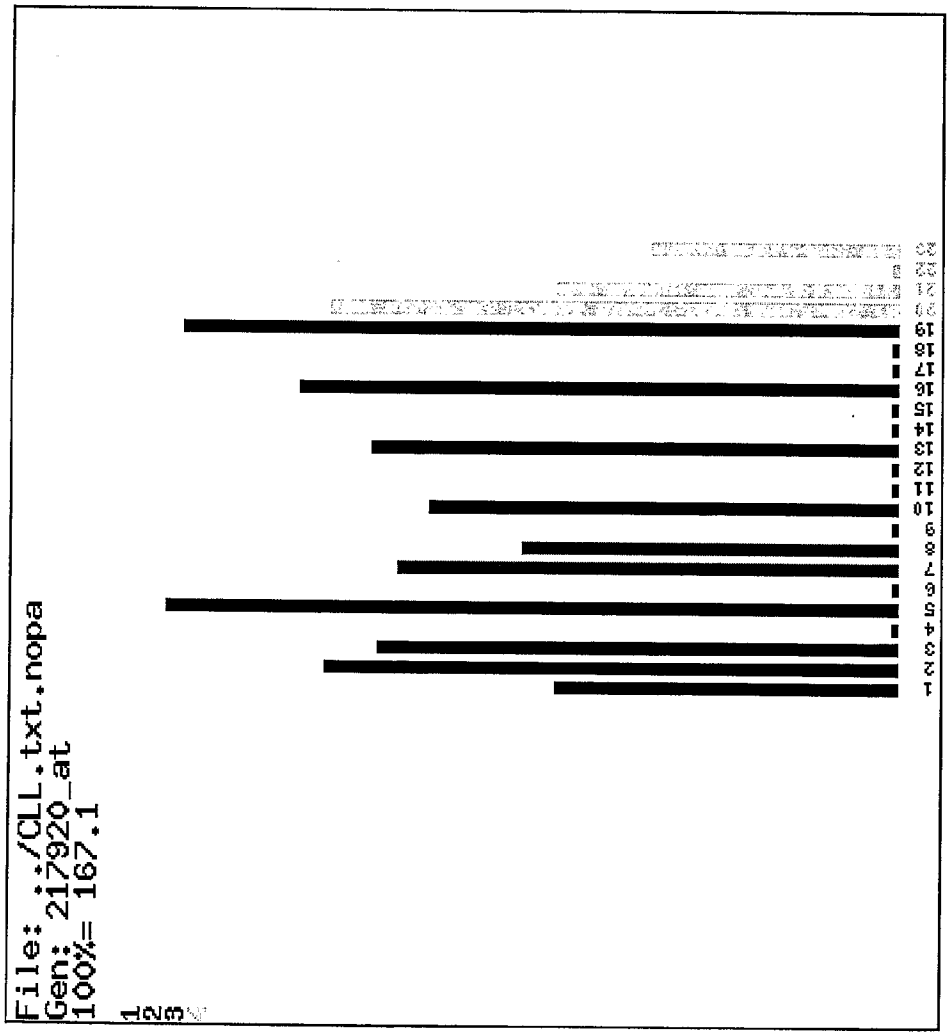

217920_at, 13q- vs. normal
File: ../CLL.txt.nopa
Gen: 217920_at
100%= 167.1
+12
11q-
13q-
17p-
normal

Figure 390

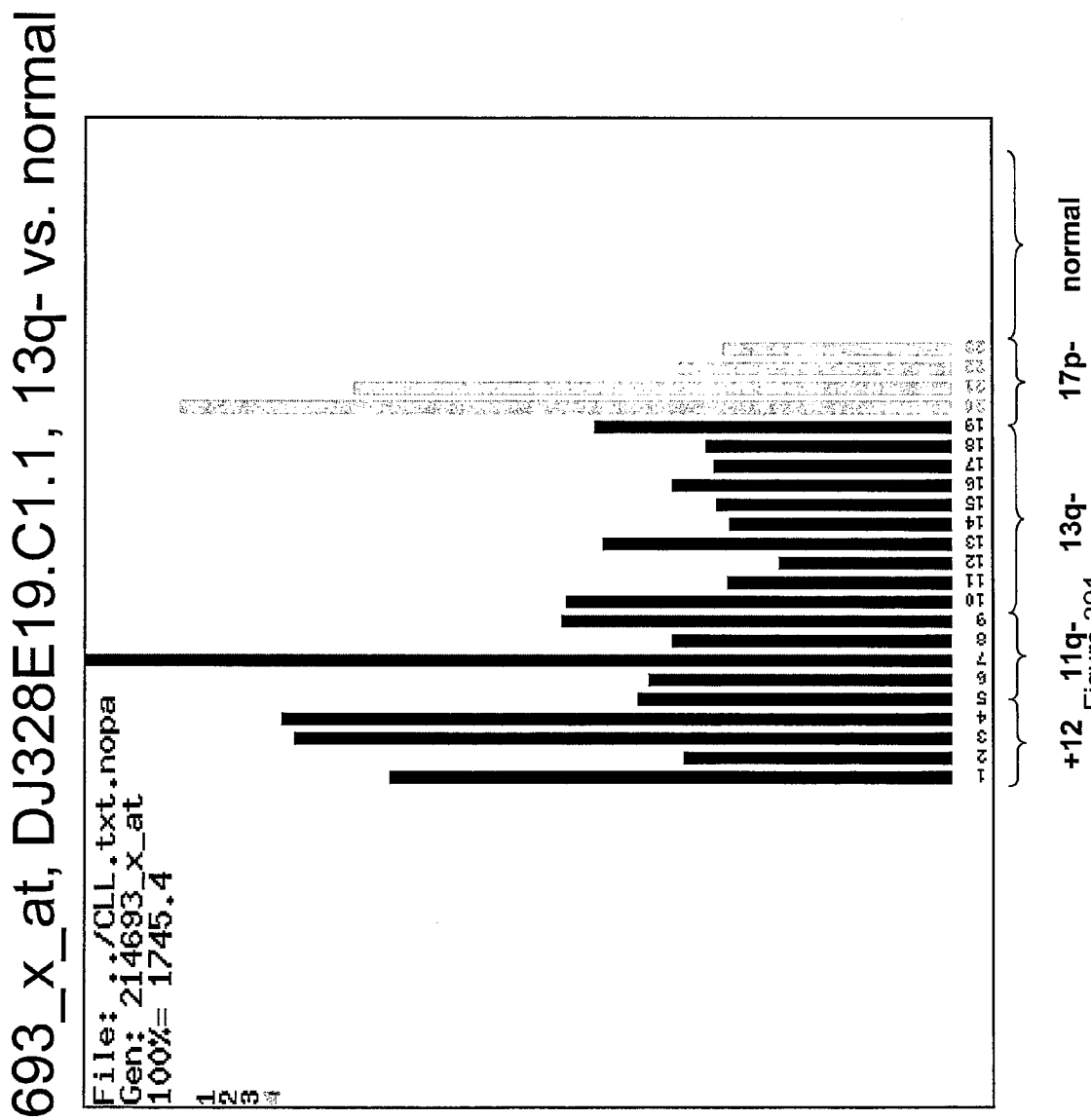

214693_x_at, DJ328E19.C1.1, 13q- vs. normal
File: ../CLL.txt.nopa
Gen: 214693_x_at
100%= 1745.4
1
2
3
+12
11q-
13q-
17p-
normal

Figure 391

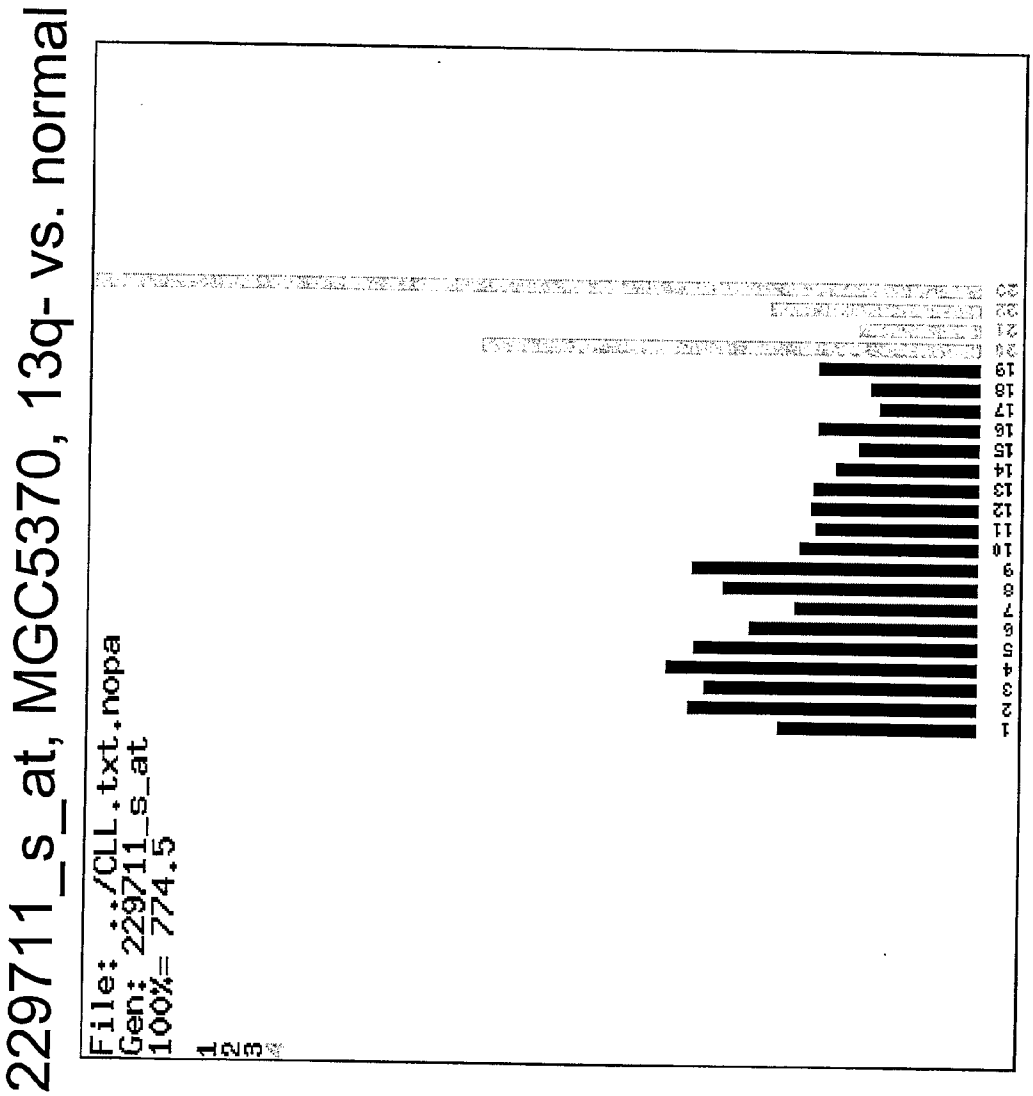

229711_s_at, MGC5370, 13q- vs. normal
File: ../CLL.txt.nopa
Gen: 229711_s_at
100%= 774.5
1
2
3
+12
11q-
13q-
17p-
normal

Figure 392

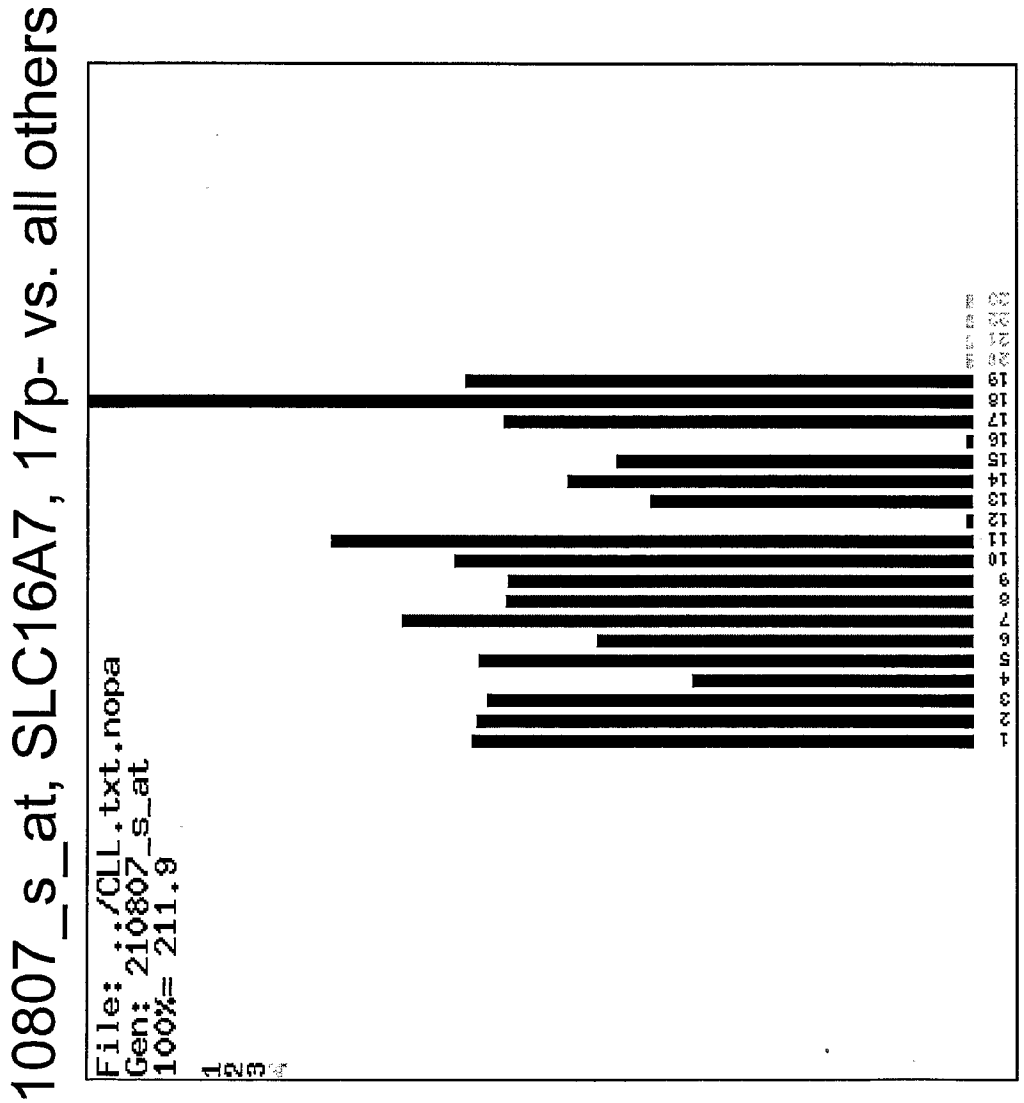

210807_s_at, SLC16A7, 17p- vs. all others
File: ../CLL.txt.nopa
Gen: 210807_s_at
100%= 211.9
+12
11q-
13q-
17p-
normal

Figure 393

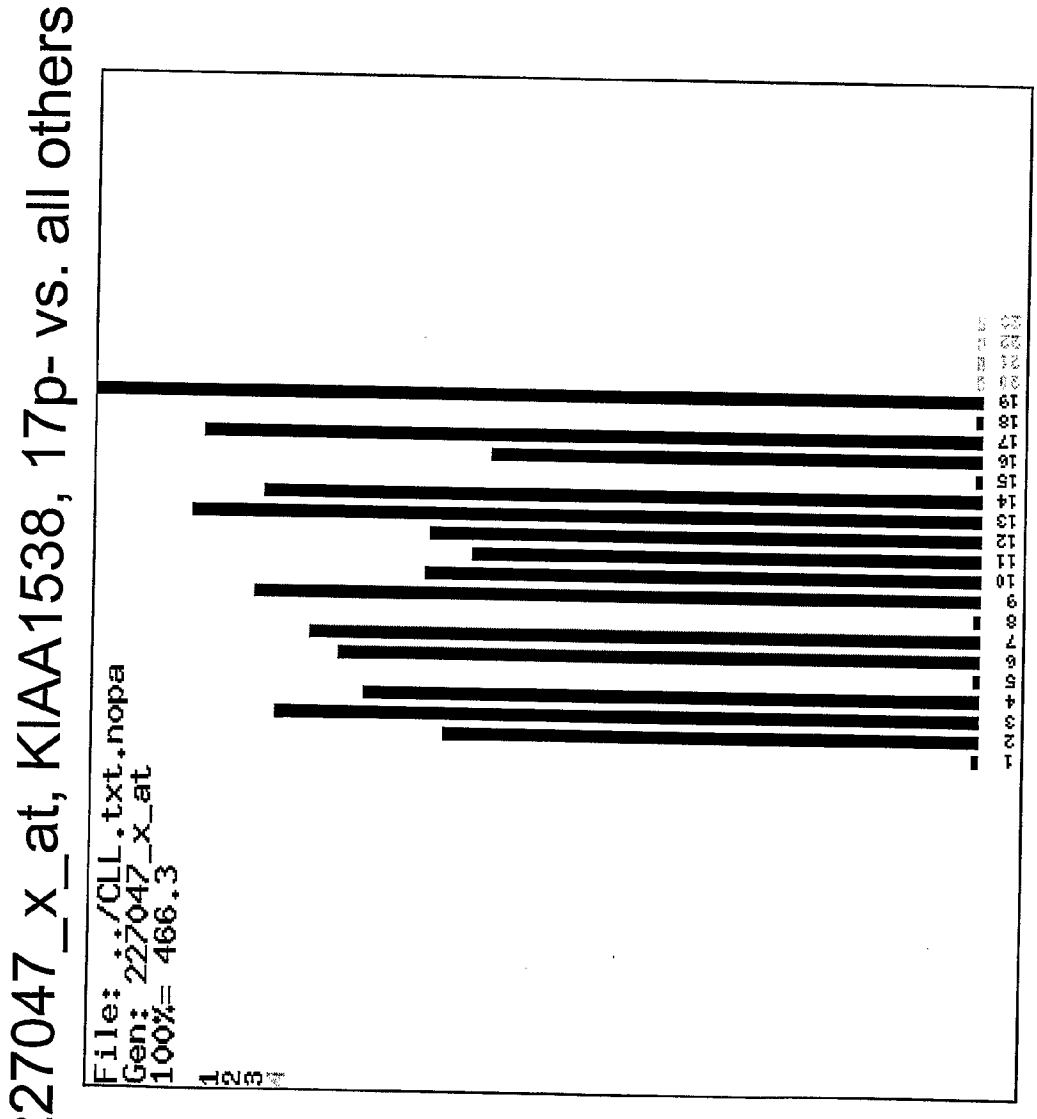

227047_x_at, KIAA1538, 17p- vs. all others
File: ../CLL.txt,nopa
Gen: 227047_x_at
100%= 466.3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22
+12
11q-
13q-
17p-
normal

Figure 394

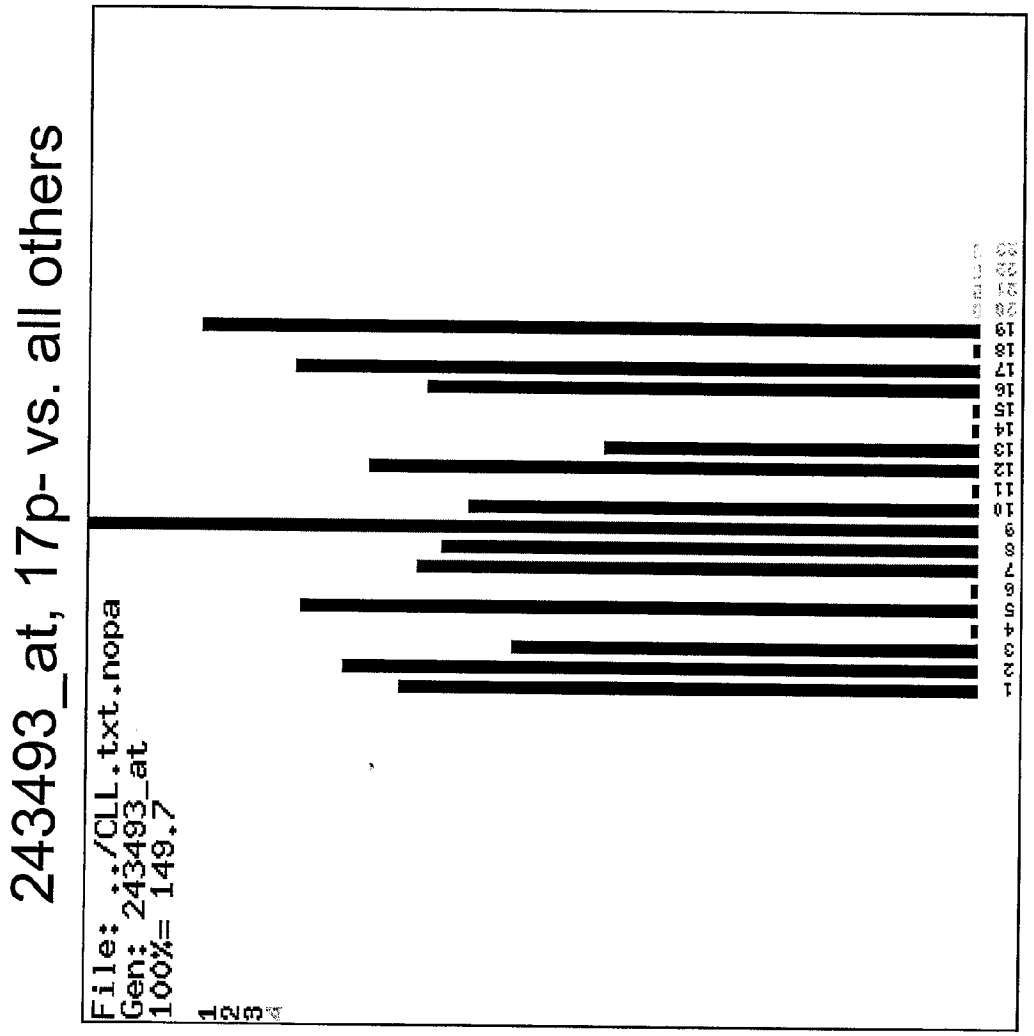

243493_at, 17p- vs. all others
File: */CLL.txt.nopa
Gen: 243493_at
100%= 149.7
+12
11q-
13q-
17p-
normal

Figure 395

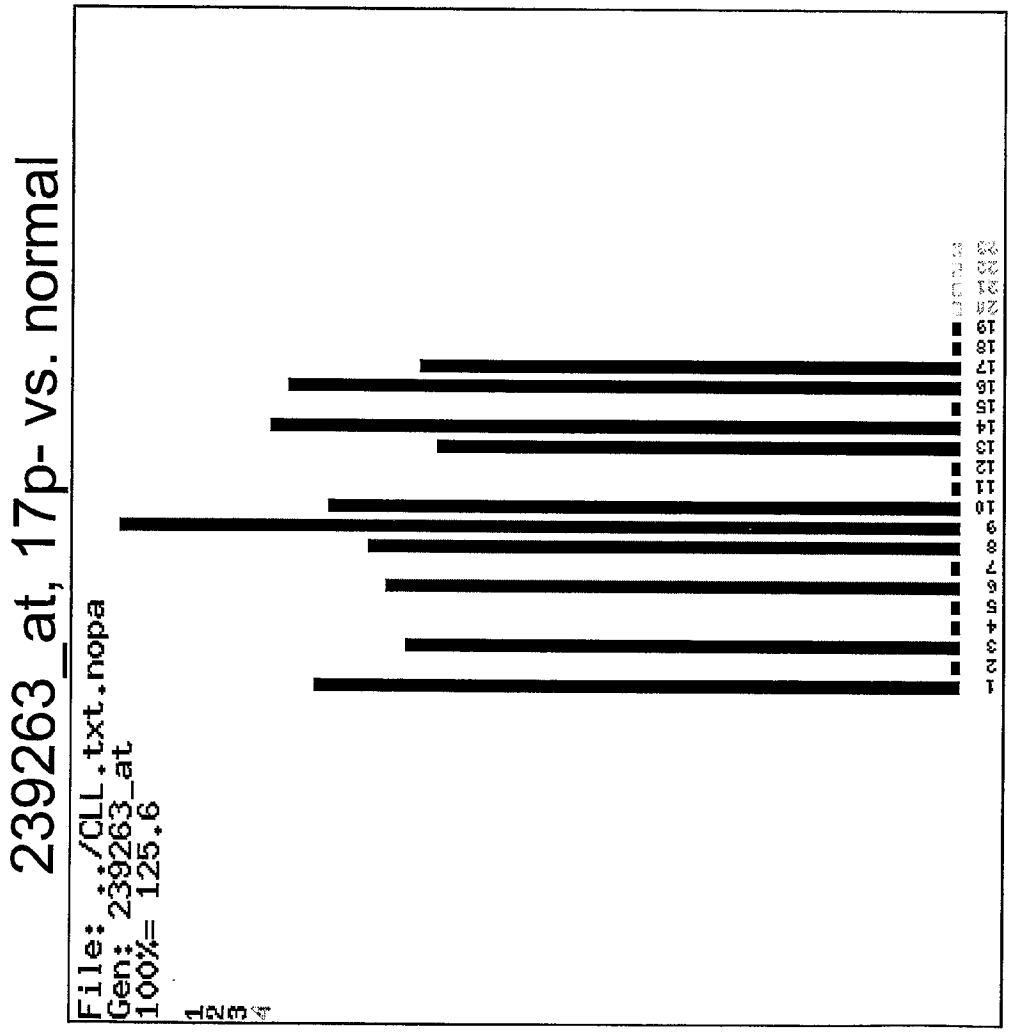

239263_at, 17p- vs. normal
File: ../CLL.txt.nopa
Gen: 239263_at
100%= 125.6
1
2
3
4
+12
11q-
13q-
17p-
normal

Figure 396

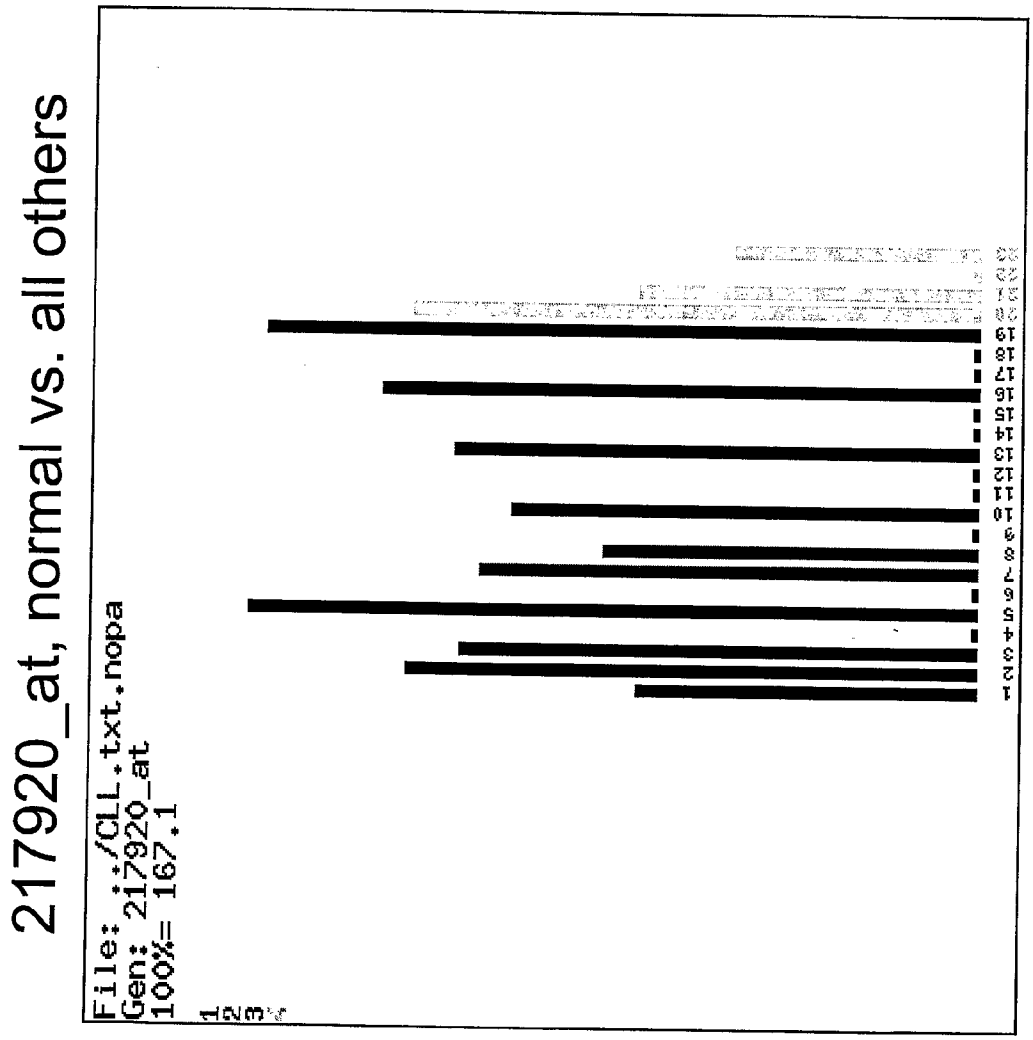

217920_at, normal vs. all others
File: ../CLL.txt.nopa
Gen: 217920_at
100%= 167.1
+12
11q-
13q-
17p-
normal

Figure 397

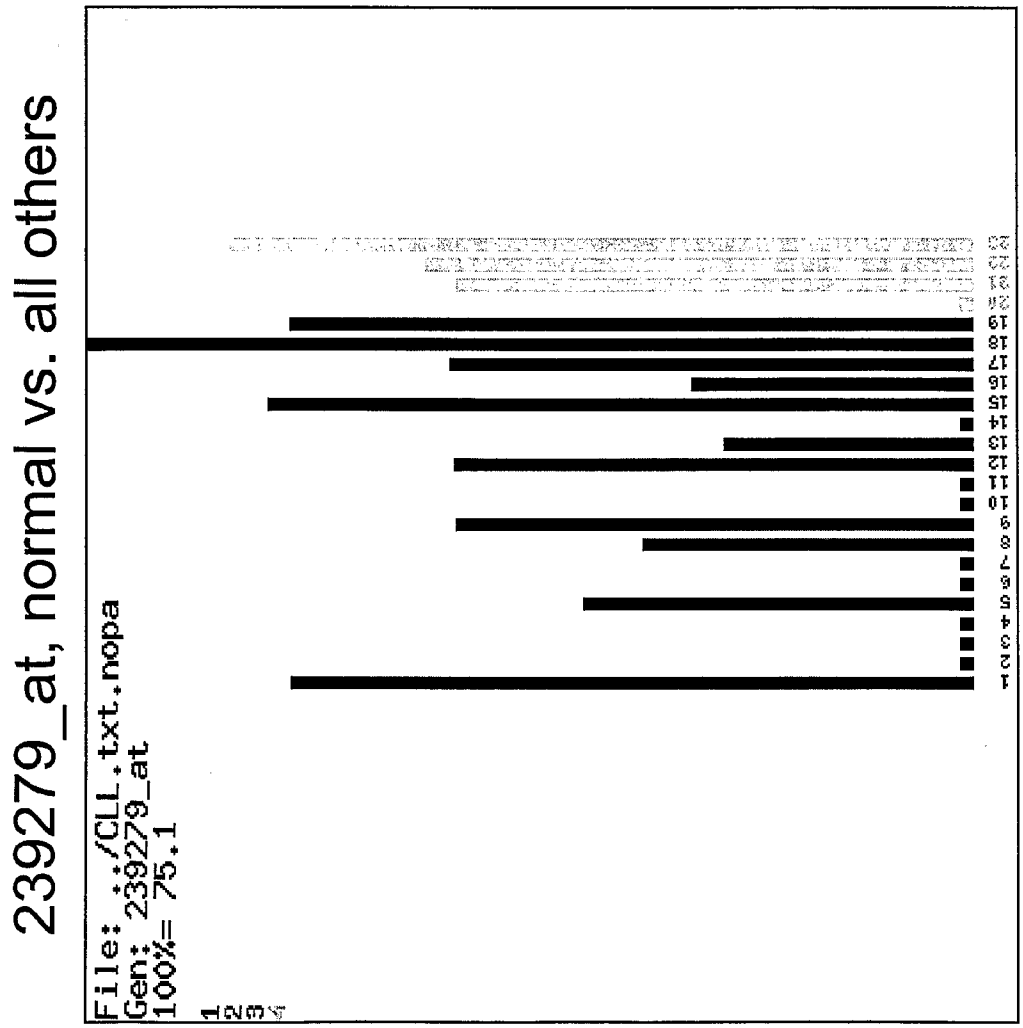

239279_at, normal vs. all others
File: ../CLL.txt.nopa
Gen: 239279_at
100%= 75.1
+12
11q-
13q-
17p-
normal

Figure 398

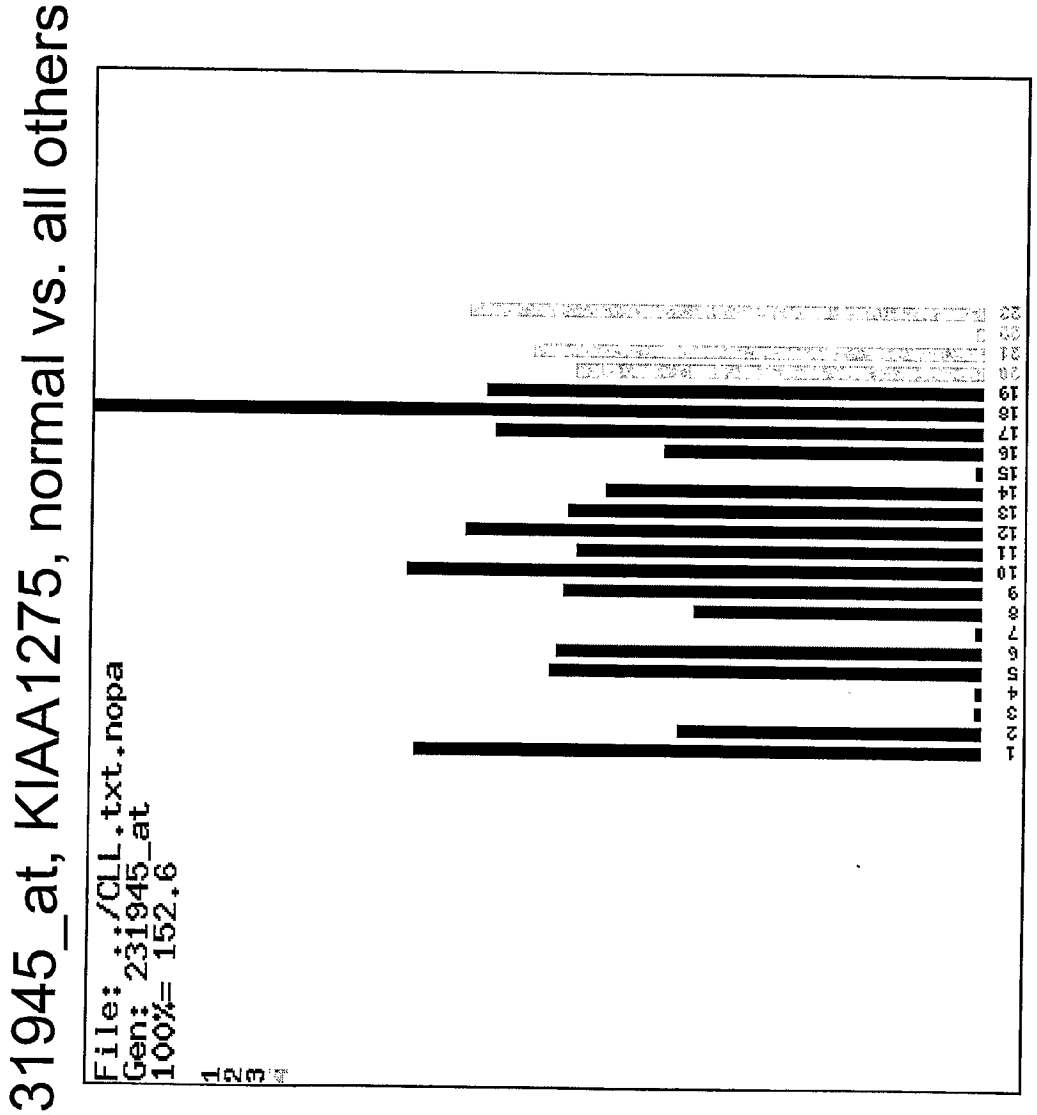

231945_at, KIAA1275, normal vs. all others
File: ../CLL.txt.nopa
Gen: 231945_at
100%= 152.6
+12
11q-
13q-
17p-
normal

Figure 399

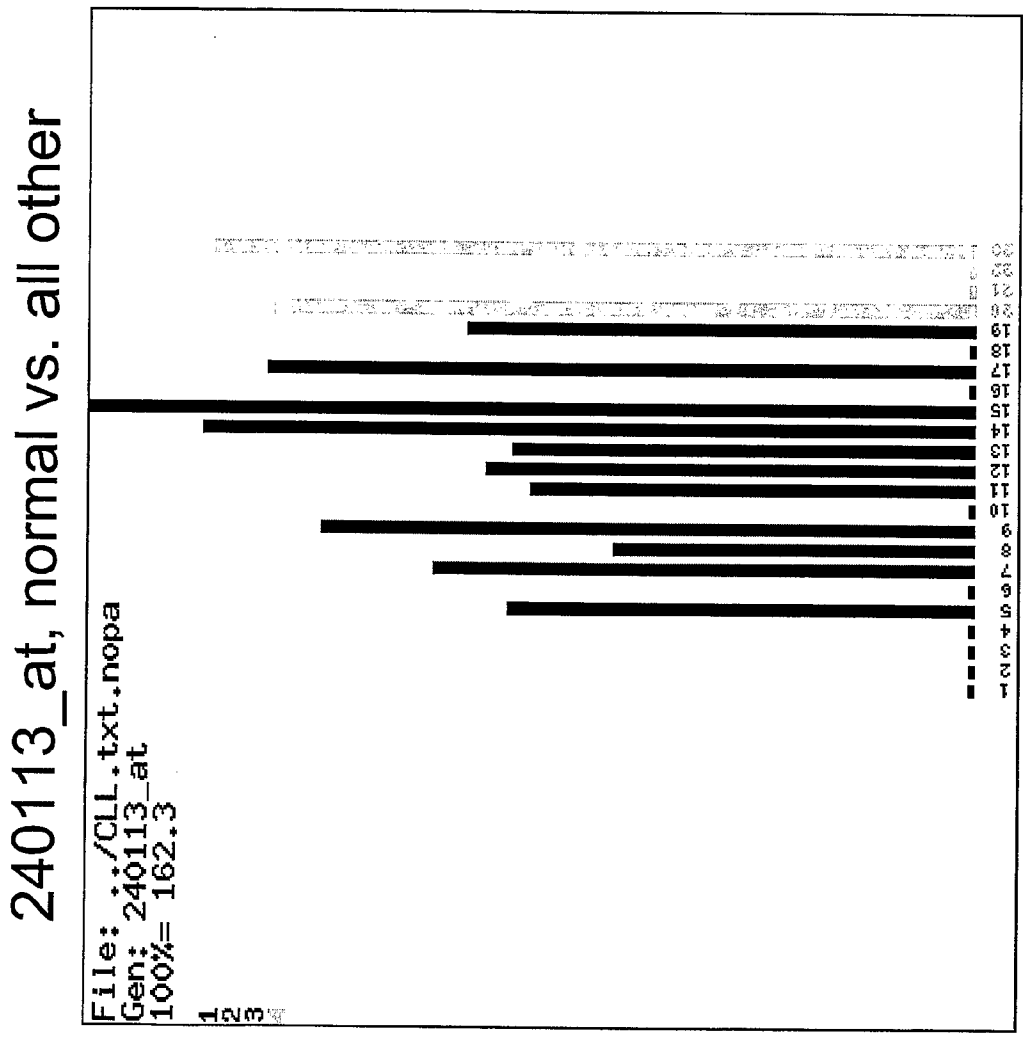

240113_at, normal vs. all other
File: ../CLL.txt.nopa
Gen: 240113_at
100%= 162.3
1 2 3
+12
11q-
13q-
17p-
normal

Figure 400

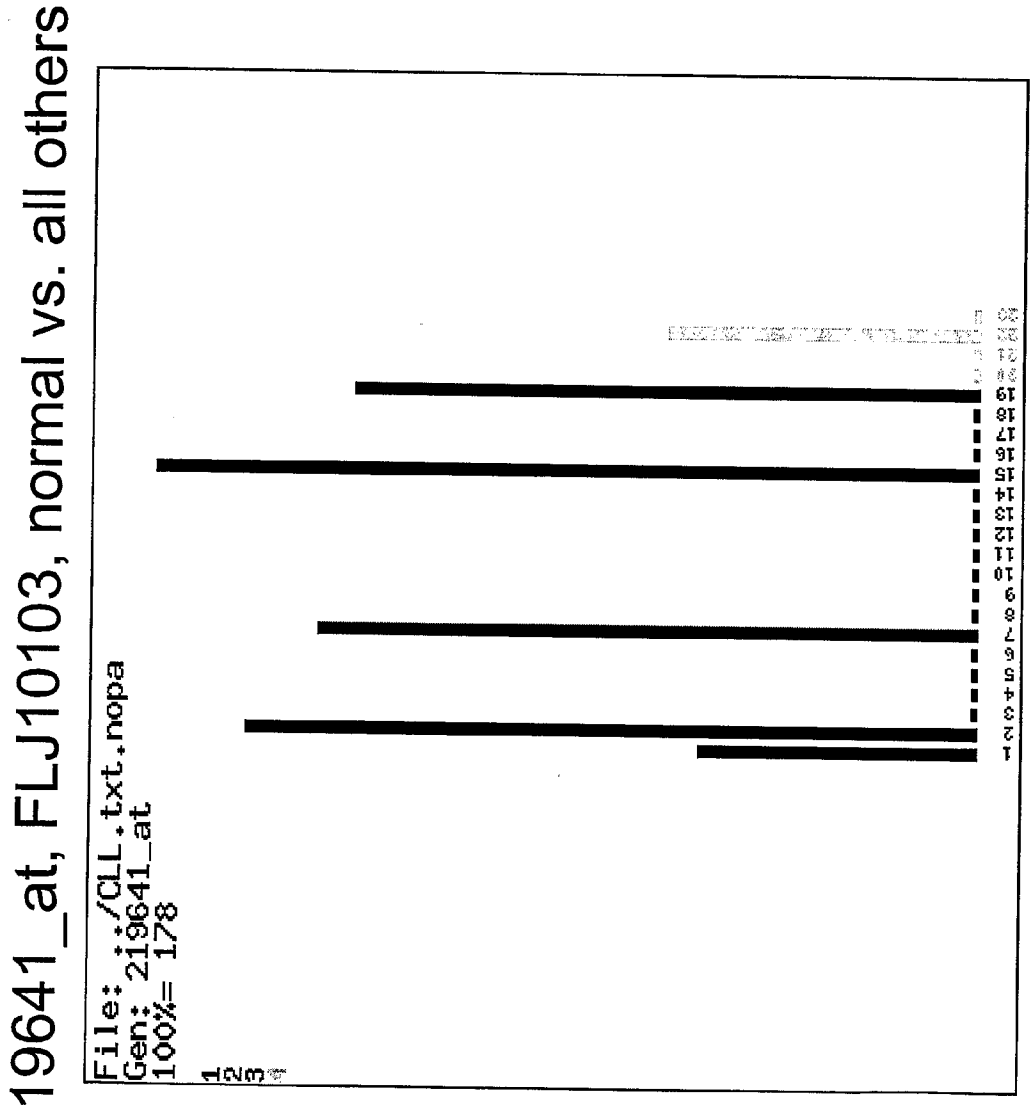

219641_at, FLJ10103, normal vs. all others
File: */CLL.txt.nopa
Gen: 219641_at
100%= 178
1
2
3
+12
11q-
13q-
17p-
normal

Figure 401

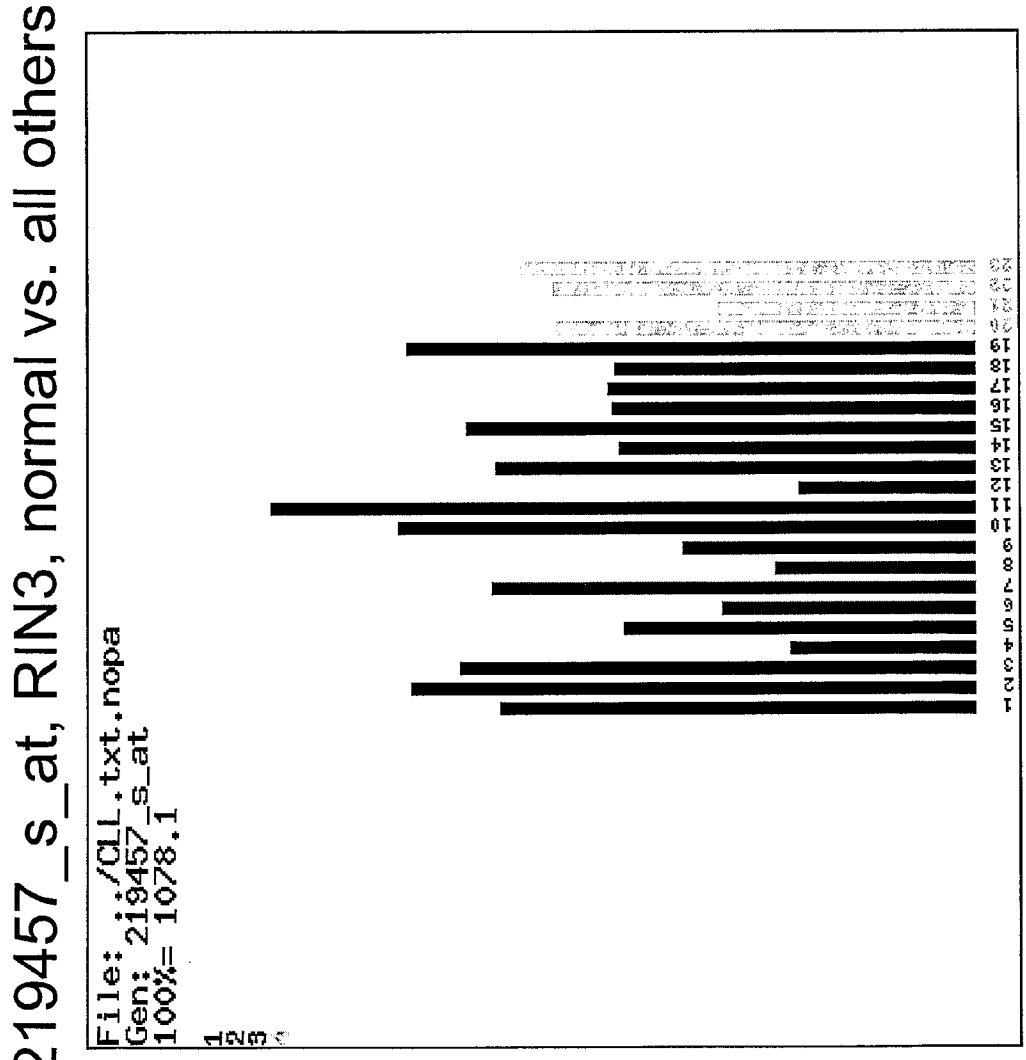

219457_s_at, RIN3, normal vs. all others
File: ../CLL.txt.nopa
Gen: 219457_s_at
100%= 1078.1
1
2
3
+12
11q-
13q-
17p-
normal

Figure 402

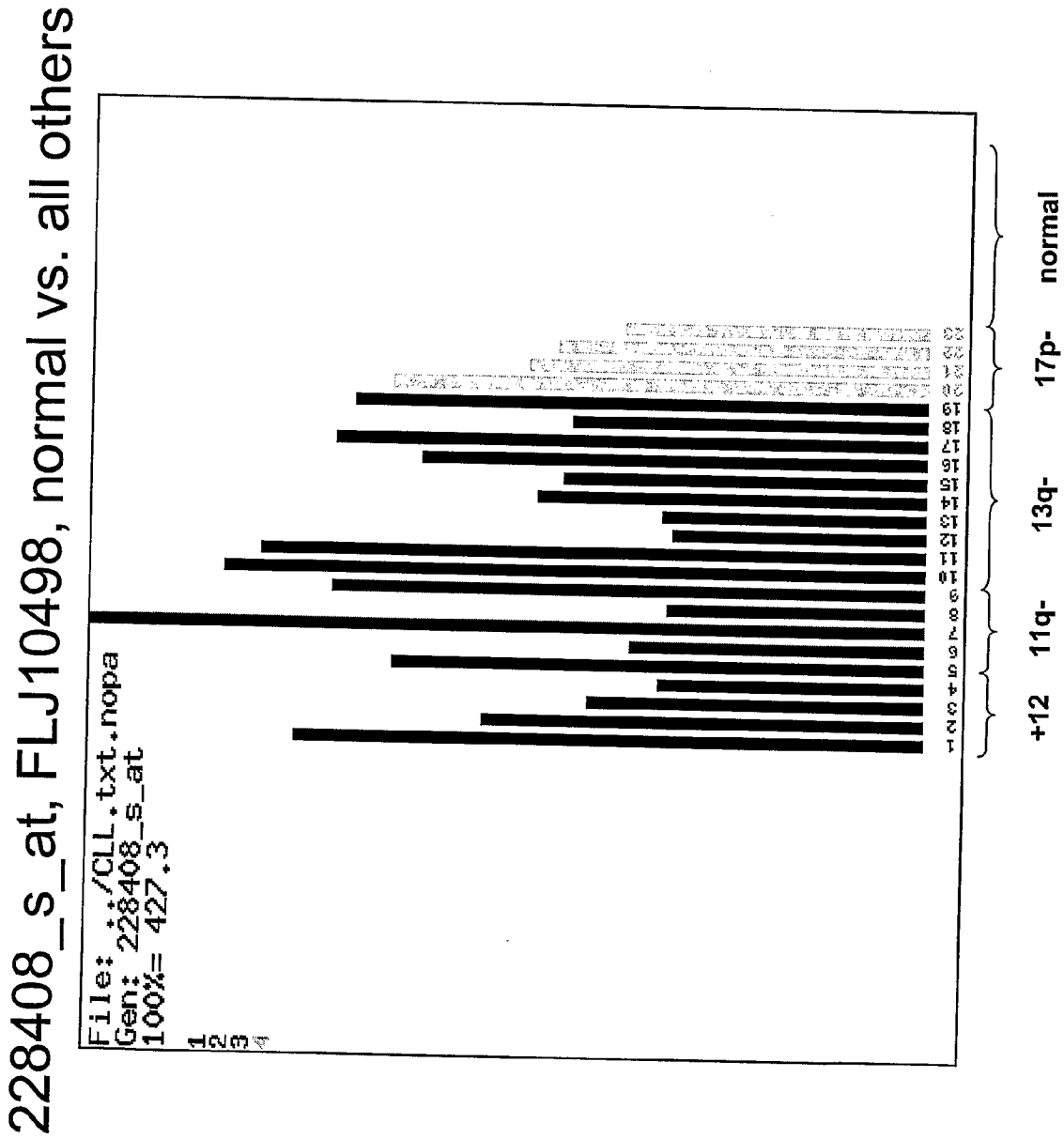

228408_s_at, FLJ10498, normal vs. all others
File: ../CLL.txt.nopa
Gen: 228408_s_at
100%= 427.3
+12
11q-
13q-
17p-
normal

Figure 403

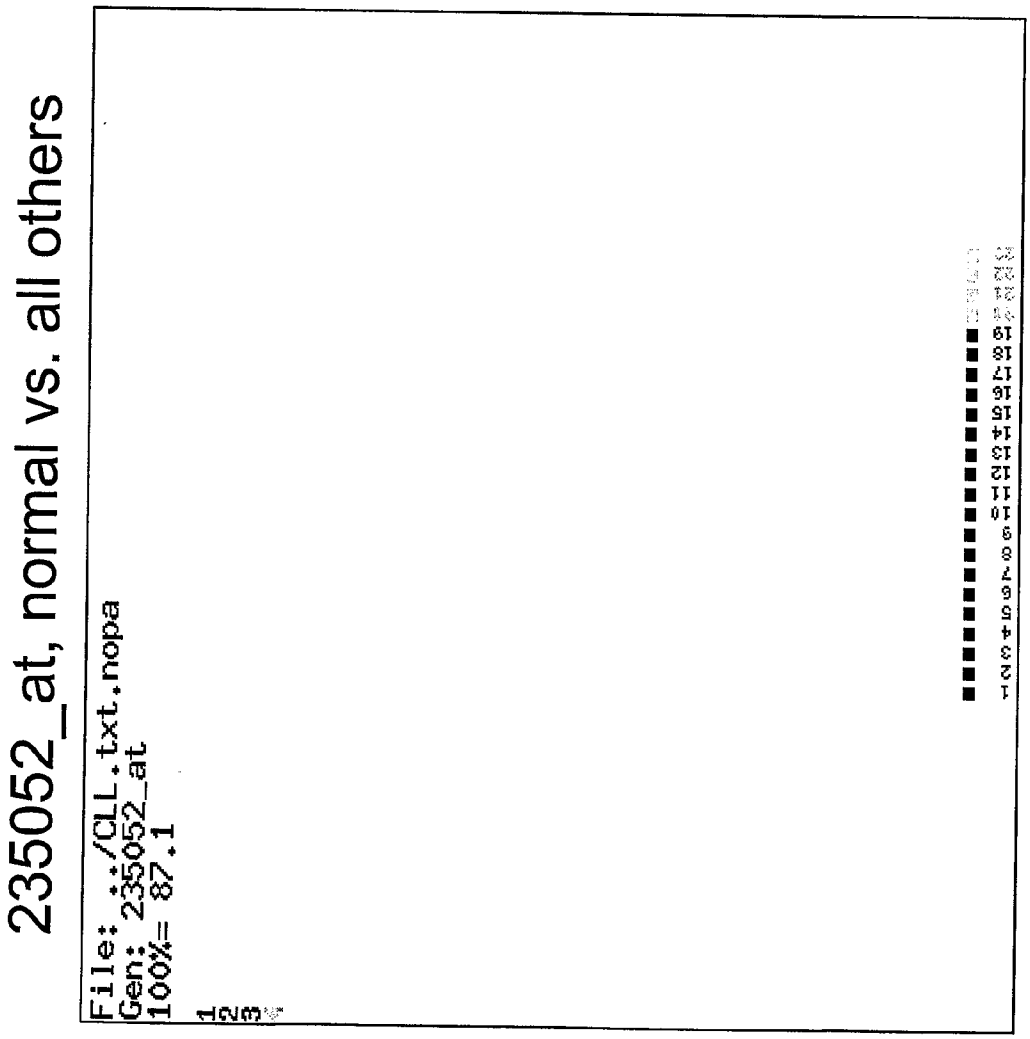

235052_at, normal vs. all others
File: ../CLL.txt.nopa
Gen: 235052_at
100%= 87.1
1 2 3
+12
11q-
13q-
17p-
normal

Figure 404

219013_at, FLJ21634, ALL vs. all others

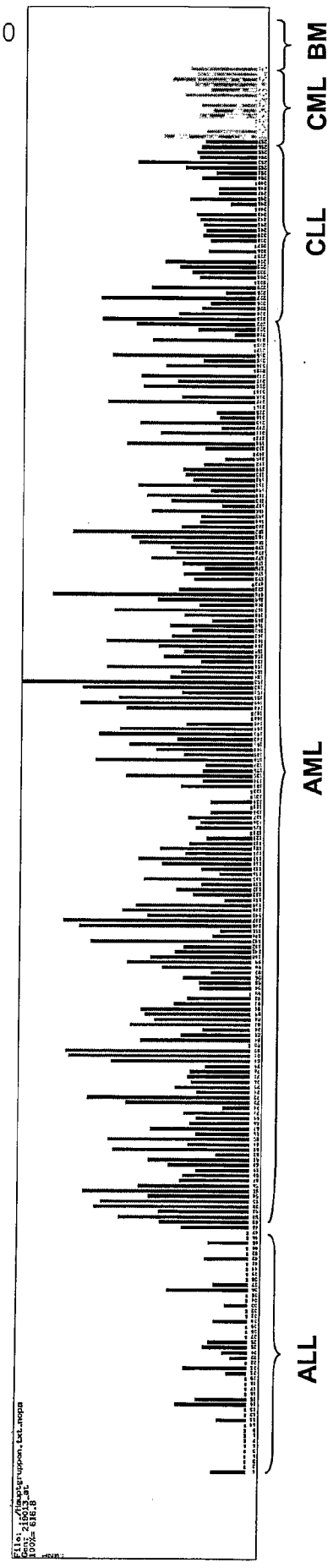


Figure 405

243362_s_at, LEF1, ALL vs. all others

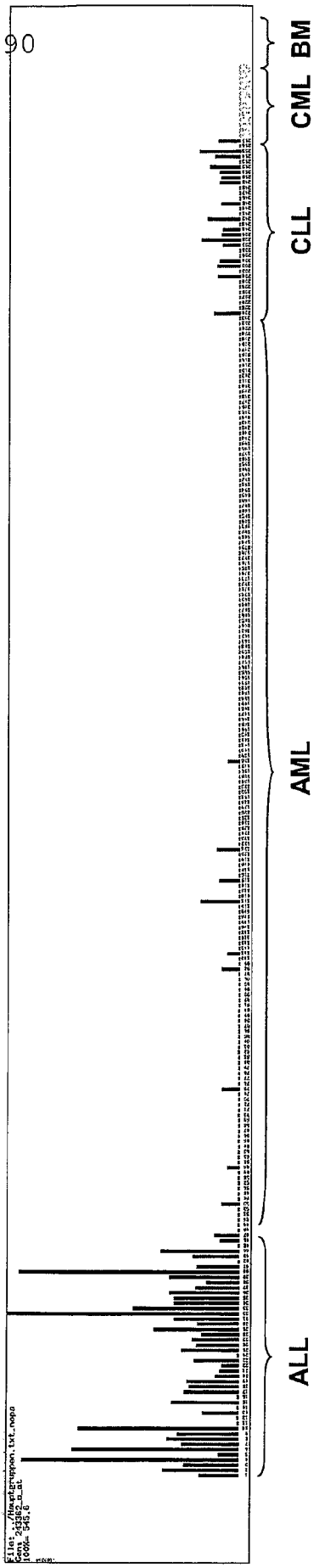


Figure 406

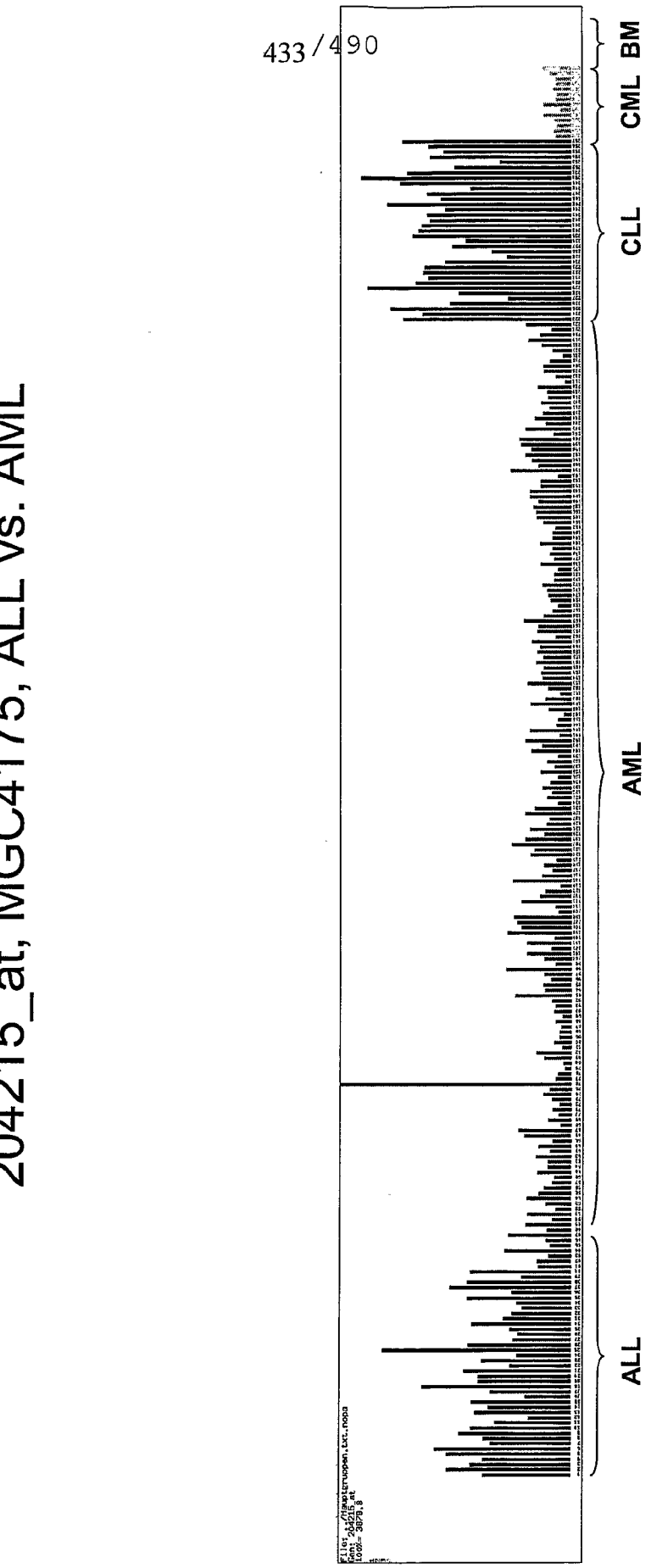


Figure 407

225927_at, MAP3K1, ALL vs. CLL

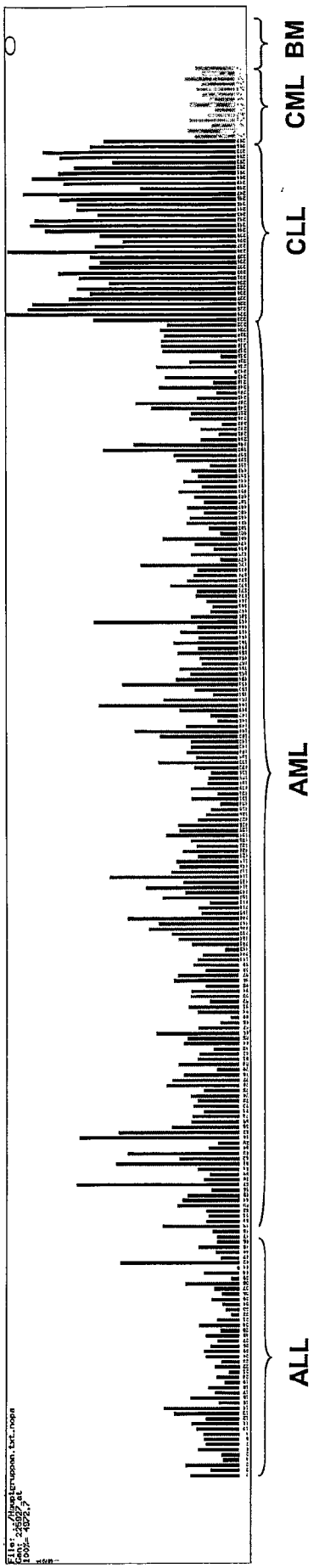


Figure 408

205557_at, BPI, ALL vs. CML

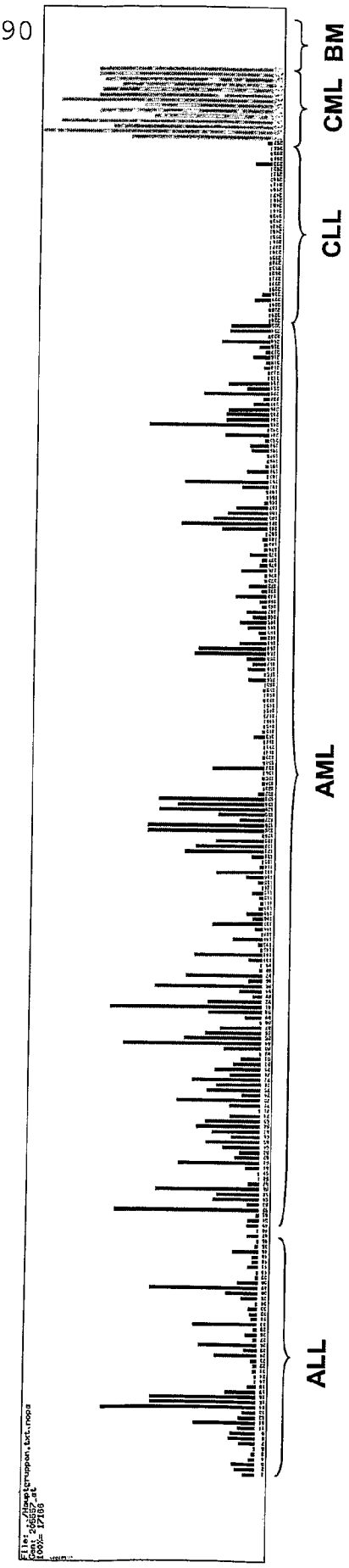


Figure 409

223280_x_at, MS4A6A, ALL vs. normal BM

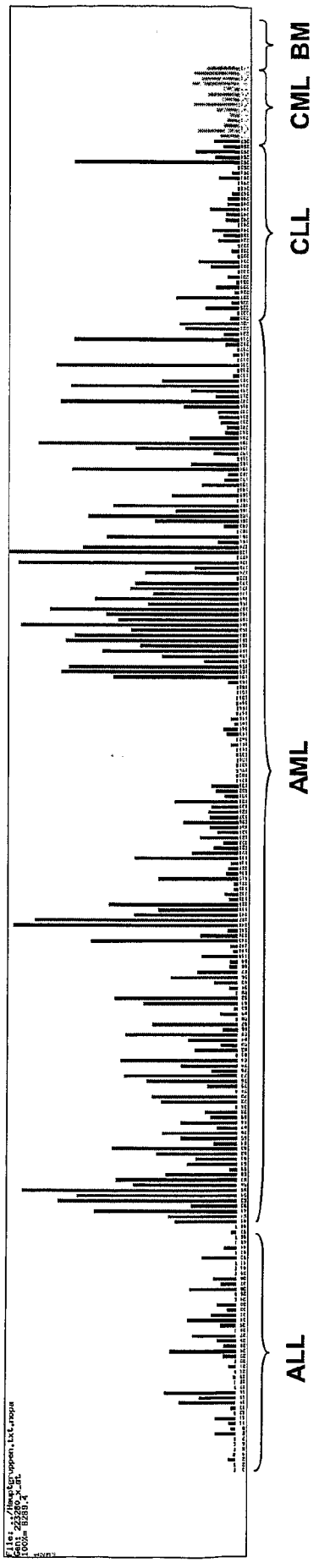


Figure 410

224356_x_at, MS4A6A, ALL vs. normal BM

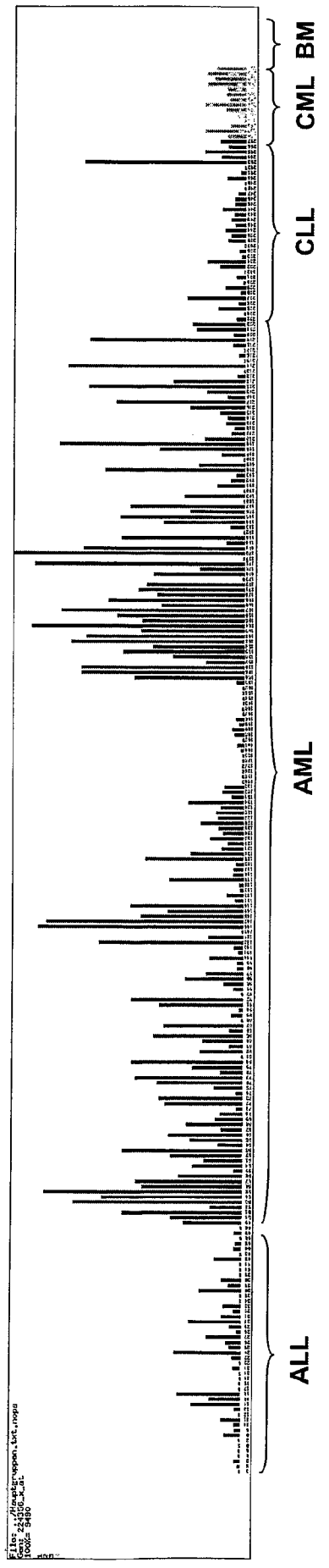


Figure 411

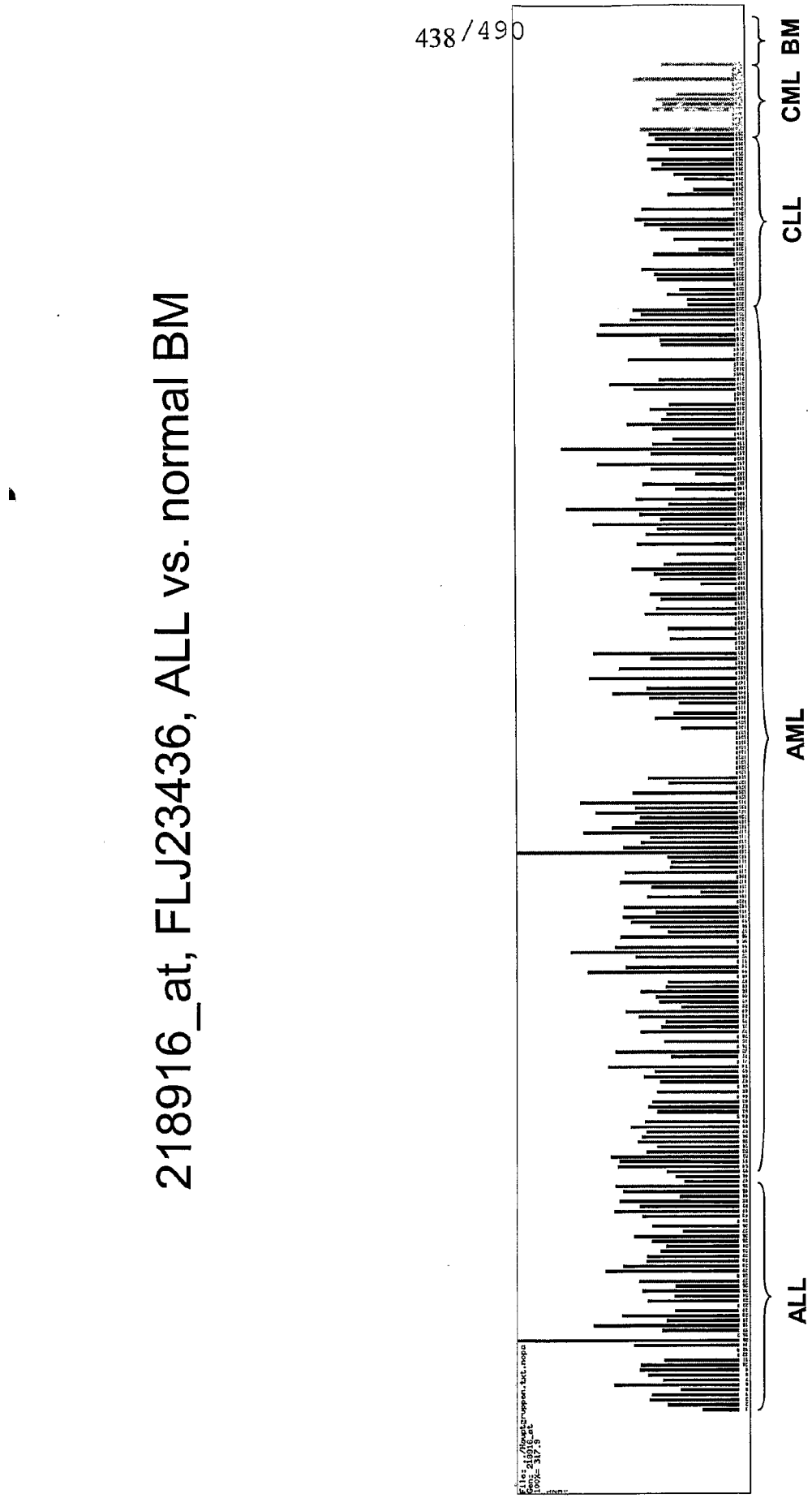


Figure 412

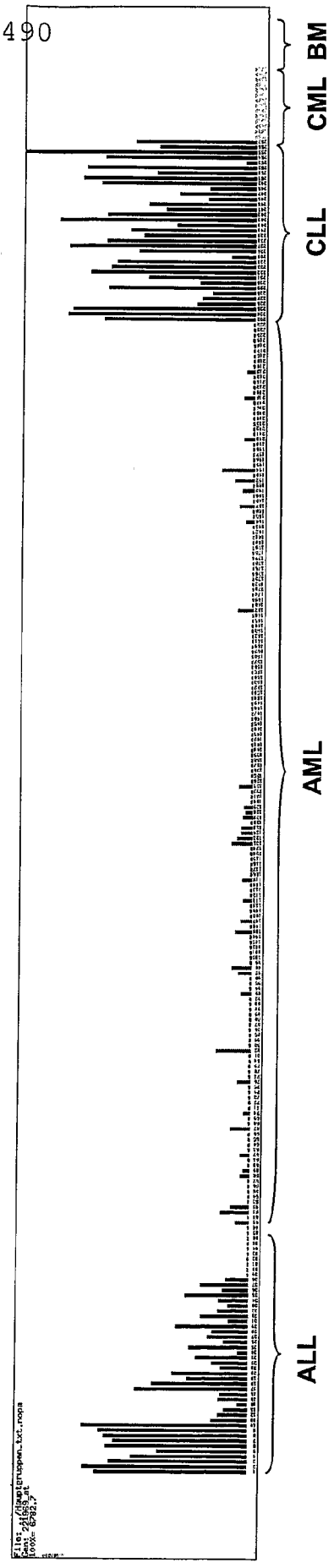


Figure 413

206398_s_at, CD19, AML vs. Rest

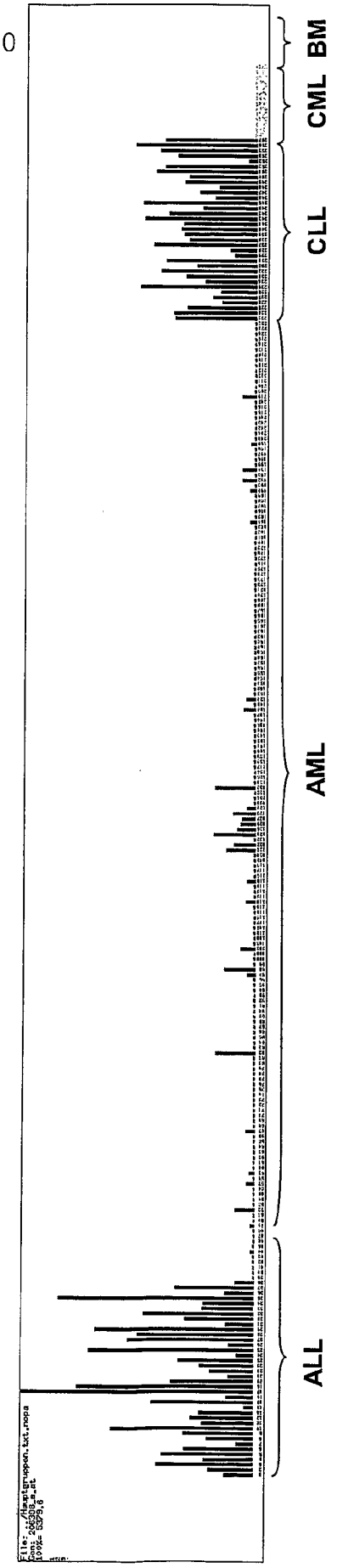


Figure 414

223514_at, CARD11, AML vs. CLL

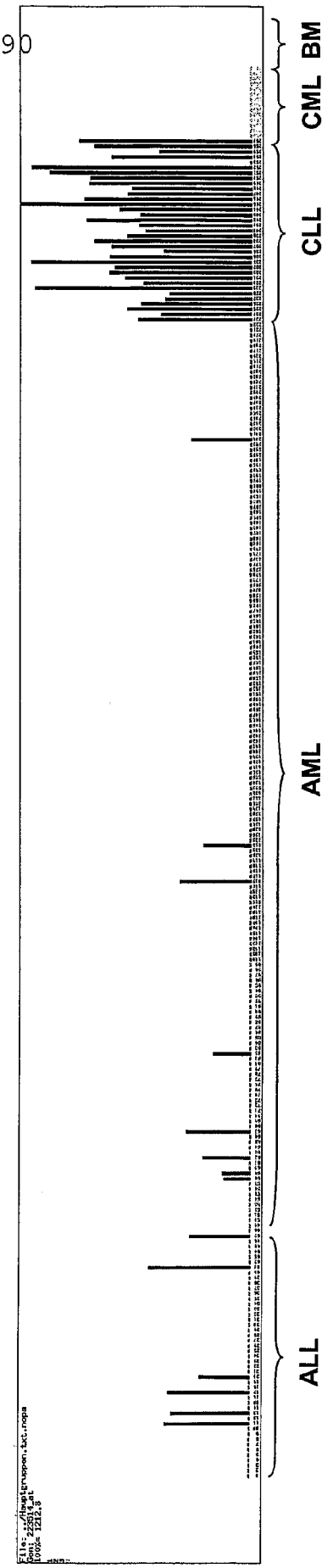


Figure 415

207802_at, SGP28, AML vs. CML

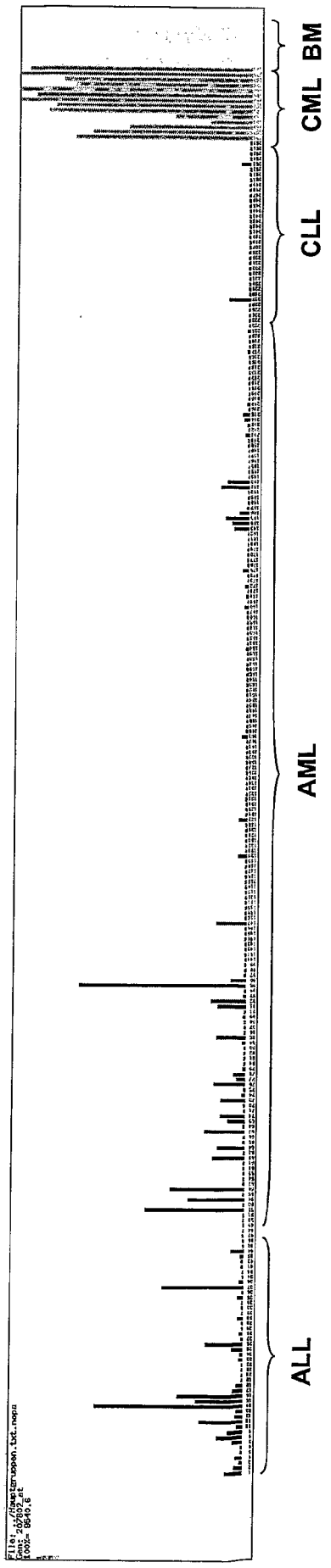


Figure 416

209772_s_at, CD24, AML vs. CML

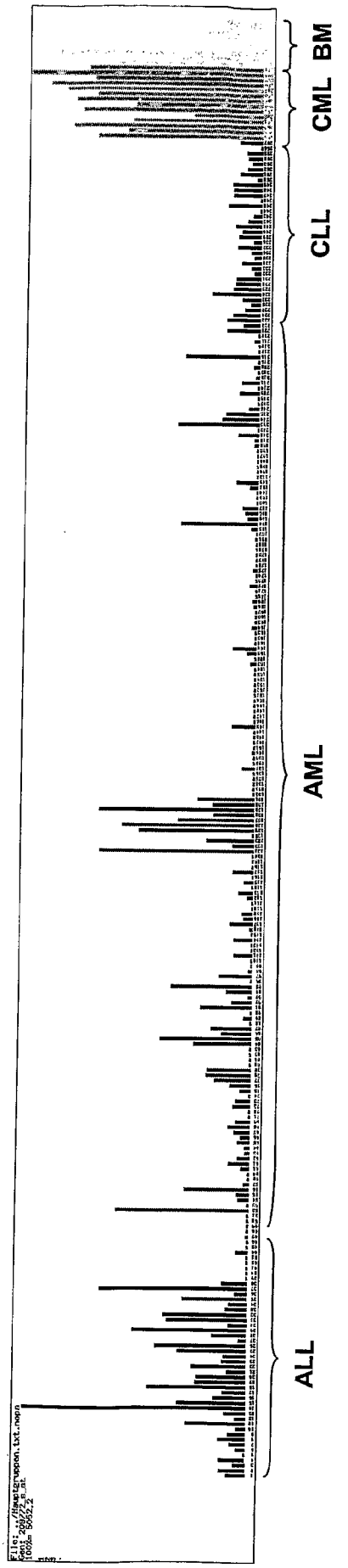


Figure 417

206676_at, CEACAM8, AML vs. CML

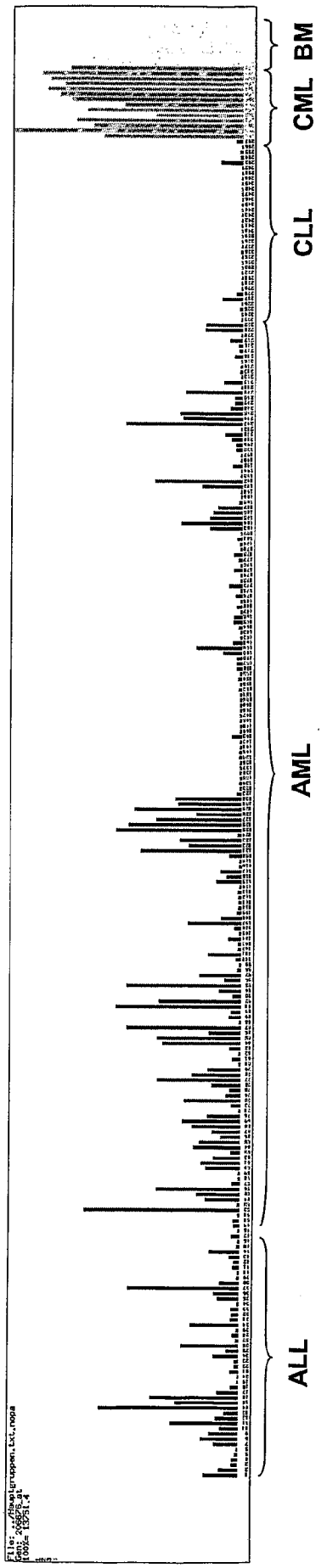


Figure 418

203936_s_at, MMP9, AML vs. CML

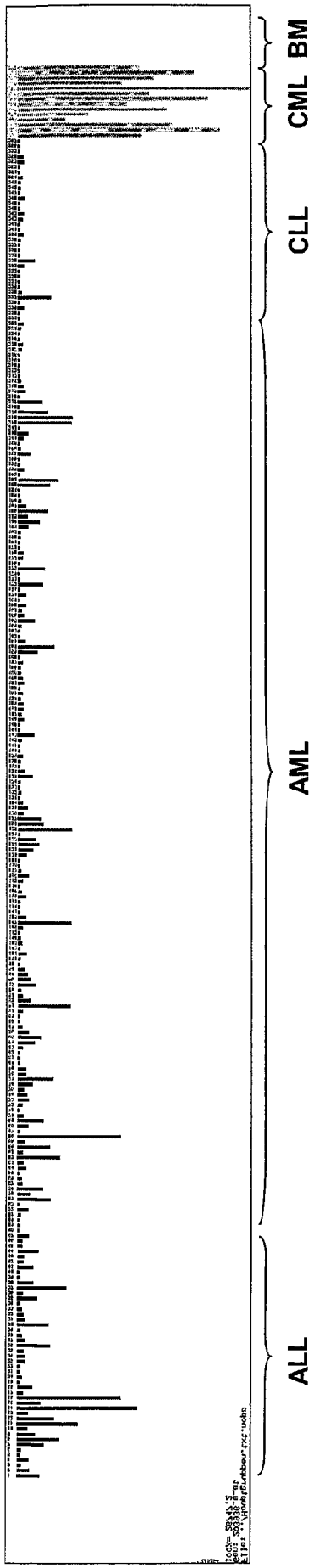


Figure 419

201029_s_at, MIC2, AML vs. CML

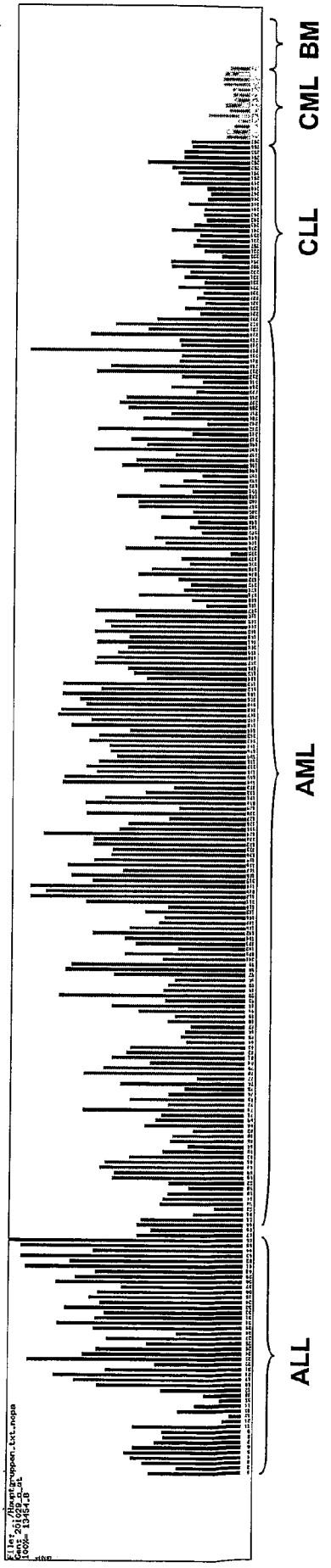


Figure 420

223894_s_at, FTS, AML vs. CML

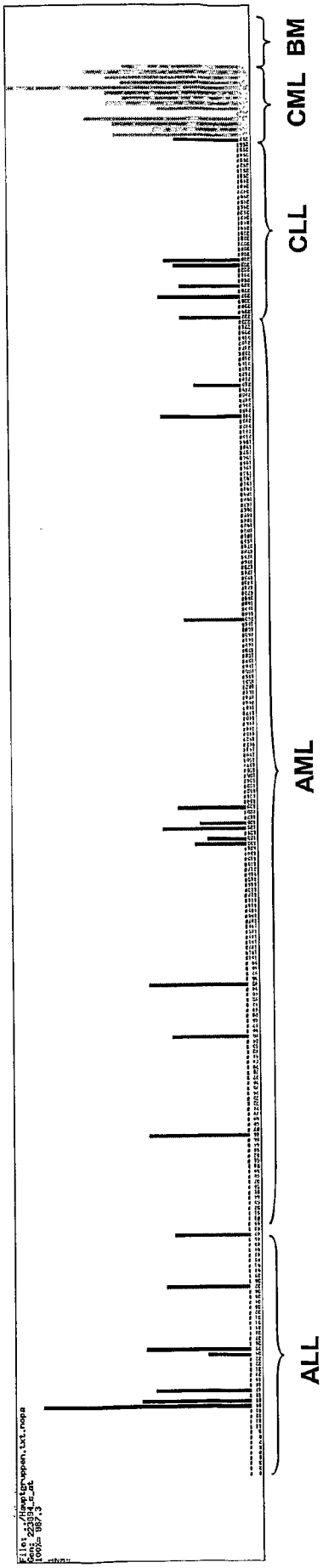


Figure 421

207269_at, DEFA4, AML vs. CML

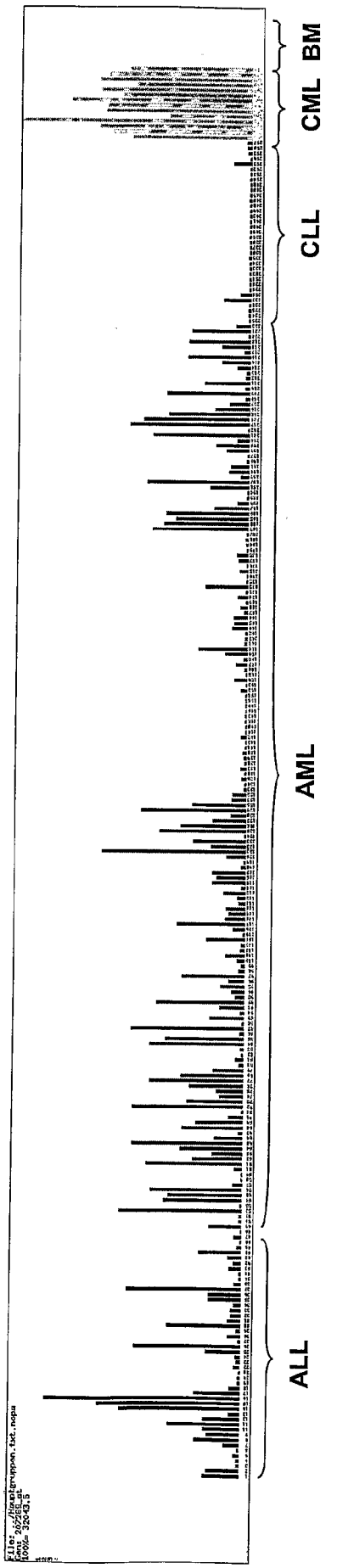


Figure 422

202018_s_at, LTF, AML vs. normal BM

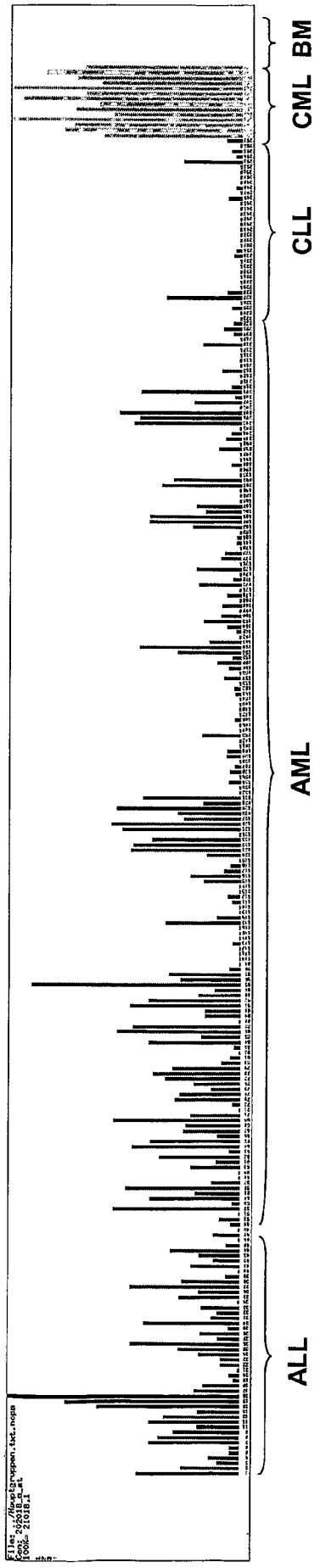


Figure 423

239287_at, CLL vs. all others

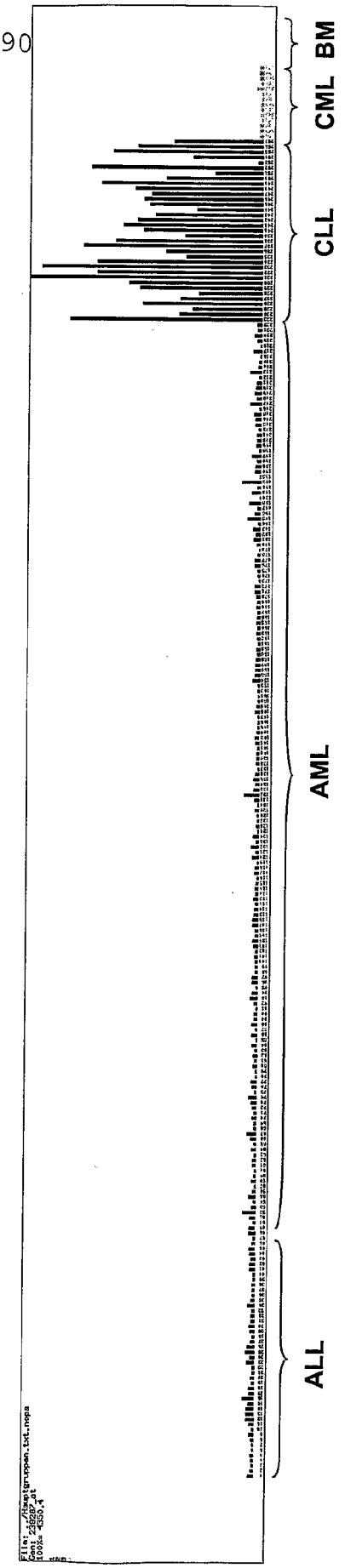


Figure 424

210254_at, CLL vs. CML

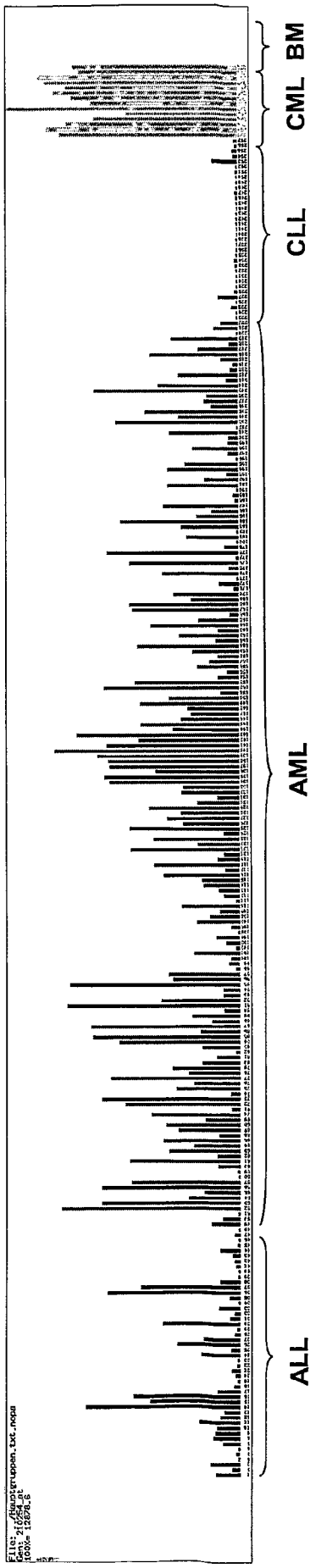


Figure 425

210613_s_at, SYNGR1, CLL vs. normal BM

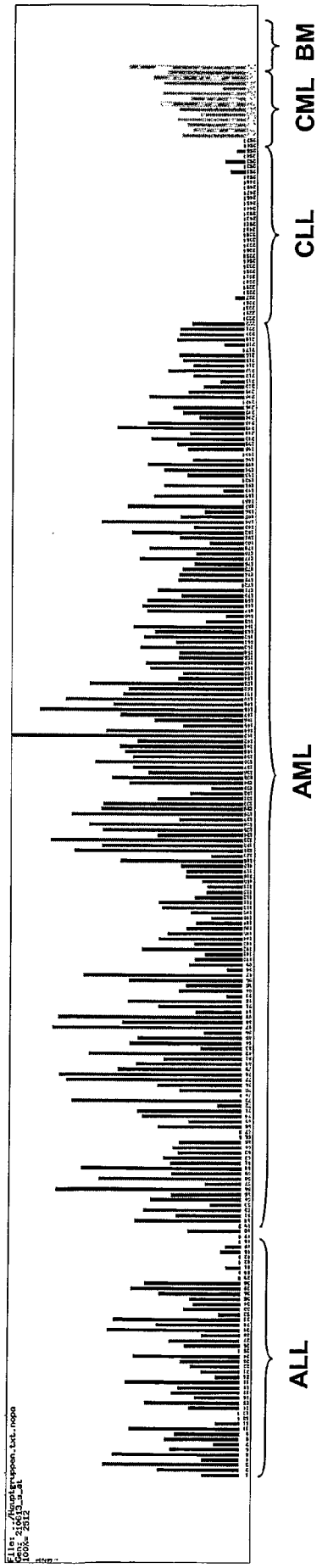


Figure 426

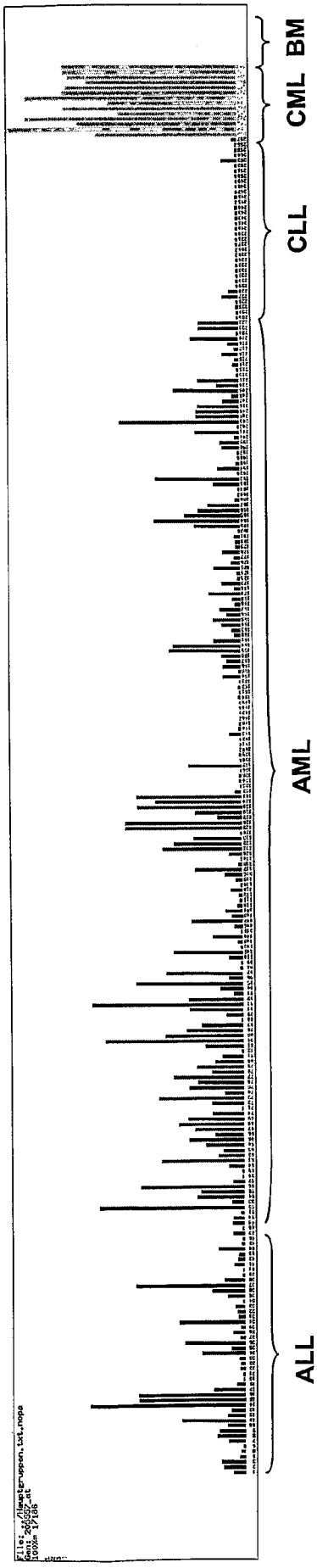


Figure 427

209772_s_at, CD24, CML vs. all others

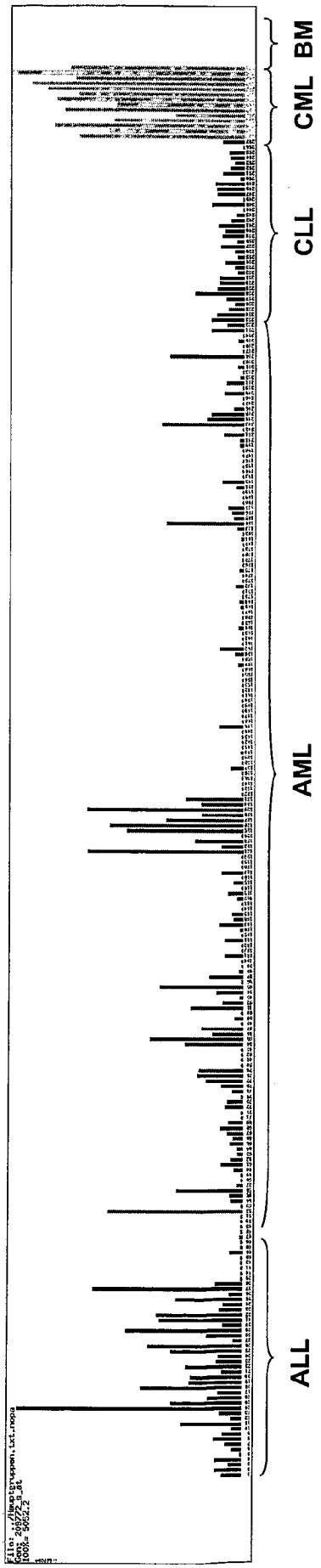


Figure 428

227198_at, CML vs. normal BM

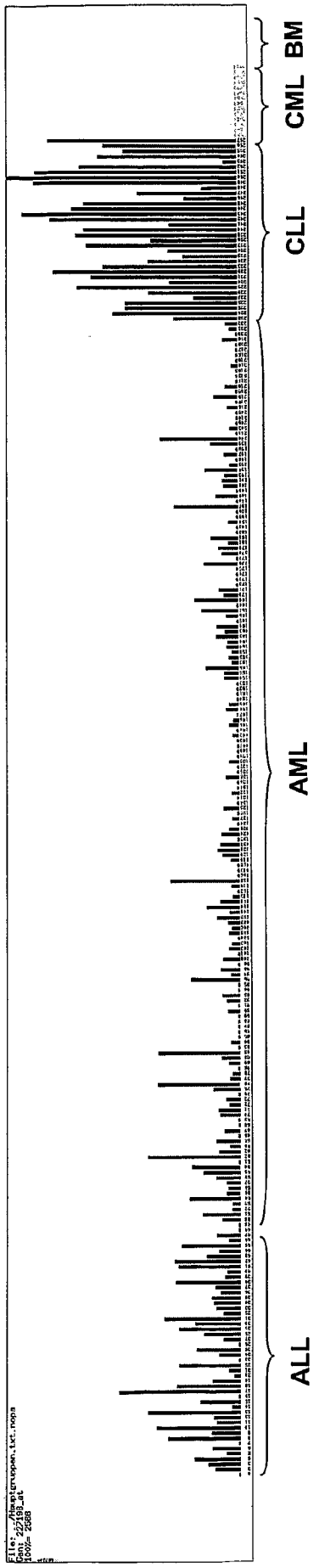


Figure 429

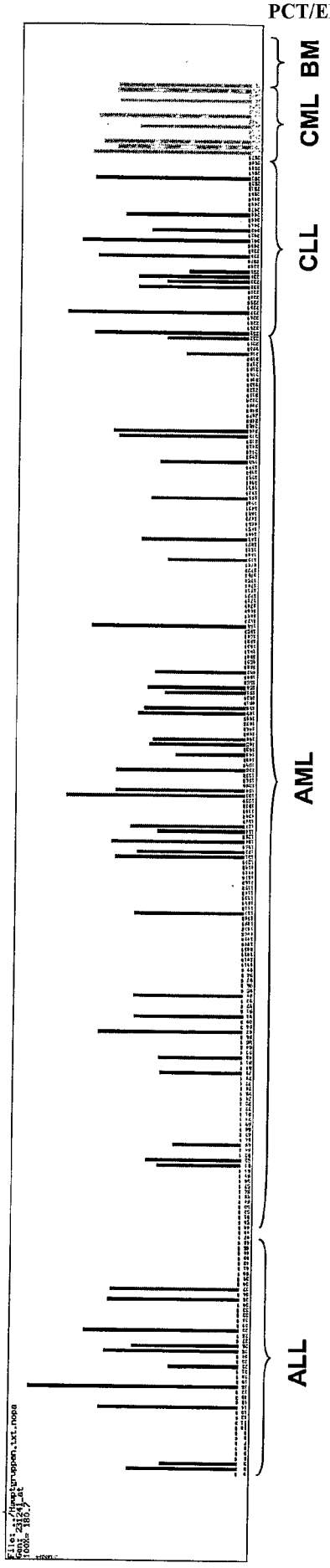


Figure 430

227497_at, normal BM vs. all others

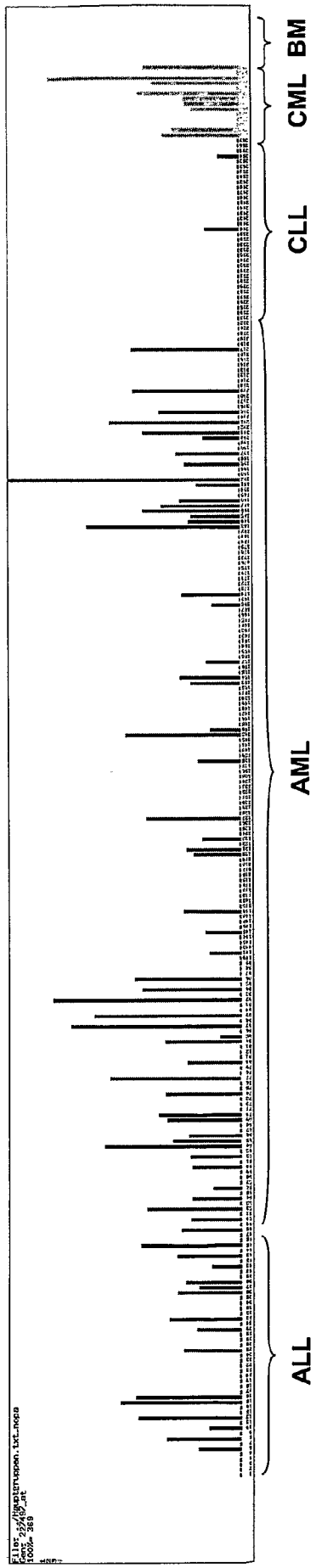


Figure 431

202580_x_at, FOXM1, CLL

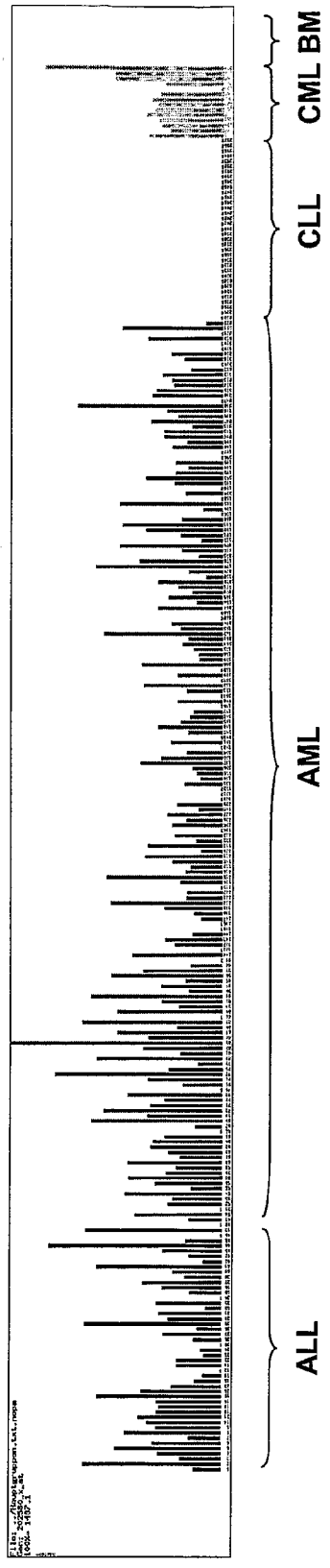


Figure 432

202709_at, FMOD, CLL

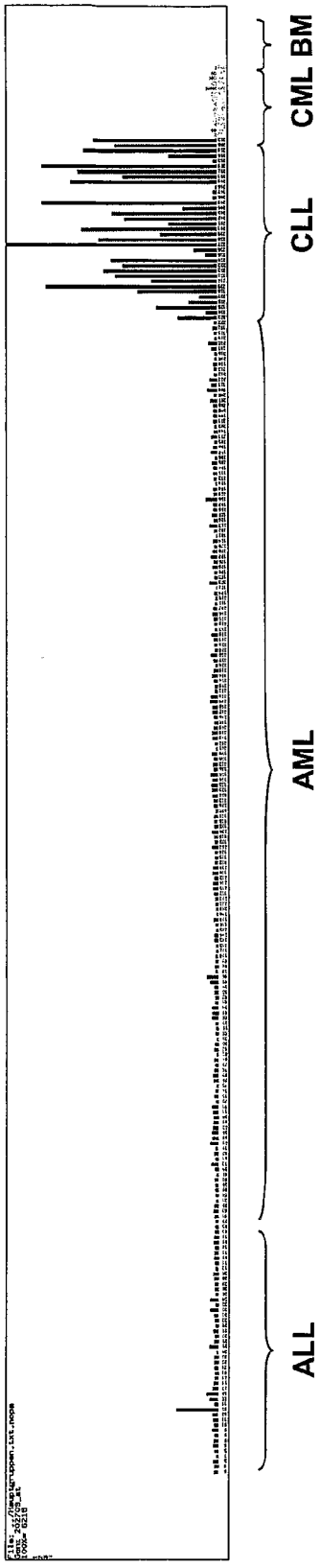


Figure 433

202503_s_at, KIAA0101, CLL

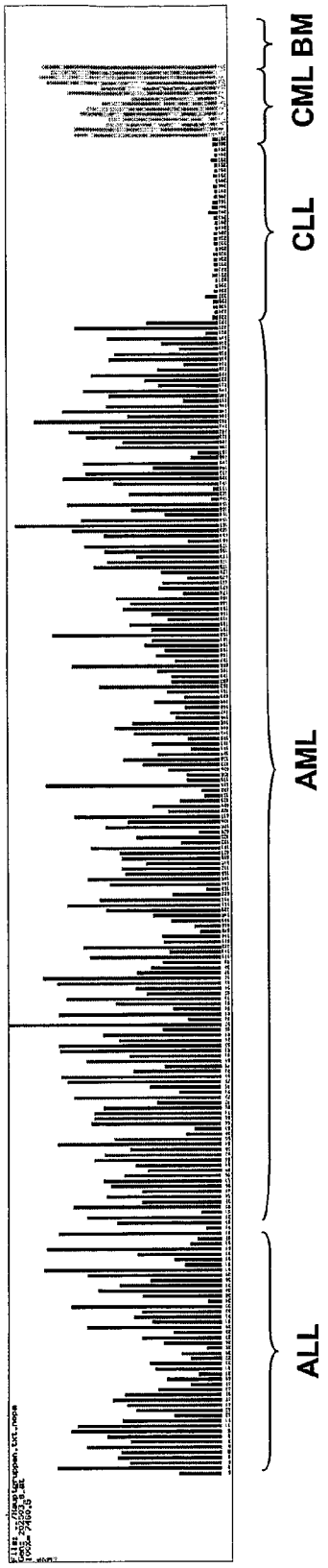


Figure 434

204882_at, KIAA0053, CLL

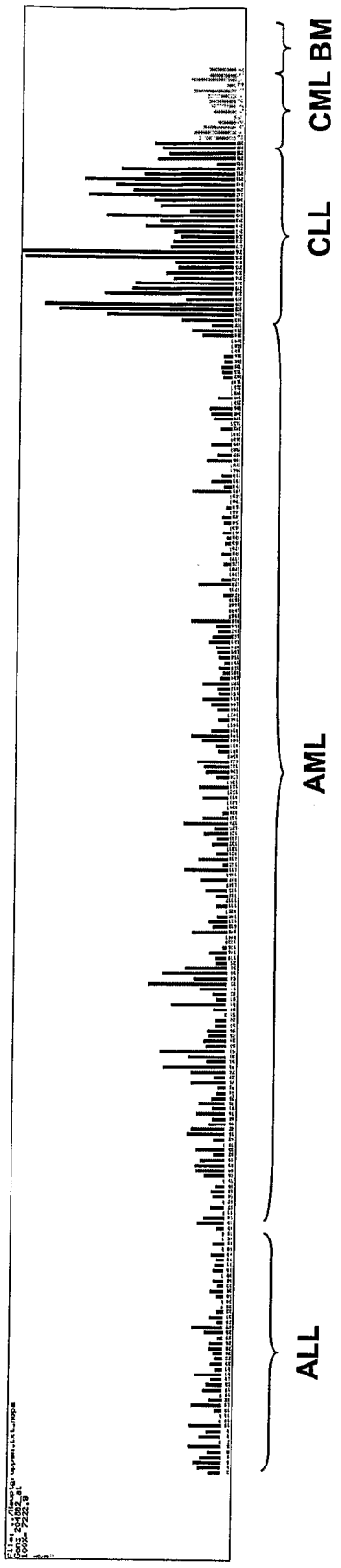


Figure 435

218090_s_at, CLL

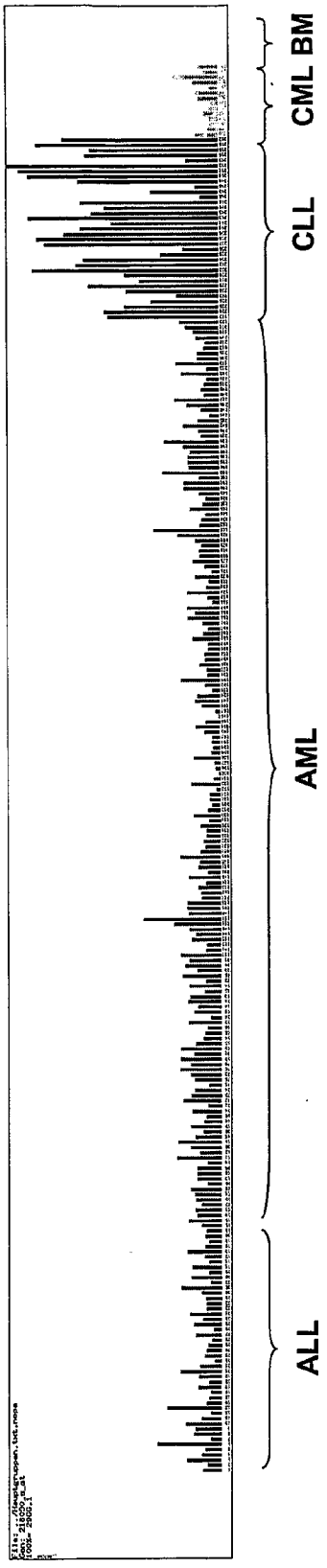


Figure 436

211352_s_at, NCOA3, CLL

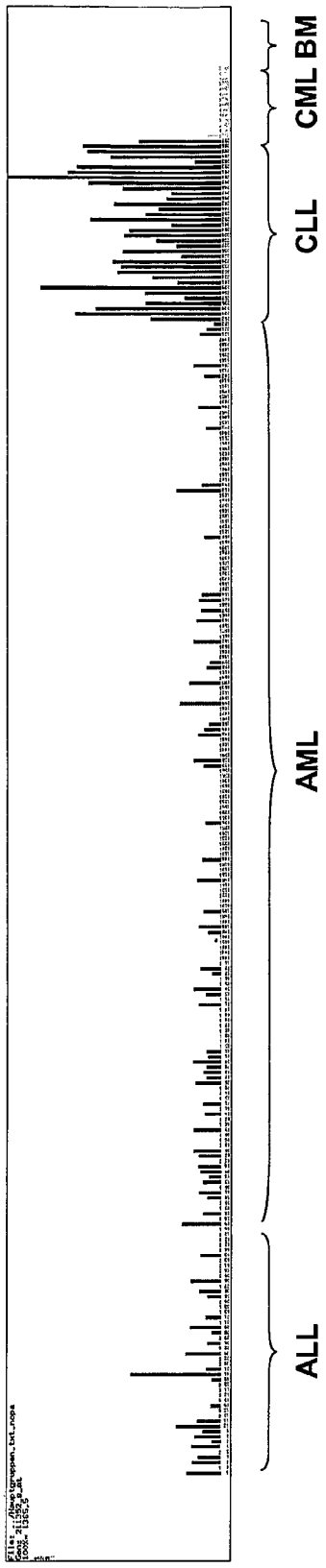


Figure 437

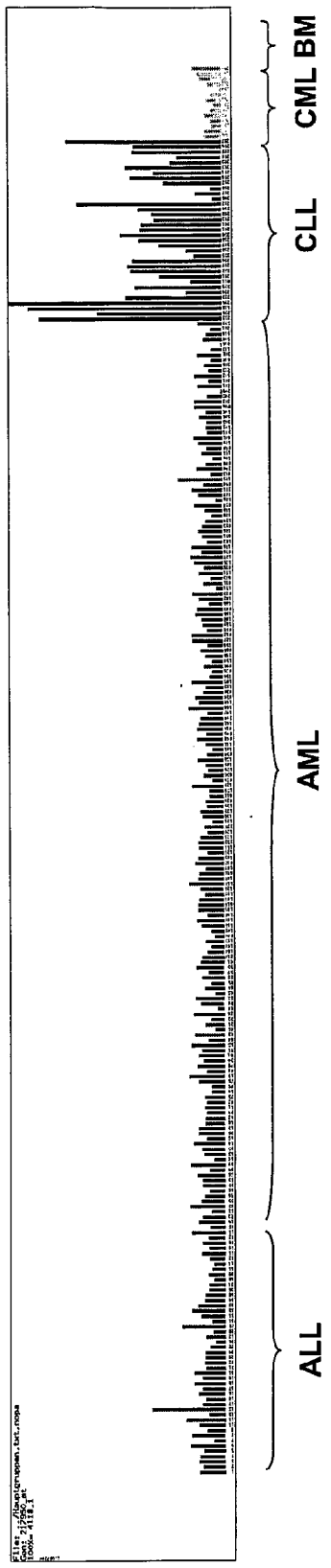


Figure 438

228471_at, CLL

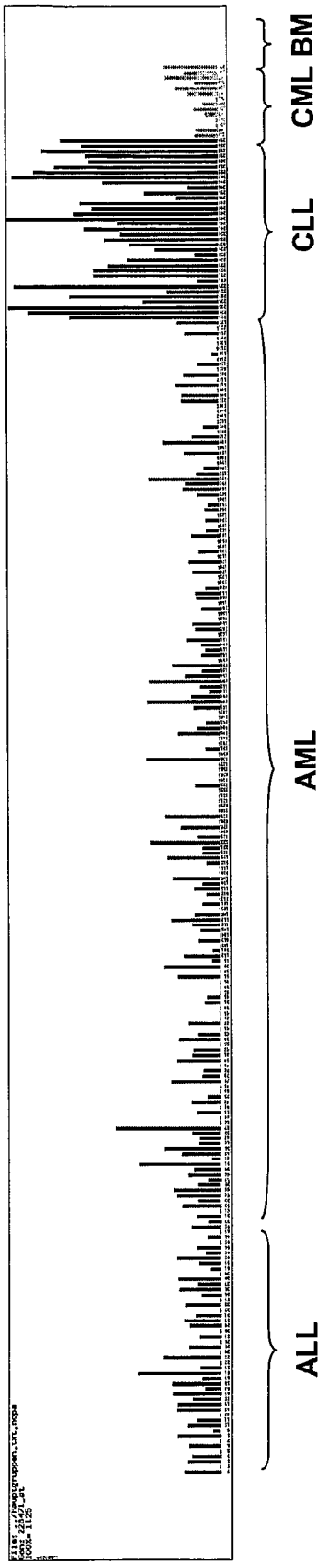


Figure 439

226147_s_at, CLL

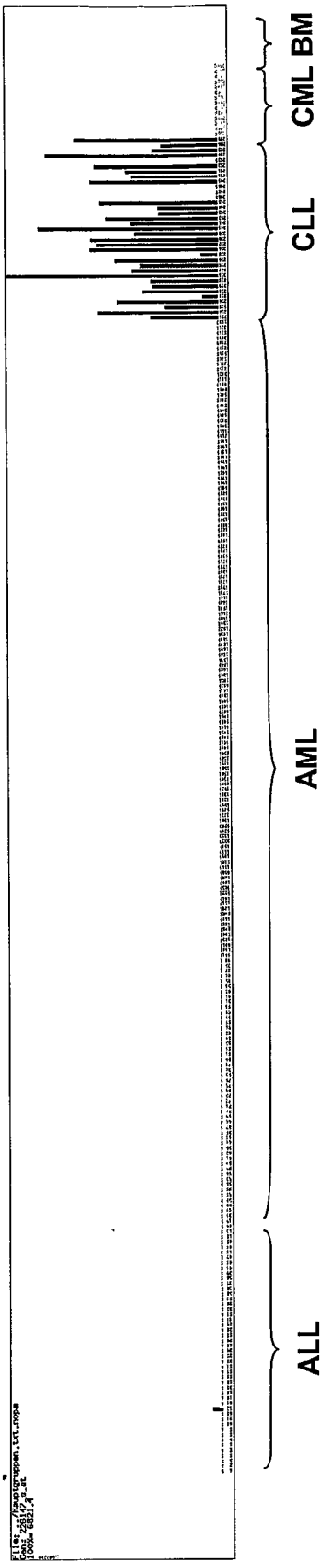


Figure 440

239287_at, CLL

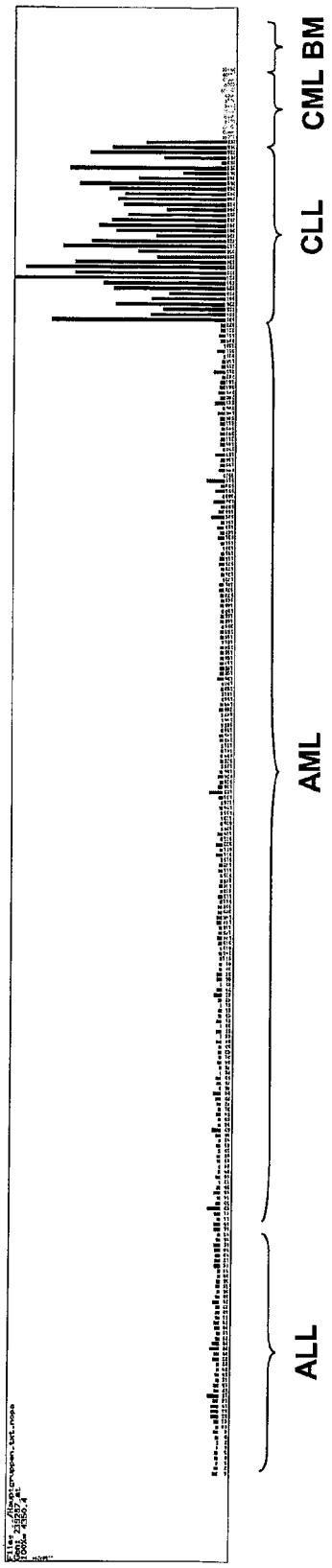


Figure 441

205051_s_at, KIT, AML

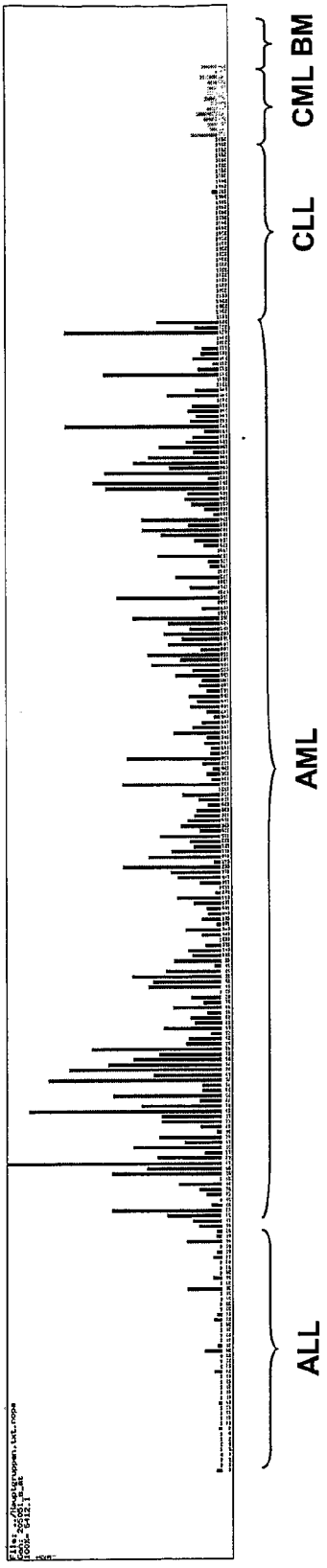


Figure 442

214761_at, OAZ, ALL

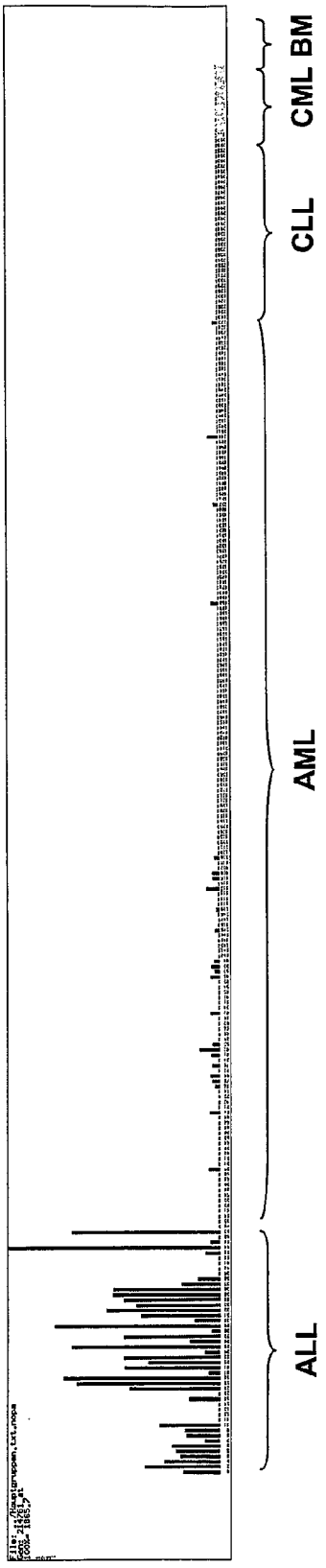


Figure 443

231854_at, CML

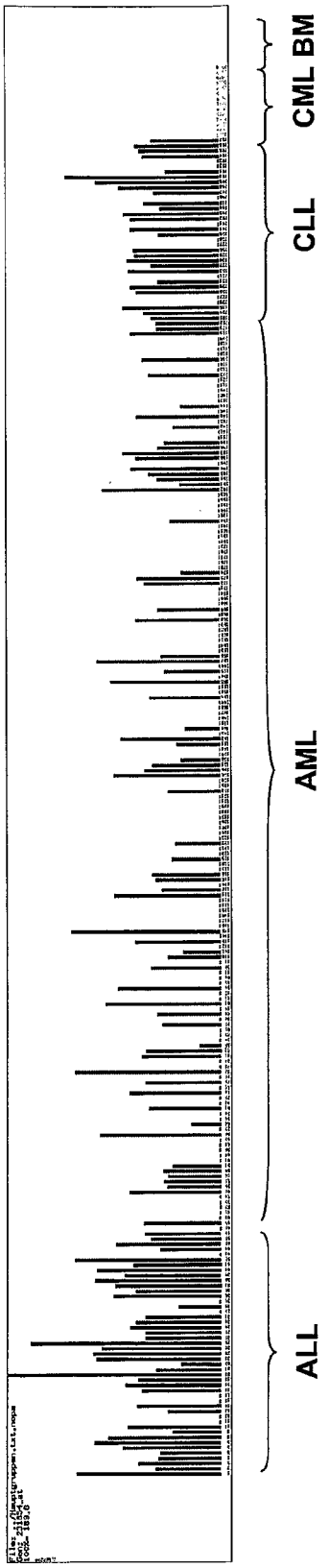


Figure 444

211404_s_at, APLP2, AML

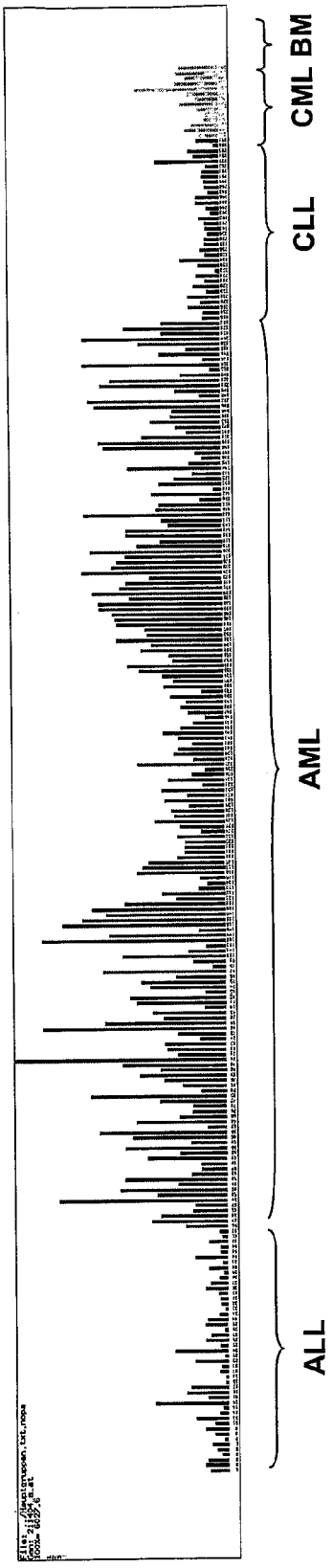


Figure 445

205382_s_at, DF, AML high

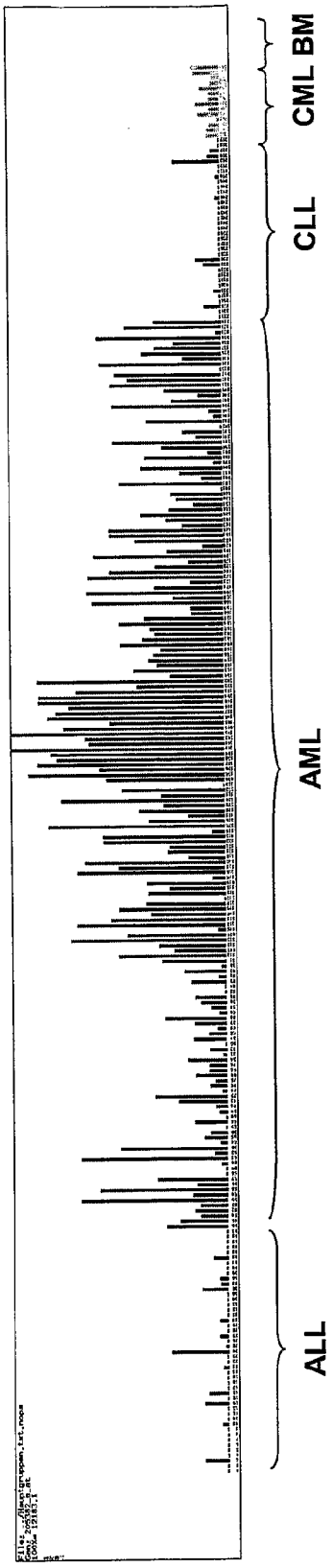


Figure 446

205599_at, TRAF1, CML absent, CLL high

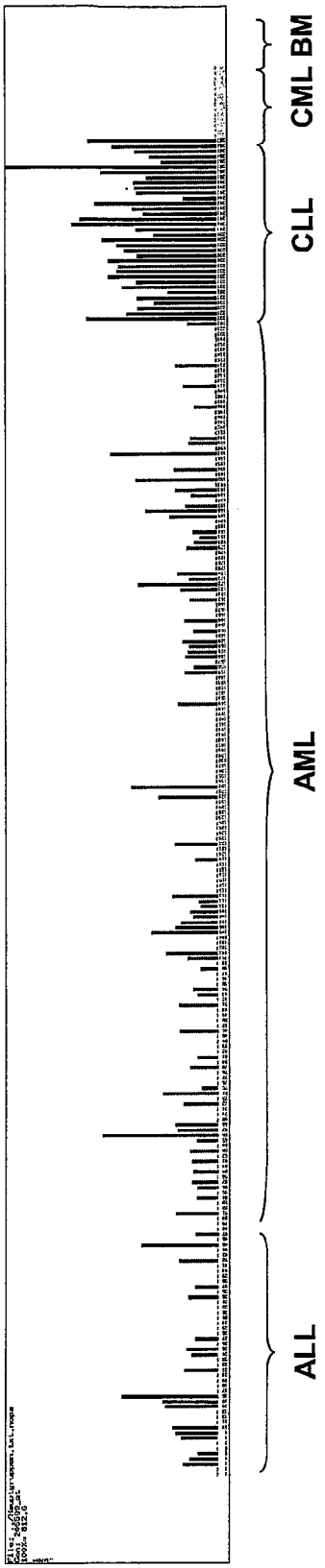


Figure 447

210948_s_at, LEF1, lymphatic high

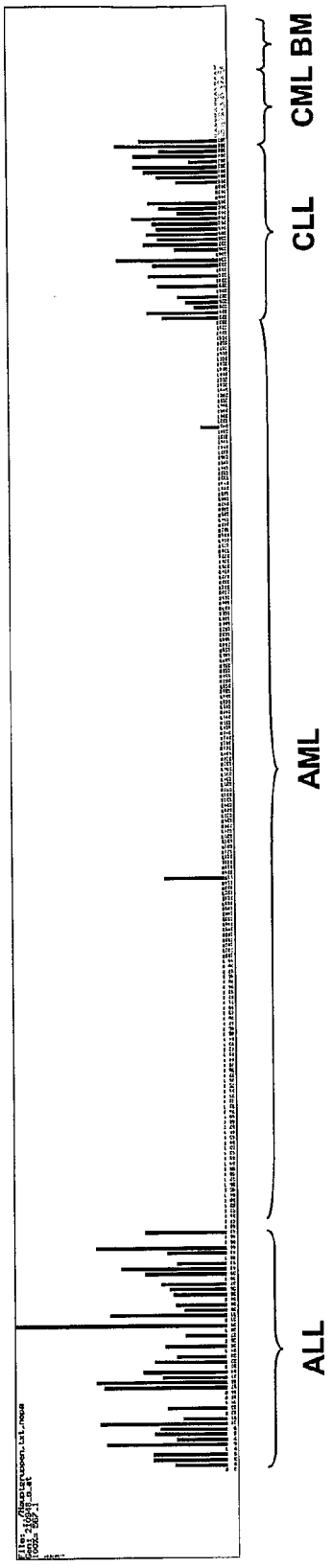


Figure 448

206398_s_at, CD19, lymphatic high

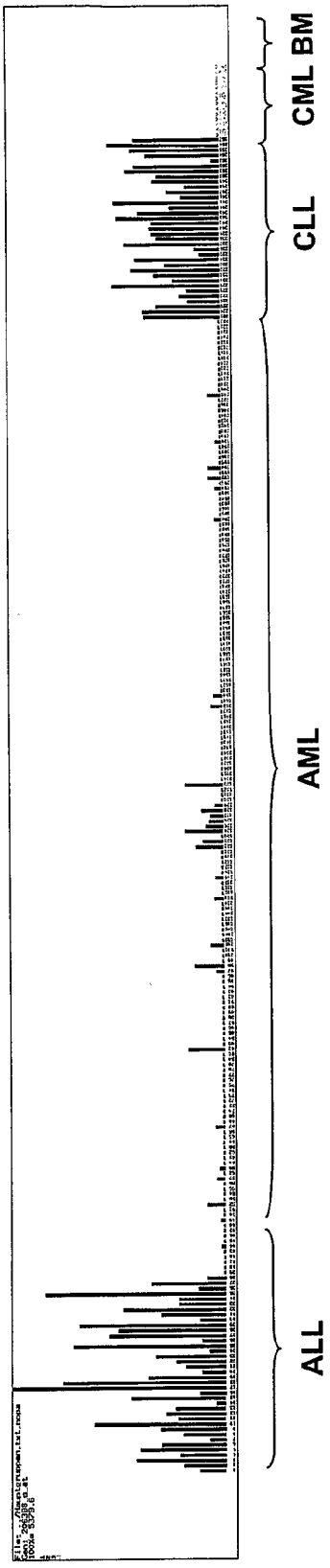


Figure 449

229487_at, ALL high

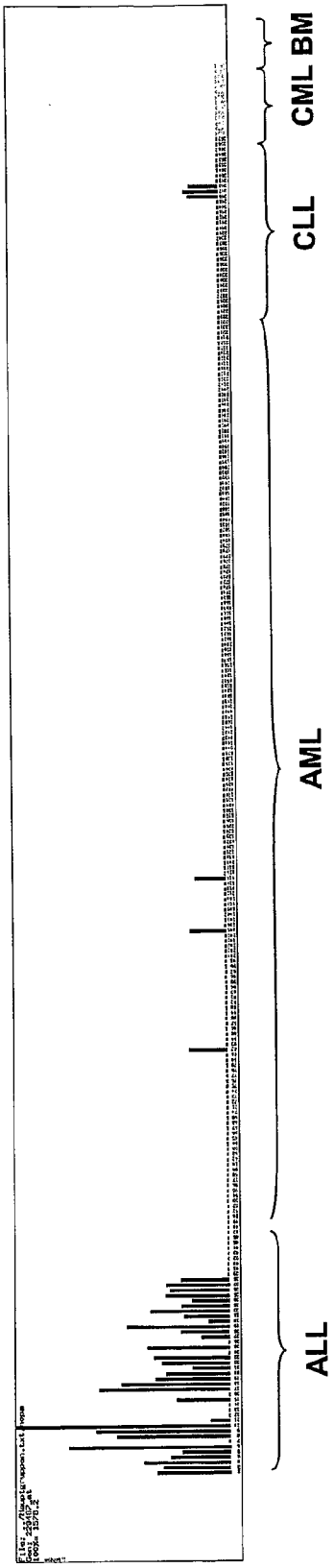


Figure 450

206255_at, BLK, lymphatic high

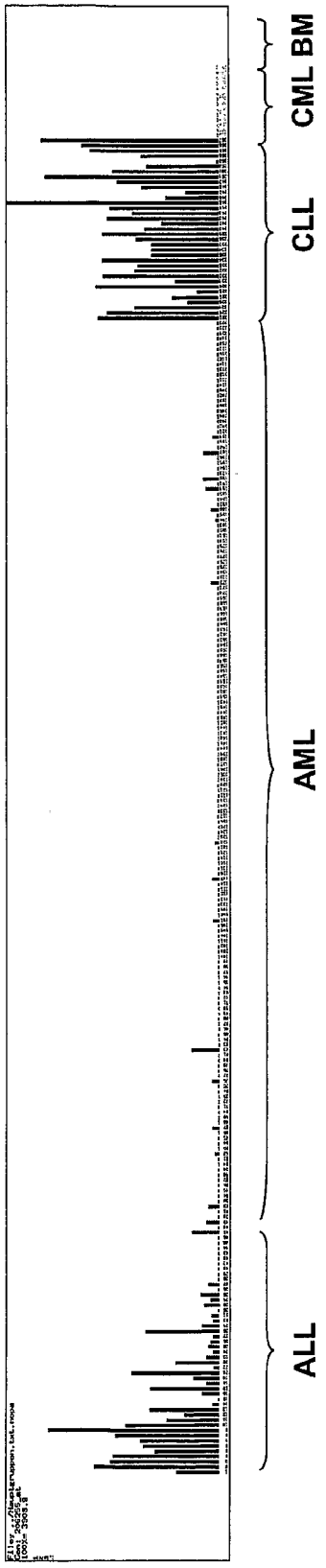


Figure 451

243362_s_at, LEF1, ALL high

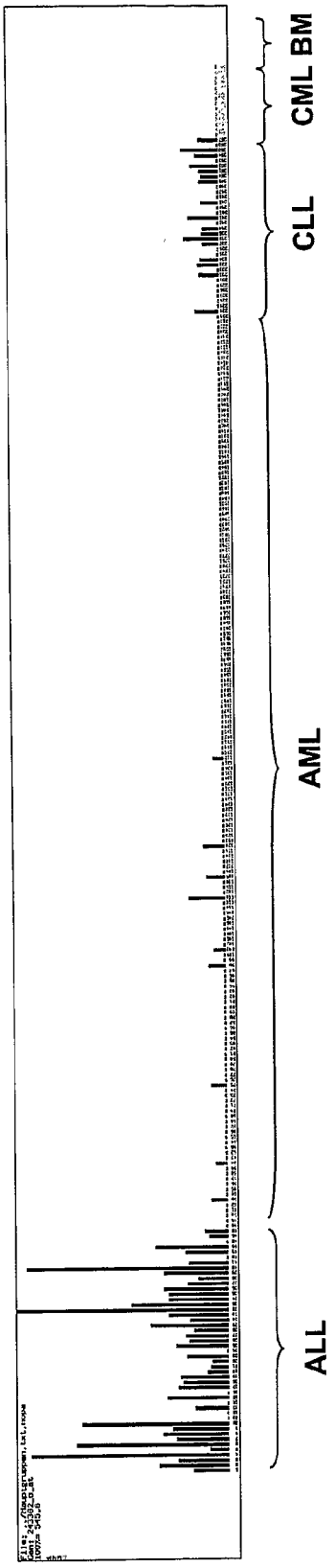


Figure 452

205049_s_at, CD79A, lymphatic high

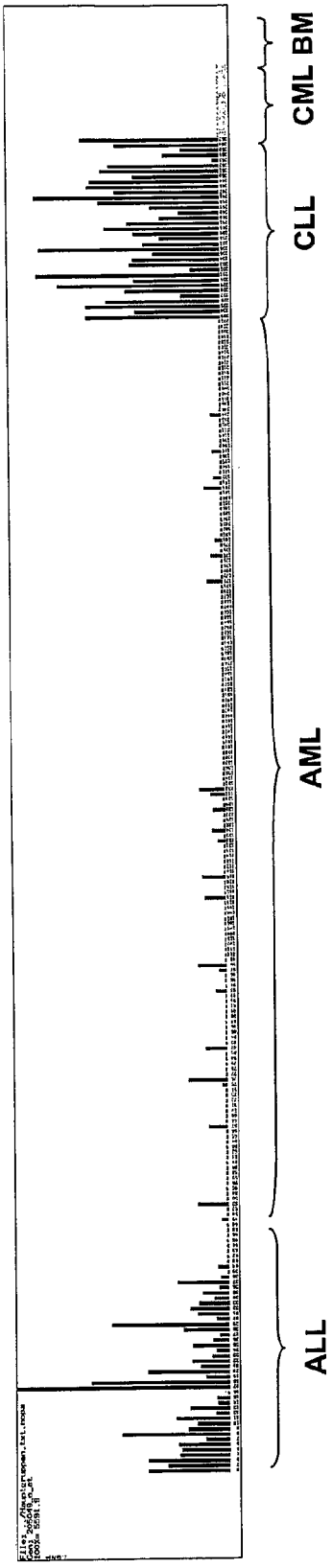


Figure 453

205382_s_at, DF, AML high

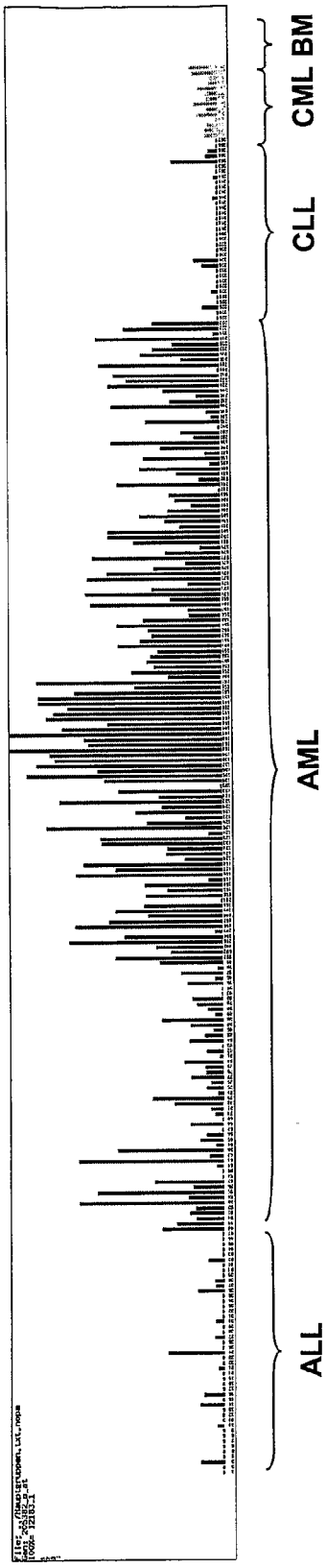


Figure 454

210487_at, DNTT, ALL high

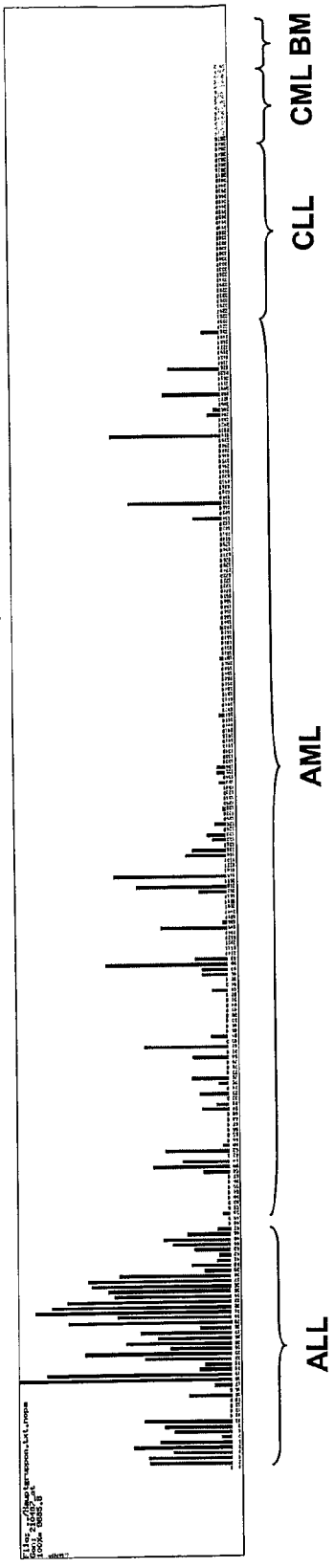


Figure 455

218516_s_at, FLJ20421, normal BM absent

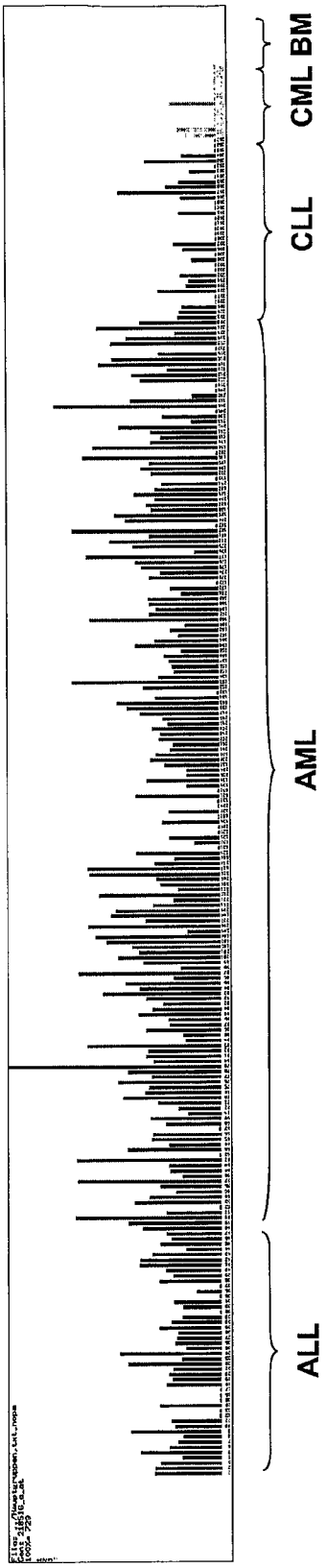


Figure 456

218916_at, FLJ23436, normal BM absent

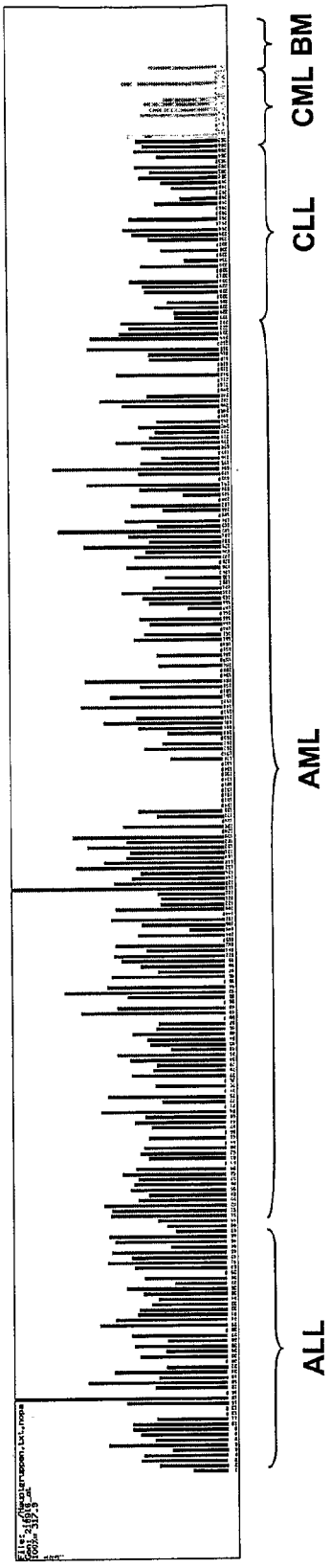


Figure 457

219753_at, STAG3, ALL high

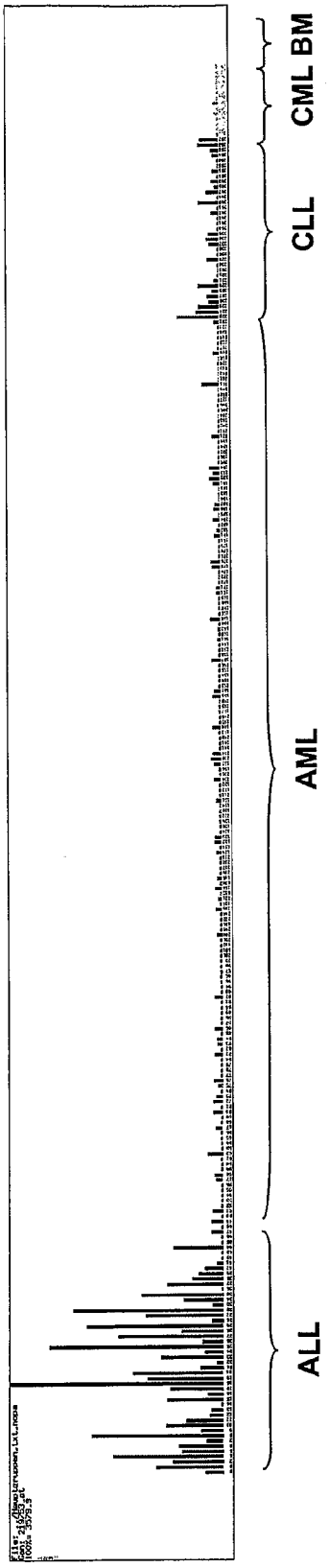


Figure 458

221969_at, PAX5, lymphatic high

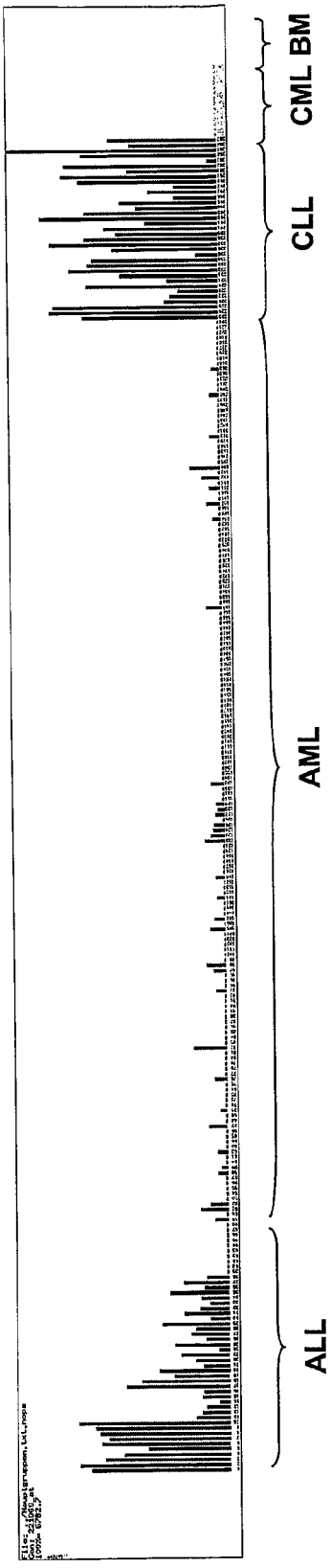


Figure 459

223703_at, CDA017, myeloid and BM high

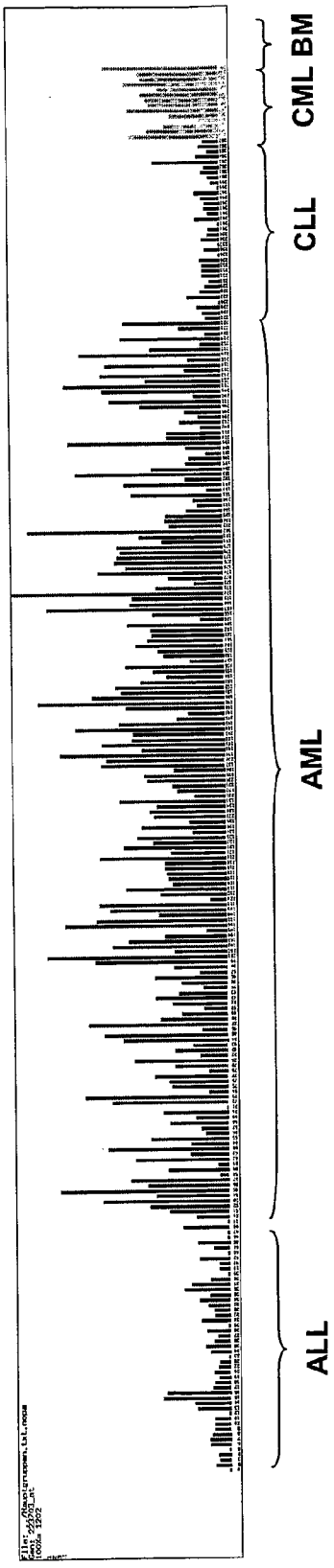


Figure 460

243363_at, LEF1, lymphatic high

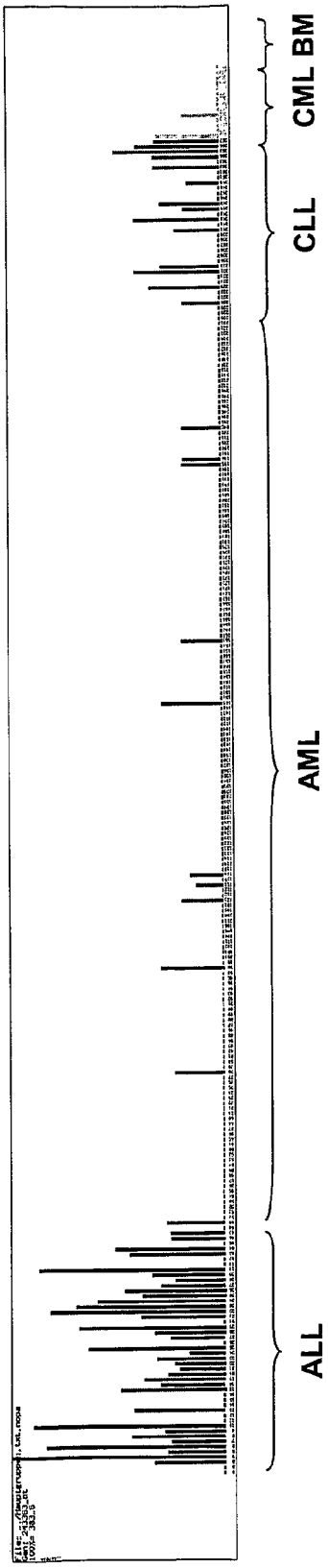


Figure 461

41577_at, PPP1R16B, CML low

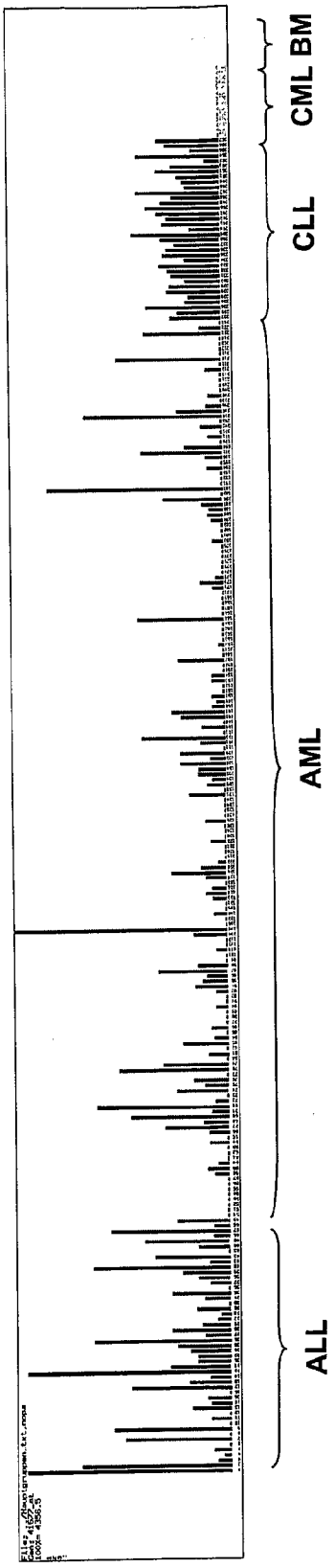


Figure 462

229790_at, TERF2, CML, BM low

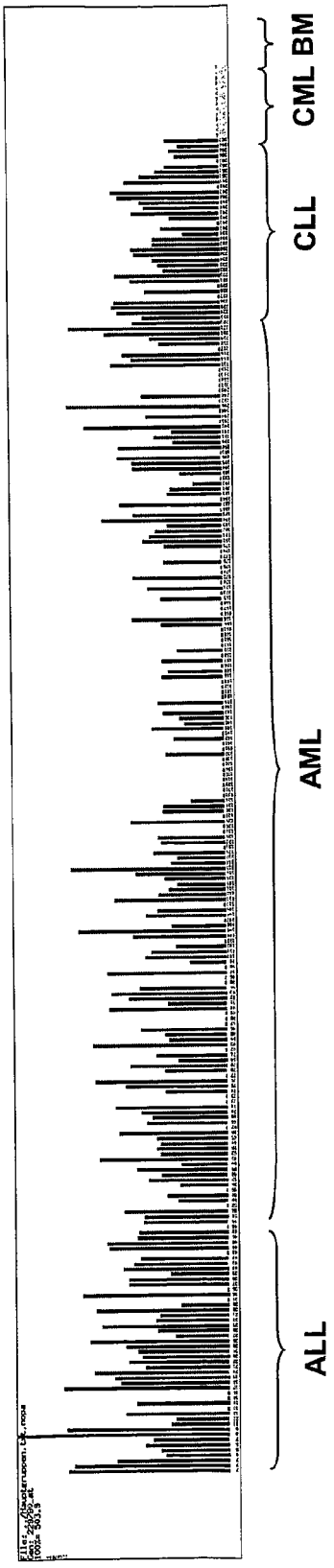


Figure 463

231736_x_at, MGST1, myeloid and BM high

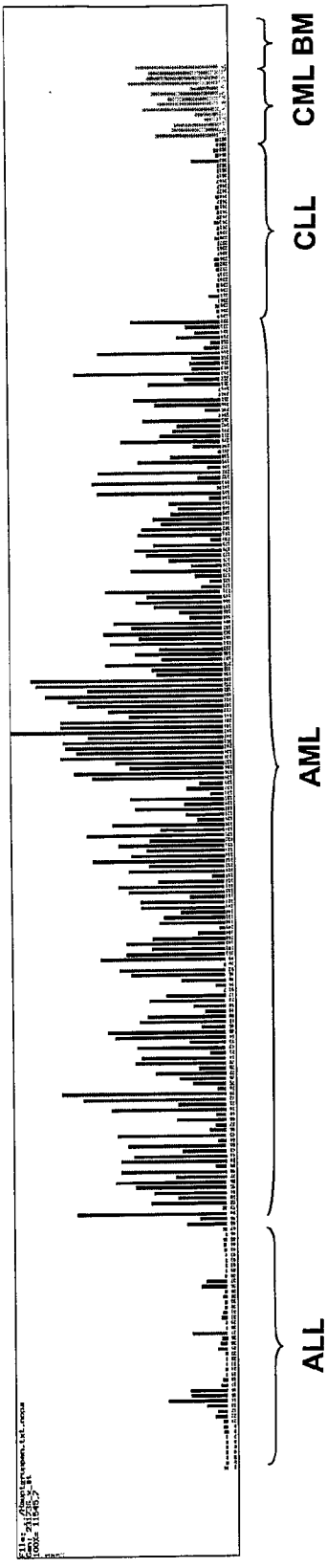


Figure 464